

STIC-Biotech/ChemLib

139347

mej

From: Whiteman, Brian  
Sent: Thursday, December 02, 2004 1:49 PM  
To: STIC-Biotech/ChemLib  
Subject: oligonucleotide search

DEC-2 2004  
STIC-Biotech/ChemLib

09/786,436, US filing date 7/16/01, priority 9/3/98

Wagner et al.

oligonucleotide search an oligonucleotide 10-50 nucleotides in length, and the oligonucleotide comprises a sequence chosen from GGGGG, GAGGG, GGGAG, GTGGG, and GGGTG; and the oligonucleotide does not comprise a CG dinucleotide (CpG motif).

the oligonucleotides are used in a method of treating a tumor in a subject

Thank you,

Brian Whiteman  
Remsen, 2D14  
mail box 2C18  
Patent Examiner - Art Unit 1635  
United States Patent and Trademark Office  
(571) 272-0764

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: 1-10  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence: # \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

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Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GAGGG

Perfect score: 5

Sequence: 1 gaggg 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.\*

1: gb\_bai.\*

2: gb\_hhg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_ats.\*

12: gb\_ay.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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C 2	5	100.0	10	6	AR029981 Sequence
C 3	5	100.0	10	6	AR030010 Sequence
C 4	5	100.0	10	6	AR030099 Sequence
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C 6	5	100.0	10	6	AR043159 Sequence
C 7	5	100.0	10	6	AR049732 Sequence
C 8	5	100.0	10	6	AR053555 Sequence
C 9	5	100.0	10	6	AR059204 Sequence
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C 22	5	100.0	10	6	AR175404 Sequence
C 23	5	100.0	10	6	BD176154 Mammalian
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C 30	5	100.0	10	6	BD238721 Preparati
C 31	5	100.0	10	6	BD238798 Preparati
C 32	5	100.0	10	6	BD238819 Preparati
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DEFINITION	AR016043	Sequence 11 from patent US 5776679.				
ACCESSION	AR016043	Sequence 11 from patent US 5776679.				
VERSION	AR016043.1	GI:3972320				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 10)					
AUTHORS	Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.					
TITLE	Assays for the DNA component of human telomerase					
JOURNAL	Patent: US 5776679-A 11 07-JUL-1998;					
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Best Local Similarity	100.0%;	Pred. No. 2.3e+07;				
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Db          9 GAGGG 5
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DEFINITION Sequence 170 from patent US 5861244.
ACCESSION  AR029981
VERSION     AR029981.1  GI:5943195
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Wang, C.-G. and Hepburn, A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 170 19-JAN-1999;
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
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Db      7 GAGGG 3

RESULT 3
LOCUS      AR030010/c          10 bp      DNA          linear      PAT 29-SEP-1999
DEFINITION Sequence 199 from patent US 5861244.
ACCESSION  AR030010
VERSION     AR030010.1  GI:5943224
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Wang, C.-G. and Hepburn, A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 199 19-JAN-1999;
FEATURES   Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
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Db      7 GAGGG 3

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LOCUS      AR030099/c          10 bp      DNA          linear      PAT 29-SEP-1999
DEFINITION Sequence 288 from patent US 5861244.
ACCESSION  AR030099
VERSION     AR030099.1  GI:5943313
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)

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AUTHORS    Wang, C.-G. and Hepburn, A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 288 19-JAN-1999;
FEATURES   Location/Qualifiers
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Qy      1 GAGGG 5
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Db      9 GAGGG 5

RESULT 5
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DEFINITION Sequence 29 from patent US 5861246.
ACCESSION  AR030218
VERSION     AR030218.1  GI:5943432
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Weissman, S.M., Mallur, G.N. and Kulkarni, P.
TITLE      Multiple selection process for binding sites of DNA-binding
JOURNAL    Patent: US 5861246-A 29 19-JAN-1999;
FEATURES   Location/Qualifiers
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Qy      1 GAGGG 5
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Db      5 GAGGG 9

RESULT 6
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DEFINITION Sequence 43 from patent US 5814453.
ACCESSION  AR043159
VERSION     AR043159.1  GI:5964167
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Beck, J. Joseph.
TITLE      Detection of fungal pathogens using the polymerase chain reaction
JOURNAL    Patent: US 5814453-A 43 29-SEP-1998;
FEATURES   Location/Qualifiers
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Qy      1 GAGGG 5
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Db      5 GAGGG 9

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DEFINITION Sequence 43 from patent US 5814453.
ACCESSION  AR043159
VERSION     AR043159.1  GI:5964167
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Beck, J. Joseph.
TITLE      Detection of fungal pathogens using the polymerase chain reaction
JOURNAL    Patent: US 5814453-A 43 29-SEP-1998;
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
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Db      5 GAGGG 9

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Db 10 GAGGG 6  
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RESULT 7  
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DEFINITION AR049732  
ACCESSION AR049732  
VERSION AR049732.1 GI:5971724  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 10)  
AUTHORS Georgopoulos,K.  
TITLE Ikaro's polypeptides  
JOURNAL Patent: US 5824770-A 35 20-OCT-1998;  
FEATURES Location/Qualifiers  
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Db 1 GAGGG 5  
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DEFINITION AR053555  
ACCESSION AR053555  
VERSION AR053555.1 GI:5978417  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 10)  
AUTHORS Falb,D.  
TITLE Compositions and methods using rchd534, a gene uregulated by shear stress  
JOURNAL Patent: US 5834248-A 20 10-NOV-1998;  
FEATURES Location/Qualifiers  
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Db 8 GAGGG 4  
RESULT 9  
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LOCUS Sequence 11 from patent US 5837857.  
DEFINITION AR059204  
ACCESSION AR059204  
VERSION AR059204.1 GI:5984781  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 10)  
AUTHORS Falb,D.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular using RCHD528 as a target  
JOURNAL Patent: US 5849578-A 20 15-DEC-1998;  
FEATURES Location/Qualifiers  
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Db 8 GAGGG 4

REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 5837857-A 11 17-NOV-1998;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
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DEFINITION AR065882  
ACCESSION AR065882  
VERSION AR065882.1 GI:5996098  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 10)  
AUTHORS Falb,D.A.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular using RCHD528 as a target  
JOURNAL Patent: US 5849578-A 20 15-DEC-1998;  
FEATURES Location/Qualifiers  
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Db 8 GAGGG 4  
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DEFINITION AR074659  
ACCESSION AR074659  
VERSION AR074659.1 GI:10001412  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 10)  
AUTHORS Ligon,J.M. and Beck,J.J.  
TITLE Detection of fungal pathogens using the polymerase chain reaction  
JOURNAL Patent: US 5955274-A 43 21-SEP-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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Db 7 GAGGG 3

RESULT 17  
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DEFINITION Sequence 41 from patent US 6077685.  
ACCESSION AR098905  
VERSION AR098905.1 GI:12808671  
KEYWORDS  
SOURCE  
ORGANISM  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Trofatter,J.A., MacCollin,M.M. and Gusella,J.F.  
TITLE Tumor suppressor merlin and antibodies thereof  
JOURNAL Patent: US 6077685-A 41 20-JUN-2000;  
FEATURES Location/Qualifiers  
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ACCESSION AR147933  
VERSION AR147933.1 GI:15112023  
KEYWORDS  
SOURCE  
ORGANISM  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Frudakis,T.N., Smith,J.M. and Reed,S.G.  
TITLE Compositions and methods for the treatment and diagnosis of breast cancer  
JOURNAL Patent: US 6225054-A 102 01-MAY-2001;  
FEATURES Location/Qualifiers  
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Qy 1 GAGGG 5  
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RESULT 19  
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DEFINITION Sequence 20 from patent US 6225084.  
ACCESSION AR148319  
VERSION AR148319.1 GI:15112409  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.

Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.  
TITLE Compositions and methods for the treatment and diagnosis of cardiovascular disease using rchd534 as a target  
JOURNAL Patent: US 6225084-A 20 01-MAY-2001;  
FEATURES Location/Qualifiers  
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RESULT 20  
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DEFINITION Sequence 35 from patent US 6228611.  
ACCESSION AR149626  
VERSION AR149626.1 GI:15114217  
KEYWORDS  
SOURCE  
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REFERENCE 1 (bases 1 to 10)  
AUTHORS Georgopoulos,K.  
TITLE Ikaros: A T cell pathway regulatory gene  
JOURNAL Patent: US 6228611-A 35 08-MAY-2001;  
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DEFINITION Sequence 11 from patent US 6258535.  
ACCESSION AR161913  
VERSION AR161913.1 GI:16228931  
KEYWORDS  
SOURCE  
ORGANISM  
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REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau,B., Ferg,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 6258535-A 11 10-JUL-2001;  
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Best Local Similarity 100.0%; Pred. No. 2.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY      1 GAGGG 5
Db      9 GAGGG 5

RESULT 22
ARI175404/c
LOCUS   ARI175404      10 bp      DNA      linear      PAT 17-DEC-2001
DEFINITION
Sequence 127 from patent US 6309823.
ACCESSION
ARI175404
VERSION
ARI175404.1 GI:17916703
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A.,
Huang,X.C., Lipschutz,R.J., Lobban,P.E., Morris,M.S. and
Sheldon,E.D.
TITLE
Arrays of nucleic acid probes for analyzing biotransformation genes
and methods of using the same
JOURNAL
Patent: US 6309823-A 127 30-OCT-2001;
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Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GAGGG 5
Db      9 GAGGG 5

RESULT 23
BD176154/c
LOCUS   BD176154      10 bp      DNA      linear      PAT 18-MAR-2003
DEFINITION
Mammalian telomerase.
ACCESSION
BD176154
VERSION
BD176154.1 GI:29121858
KEYWORDS
JP 200272489-A/13.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE
Mammalian telomerase
JOURNAL
Patent: JP 200272489-A 13 24-SEP-2002;
COMMENT
OS Unidentified
PN JP 200272489-A/13
PD 24-SEP-2002
PF 06-MAR-2002 JP 2002061125
PR 07-JUL-1994 US 08/272102,27-OCT-1994 US 08/330123 PR
07-JUN-1995 US 08/472802,07-JUN-1995 US 08/482115 PI BRYANT
VILLEPONTEAU,JUNLI FENG,WALTER FUNK,WILLIAM H ANDREWS PC
C12N15/09,C12N9/99,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
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CC Topology: Linear;
CC Mammalian telomerase
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QY      1 GAGGG 5
Db      9 GAGGG 5

RESULT 24
BD177264
LOCUS   BD177264      10 bp      DNA      linear      PAT 16-APR-2003
DEFINITION
Method for discriminating individuals by the RAPD process.
ACCESSION
BD177264
VERSION
BD177264.1 GI:30014525
KEYWORDS
JP 2002291475-A/5.
SOURCE
synthetic construct
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Matsuda,M., Kojima,E., Izumi,K. and Murakami,K.
TITLE
Method for discriminating individuals by the RAPD process
JOURNAL
Patent: JP 2002291475-A 5 08-OCT-2002;
NIPPON PAPER INDUSTRIES CO LTD
COMMENT
OS Artificial Sequence
PN JP 2002291475-A/5
PD 08-OCT-2002
PF 29-MAR-2001 JP 2001097703
PI MANABU MATSUDA,EIJI KOJIMA,KIMIKO IZUMI,KUNICHIKA MURAKAMI PC
C12N15/09,C12Q1/68//A01H1/00,C12N15/00
CC primer for PCR
FH Key
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Location/Qualifiers
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QY      1 GAGGG 5
Db      2 GAGGG 6

RESULT 25
BD238590
LOCUS   BD238590      10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION
Preparation and use of superior vaccines.
ACCESSION
BD238590
VERSION
BD238590.1 GI:33048360
KEYWORDS
JP 2002534056-A/8.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Roberts,B.L. and Shankara,S.
TITLE
Preparation and use of superior vaccines
JOURNAL
Patent: JP 2002534056-A 8 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/8
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR

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Db 6 GAGGG 10

RESULT 28
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LOCUS BD238717 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238717
VERSION BD238717.1 GI:33048487
KEYWORDS JP 2002534056-A/135.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 135 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/135
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/05,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
C12N1/19
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
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PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
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Query Match 100.0%; Score 5; DB 6; Length 10;
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LOCUS BD238721 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238721
VERSION BD238721.1 GI:33048491
KEYWORDS JP 2002534056-A/139.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 135 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/135
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/05,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC
C12N1/19
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566,PC
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CC Preparation and use of superior vaccines
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 139 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/139  
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08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
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PC C12N15/00,C12N5/00,C12N15/00  
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Qy 1 GAGGG 5  
Db 5 GAGGG 9  
RESULT 31  
BD238798/c  
LOCUS BD238798 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238798  
VERSION BD238798.1 GI:33048568  
KEYWORDS JP 2002534056-A/216.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 216 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/216  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR

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19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR  
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19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR  
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR  
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08-DEC-1998 US 60/111715  
PI BRUCE L ROBERTS,SRINIVAS SHANKARA  
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC  
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC  
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Qy 1 GAGGG 5  
Db 5 GAGGG 1  
RESULT 32  
BD238819/c  
LOCUS BD238819 10 bp DNA linear PAT 17-JUL-2003  
DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238819  
VERSION BD238819.1 GI:33048589  
KEYWORDS JP 2002534056-A/237.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 237 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
PN JP 2002534056-A/237  
PD 15-OCT-2002  
PF 18-JUN-1999 JP 2000554749  
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR  
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19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
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C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
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Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db |||||
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RESULT 33
BD238828/c
LOCUS BD238828 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238828
VERSION BD238828.1 GI:33048598
KEYWORDS JP 2002534056-A/246
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts, B.L. and Shankara, S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 246 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/246
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
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19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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CC Preparation and use of superior vaccines
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Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db |||||
5 GAGGG 1

RESULT 34
BD238938
LOCUS BD238938 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238938
VERSION BD238938.1 GI:33048708
KEYWORDS JP 2002534056-A/356
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts, B.L. and Shankara, S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 356 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
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DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239150
VERSION     BD239150.1 GI:33048920
KEYWORDS   JP 2002534056-A/568.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 568 15-OCT-2002;
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DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239242
VERSION     BD239242.1 GI:33049012
KEYWORDS   JP 2002534056-A/660.

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DEFINITION Preparation and use of superior vaccines.
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REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 568 15-OCT-2002;
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LOCUS      BD239242          10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239242
VERSION     BD239242.1 GI:33049012
KEYWORDS   JP 2002534056-A/660.
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REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 660 15-OCT-2002;  
GENZYME CORP  
COMMENT OS Homo sapiens (human)  
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DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239296  
VERSION BD239296.1 GI:33049066  
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ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 714 15-OCT-2002;  
GENZYME CORP  
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DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD239347  
VERSION BD239347.1 GI:33049117  
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ORGANISM Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 765 15-OCT-2002;  
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239356
VERSION BD239356.1 GI:33049126
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REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 774 15-OCT-2002;
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239356
VERSION BD239356.1 GI:33049126
KEYWORDS JP 2002534056-A/774.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 774 15-OCT-2002;
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD239370
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 788 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/788
PD 15-OCT-2002
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PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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ACCESSION BD239497
VERSION BD239497.1 GI:33049267
KEYWORDS JP 2002534056-A/915.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Roberte, B.L. and Shankara, S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 915 15-OCT-2002;
GENZYME CORP

COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/915
PD 15-OCT-2002
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PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
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KEYWORDS JP 2002534056-A/1038.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS Roberte, B.L. and Shankara, S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1038 15-OCT-2002;
GENZYME CORP

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DEFINITION Preparation and use of superior vaccines.
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VERSION BD239582.1 GI:33049352
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA
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ACCESSION BD239646
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Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 1064 15-OCT-2002;
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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c 239 5 100.0 10 3 AaZ82042 Metastati  
240 5 100.0 10 3 AaZ83070 Metastati

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C 241		5	100.0	10	3	AAZ833295	Aaz833295	Metastati	314	5	100.0	10	4	AAH63653	Aah63653	Human ubi
C 242		5	100.0	10	3	AAZ83857	Aaz83857	Metastati	315	5	100.0	10	4	AAH63183	Aah63183	Human col
C 243		5	100.0	10	3	AAZ85580	Aaz85580	Metastati	C 316	5	100.0	10	4	AAH63802	Aah63802	Human ubi
C 244		5	100.0	10	3	AAZ86648	Aaz86648	Metastati	C 317	5	100.0	10	4	AAH63211	Aah63211	Human col
C 245		5	100.0	10	3	AAZ874009	Aaz874009	Human den	C 318	5	100.0	10	4	AAH64264	Aah64264	Human ubi
C 246		5	100.0	10	3	AAZ874113	Aaz874113	Human den	C 319	5	100.0	10	4	AAH64574	Aah64574	Human ubi
C 247		5	100.0	10	3	AAZ874045	Aaz874045	Human den	C 320	5	100.0	10	4	AAH63412	Aah63412	Human can
C 248		5	100.0	10	3	AAZ874081	Aaz874081	Human den	C 321	5	100.0	10	4	AAH63840	Aah63840	Human ubi
C 249		5	100.0	10	3	AAZ86451	Aaz86451	Human mac	C 322	5	100.0	10	4	AAH64708	Aah64708	Human hig
C 250		5	100.0	10	3	AAZ86523	Aaz86523	Human mac	C 323	5	100.0	10	4	AAH63801	Aah63801	Human ubi
C 251		5	100.0	10	3	AAZ86133	Aaz86133	Human mon	C 324	5	100.0	10	4	AAH64621	Aah64621	Human col
C 252		5	100.0	10	3	AAZ86547	Aaz86547	Human mac	C 325	5	100.0	10	4	AAH63466	Aah63466	Human col
C 253		5	100.0	10	3	AAZ86490	Aaz86490	Human mac	C 326	5	100.0	10	4	AAH64099	Aah64099	Human ubi
C 254		5	100.0	10	3	AAZ86395	Aaz86395	Human mac	C 327	5	100.0	10	4	AAH64338	Aah64338	Human ubi
C 255		5	100.0	10	3	AAZ86564	Aaz86564	Human mac	C 328	5	100.0	10	4	AAH63689	Aah63689	Human ubi
C 256		5	100.0	10	3	AAZ86297	Aaz86297	Human mac	C 329	5	100.0	10	4	AAH63757	Aah63757	Human ubi
C 257		5	100.0	10	3	AAZ86487	Aaz86487	Human mac	C 330	5	100.0	10	4	AAH63841	Aah63841	Human ubi
C 258		5	100.0	10	3	AAZ860744	Aaz860744	5' PCR pr	C 331	5	100.0	10	4	AAH63462	Aah63462	Human ubi
C 259		5	100.0	10	3	AAZ80824	Aaz80824	Human bre	C 332	5	100.0	10	4	AAH64021	Aah64021	Human ubi
C 260		5	100.0	10	3	AAZ89116	Aaz89116	Rice prim	C 333	5	100.0	10	4	AAH63839	Aah63839	Human ubi
C 261		5	100.0	10	3	AAZ803349	Aaz803349	Human ade	C 334	5	100.0	10	4	AAH64500	Aah64500	Human ubi
C 262		5	100.0	10	3	AAZ803415	Aaz803415	Human ade	C 335	5	100.0	10	4	AAH63176	Aah63176	Human col
C 263		5	100.0	10	3	AAZ803325	Aaz803325	Human ade	C 336	5	100.0	10	4	AAH63179	Aah63179	Human col
C 264		5	100.0	10	3	AAZ803435	Aaz803435	Human ade	C 337	5	100.0	10	4	AAH63307	Aah63307	Human col
C 265		5	100.0	10	3	AAZ803372	Aaz803372	Human ade	C 338	5	100.0	10	4	AAH63435	Aah63435	Human ubi
C 266		5	100.0	10	3	AAZ803394	Aaz803394	Human ade	C 339	5	100.0	10	4	AAH63528	Aah63528	Human ubi
C 267		5	100.0	10	3	AAZ879748	Aaz879748	Human col	C 340	5	100.0	10	4	AAH63782	Aah63782	Human CHR
C 268		5	100.0	10	3	AAZ879732	Aaz879732	Human col	C 341	5	100.0	10	4	AAH637284	Aah637284	Human CHR
C 269		5	100.0	10	3	AAZ879752	Aaz879752	Human col	C 342	5	100.0	10	4	AAH63710	Aah63710	Human CHR
C 270		5	100.0	10	3	AAZ879778	Aaz879778	Human bre	C 343	5	100.0	10	4	AAH637286	Aah637286	Human CHR
C 271		5	100.0	10	3	AAZ879834	Aaz879834	Human lun	C 344	5	100.0	10	4	AAH637303	Aah637303	Human CHR
C 272		5	100.0	10	3	AAZ879787	Aaz879787	Human kid	C 345	5	100.0	10	4	AAH616618	Aah616618	Gastric a
C 273		5	100.0	10	3	AAZ879900	Aaz879900	Human den	C 346	5	100.0	10	4	AAH670100	Aah670100	Human TNF
C 274		5	100.0	10	3	AAZ879848	Aaz879848	Human den	C 347	5	100.0	10	4	AAH628600	Aah628600	Human int
C 275		5	100.0	10	3	AAZ879863	Aaz879863	Human den	C 348	5	100.0	10	4	AAH628624	Aah628624	Human int
C 276		5	100.0	10	3	AAZ89808	Aaz89808	Different	C 349	5	100.0	10	4	AAH32933	Aah32933	LPS activ
C 277		5	100.0	10	3	AAZ89178	Aaz89178	Human ade	C 350	5	100.0	10	4	AAH32701	Aah32701	LPS activ
C 278		5	100.0	10	3	AAZ89135	Aaz89135	Human ade	C 351	5	100.0	10	4	AAH32861	Aah32861	LPS activ
C 279		5	100.0	10	3	AAZ891088	Aaz891088	Human ade	C 352	5	100.0	10	4	AAH32868	Aah32868	LPS activ
C 280		5	100.0	10	3	AAZ89157	Aaz89157	Human ade	C 353	5	100.0	10	4	AAH32908	Aah32908	LPS activ
C 281		5	100.0	10	3	AAZ89197	Aaz89197	Human ade	C 354	5	100.0	10	4	AAH32790	Aah32790	LPS activ
C 282		5	100.0	10	3	AAZ89112	Aaz89112	Human ade	C 355	5	100.0	10	4	AAH32892	Aah32892	LPS activ
C 283		5	100.0	10	3	AAZ88020	Aaz88020	Human umb	C 356	5	100.0	10	4	ABA81675	Aba81675	Human pho
C 284		5	100.0	10	3	AAZ861013	Aaz861013	Protein b	C 357	5	100.0	10	4	ABA81650	Aba81650	Human pho
C 285		5	100.0	10	3	AAZ868567	Aaz868567	Green flu	C 358	5	100.0	10	4	ABA81634	Aba81634	Human pho
C 286		5	100.0	10	3	AAZ895171	Aaz895171	Primer #1	C 359	5	100.0	10	5	AAH41727	Aah41727	Anti-PEP
C 287		5	100.0	10	3	AAZ874377	Aaz874377	Mouse tra	C 360	5	100.0	10	5	AAH41710	Aah41710	Anti-PEP
C 288		5	100.0	10	3	AAZ874368	Aaz874368	Mouse tra	C 361	5	100.0	10	5	ABA06213	Aba06213	Human nor
C 289		5	100.0	10	4	AAH18990	Aah18990	UCP3 poly	C 362	5	100.0	10	5	ABA06157	Aba06157	Human nor
C 290		5	100.0	10	4	AAH19960	Aah19960	Mouse Tre	C 363	5	100.0	10	5	AAH70443	Aah70443	Human DRD
C 291		5	100.0	10	4	AAH19987	Aah19987	Mouse Tre	C 364	5	100.0	10	5	AAH70431	Aah70431	Human DRD
C 292		5	100.0	10	4	AAH167375	Aah167375	Human FKB	C 365	5	100.0	10	5	AAH69606	Aah69606	Human IL4
C 293		5	100.0	10	4	AAH167352	Aah167352	Human FKB	C 366	5	100.0	10	5	AAH69623	Aah69623	Human IL4
C 294		5	100.0	10	4	AAH167369	Aah167369	Human FKB	C 367	5	100.0	10	5	AAH74011	Aah74011	Human SIC
C 295		5	100.0	10	4	AAH167354	Aah167354	Human FKB	C 368	5	100.0	10	5	AAH74010	Aah74010	Human SIC
C 296		5	100.0	10	4	AAH167355	Aah167355	Human FKB	C 369	5	100.0	10	5	ABA83151	Aba83151	Glutathio
C 297		5	100.0	10	4	AAH167380	Aah167380	Human FKB	C 370	5	100.0	10	5	AAH37150	Aah37150	Yeast NOR
C 298		5	100.0	10	4	AAH58695	Aah58695	DNA segme	C 371	5	100.0	10	5	AAH37652	Aah37652	Yeast NOR
C 299		5	100.0	10	4	AAH06118	Aah06118	Human b3	C 372	5	100.0	10	5	AAH40937	Aah40937	Yeast NOR
C 300		5	100.0	10	4	AAH27548	Aah27548	Ligation	C 373	5	100.0	10	5	AAH42839	Aah42839	Yeast NOR
C 301		5	100.0	10	4	AAH27547	Aah27547	Ligation	C 374	5	100.0	10	5	AAH42840	Aah42840	Yeast NOR
C 302		5	100.0	10	4	AAH77673	Aah77673	Rice S-5	C 375	5	100.0	10	5	AAH43929	Aah43929	Yeast NOR
C 303		5	100.0	10	4	AAH04436	Aah04436	Human DAX	C 376	5	100.0	10	5	AAH36456	Aah36456	Yeast NOR
C 304		5	100.0	10	4	AAH04440	Aah04440	Human DAX	C 377	5	100.0	10	5	AAH40041	Aah40041	Yeast NOR
C 305		5	100.0	10	4	AAH04443	Aah04443	Human DAX	C 378	5	100.0	10	5	AAH42573	Aah42573	Yeast NOR
C 306		5	100.0	10	4	AAH04420	Aah04420	Human DAX	C 379	5	100.0	10	5	AAH35078	Aah35078	Yeast NOR
C 307		5	100.0	10	4	AAH63433	Aah63433	Human ubi	C 380	5	100.0	10	5	AAH36719	Aah36719	Yeast NOR
C 308		5	100.0	10	4	AAH63629	Aah63629	Human ubi	C 381	5	100.0	10	5	AAH40953	Aah40953	Yeast NOR
C 309		5	100.0	10	4	AAH63735	Aah63735	Human ubi	C 382	5	100.0	10	5	AAH38210	Aah38210	Yeast NOR
C 310		5	100.0	10	4	AAH63729	Aah63729	Human ubi	C 383	5	100.0	10	5	AAH39594	Aah39594	Yeast NOR
C 311		5	100.0	10	4	AAH63956	Aah63956	Human ubi	C 384	5	100.0	10	5	AAH41459	Aah41459	Yeast NOR
C 312		5	100.0	10	4	AAH64152	Aah64152	Human ubi	C 385	5	100.0	10	5	AAH42052	Aah42052	Yeast NOR
C 313		5	100.0	10	4	AAH63406	Aah63406	Human can	C 386	5	100.0	10	5	AAH43475	Aah43475	Yeast NOR

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C 389 Aaf36707 Yeast NOR 5 100.0 10 5 AAF36707  
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C 465 ABL52189 Human PER 5 100.0 10 6 ABL52189  
C 466 AAL38366 Human PER 5 100.0 10 6 AAL38366  
467 Abk81953 Oligonuc1 5 100.0 10 6 ABK81953  
C 468 ABL01179 Human AKR 5 100.0 10 6 ABL01179  
C 469 ABL01221 Human AKR 5 100.0 10 6 ABL01221  
470 Aaf98896 Colony st 5 100.0 10 6 AAS98896  
471 Aaf98852 Colony st 5 100.0 10 6 AAS98852  
C 472 AAD5885 Primer #7 5 100.0 10 6 AAD5885  
473 Aaf99670 Breast tu 5 100.0 10 6 AAS99670  
C 474 ABL42863 Human mat 5 100.0 10 6 ABL42863  
C 475 ABL42756 Human mat 5 100.0 10 6 ABL42756  
C 476 ABL42716 Human mat 5 100.0 10 6 ABL42716  
C 477 ABL99006 Mouse neu 5 100.0 10 6 ABL99006  
478 ABL57659 Human SCY 5 100.0 10 6 ABL57659  
479 ABL57662 Human SCY 5 100.0 10 6 ABL57662  
480 ABL57671 Human SCY 5 100.0 10 6 ABL57671  
C 481 Abk70541 Human G P 5 100.0 10 6 ABK70541  
482 ABL60194 Human MUC 5 100.0 10 6 ABL60194  
483 ABL60200 Human MUC 5 100.0 10 6 ABL60200  
484 Abk89140 RNA seque 5 100.0 10 6 ABK89140  
C 485 ABL51966 Human FMO 5 100.0 10 6 ABL51966  
C 486 ABL51949 Human FMO 5 100.0 10 6 ABL51949  
487 ABL51956 Human FMO 5 100.0 10 6 ABL51956  
C 488 ABL51960 Human FMO 5 100.0 10 6 ABL51960  
C 489 AAD5283 Human PON 5 100.0 10 6 AAD5283  
490 Abk81400 SCYA21 ge 5 100.0 10 6 ABK81400  
491 Abk96075 Human LIP 5 100.0 10 6 ABK96075  
492 Abk96052 Human LIP 5 100.0 10 6 ABK96052  
493 ABL96200 Human Ace 5 100.0 10 6 ABL96200  
494 ABL96191 Human Ace 5 100.0 10 6 ABL96191  
C 495 ABL97044 ZFP36 ext 5 100.0 10 6 ABL97044  
C 496 ABL97036 ZFP36 ext 5 100.0 10 6 ABL97036  
C 497 AAD26176 Human end 5 100.0 10 6 AAD26176  
498 AAD26165 Human end 5 100.0 10 6 AAD26165  
C 499 Abk16982 Pyridoxal 5 100.0 10 6 ABK16982  
C 500 AD113702 Cycloplasm 5 100.0 10 12 AD113702

## ALIGNMENTS

## RESULT 1

AAN92503  
ID AAN92503 standard; DNA; 10 BP.  
XX AC AAN92503;  
XX AC AAN92503;  
DT 25-MAR-2003 (revised)  
DT 10-MAY-1990 (first entry)  
XX XX  
DE Sequence corresponding to ribosome binding region.  
XX XX  
KW Ribosome binding region; anti-hyperlipidaemia agent;  
XX anti-arteriosclerosis agent; ss.  
OS Escherichia coli.  
XX PN EP345155-A.  
XX PD 06-DEC-1989.  
XX XX  
PF 31-MAY-1989; 89EP-00401495.  
XX XX  
PR 31-MAY-1988; 88JP-00133549.  
PR 26-APR-1989; 89JP-00107027.  
XX XX  
PA (MITU ) MITSUBISHI KASEI CORP.  
XX XX





CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 3 GAGGG 7

RESULT 4

AAQ71097/c

ID AAQ71097 standard; cDNA; 10 BP.

XX AC AAQ71097;

XX DT 25-MAR-2003 (revised)

XX DT 20-APR-1995 (first entry)

XX DE Merlin exon 11 splice acceptor site.

XX KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;

XX KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;

XX KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;

XX KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;

XX KW merlin-associated tumour; D22S1; posterior capsular lens opacity;

XX KW deafness; balance disorder; paralysis; ss.

XX OS Homo sapiens.

XX PN EP613945-A2.

XX PD 07-SEP-1994.

XX PF 25-FEB-1994; 94EP-00301367.

XX PR 25-FEB-1993; 93US-00022034.

XX PR 04-MAR-1993; 93US-00026063.

XX PR 19-AUG-1993; 93US-00108808.

XX PR 22-DEC-1993; 93US-00171718.

XX PA (GCHO ) GEN HOSPITAL CORP.

XX PI Trofatter JA, Maccollin MM, Gusella JF;

XX WPI; 1994-272992/34.

XX DR The tumour suppressor gene merlin - for treatment and diagnosis of

XX PT tumours and neurofibromatosis (NF2).

XX PS Example 6; Page 26; 86pp; English.

XX CC The sequences given in AAQ71078-109 represent the splice donor and

XX CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-

XX CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2

XX CC "gene" has been shown by linkage studies to be assigned to chromosome 22.

XX CC The missing or mutated gene in NF2 patients has been shown to be the

XX CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-

XX CC like protein), which possesses tumour suppressor activity, and whose

XX CC tumour suppressor activity is mediated by inter- actions with the

XX CC cytoskeleton. The merlin gene is found on chromosome 22 between the known

XX CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene

XX CC is either lost or mutated. A mutant merlin protein may be encoded by a

XX CC gene in which a mutation of A to T at the first position of the codon

XX CC encoding amino acid 220 causes the substitution of Tyr for Asn. The

XX CC merlin gene may be used in gene therapy for the treatment of a merlin-

XX CC associated tumour or NF2, or for prevention of schwannoma, meningioma,

XX CC posterior capsular lens opacities, deafness or hearing loss, balance

XX CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)

SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 6 GAGGG 2

RESULT 5

AAQ71099/c

ID AAQ71099 standard; cDNA; 10 BP.

XX AC AAQ71099;

XX DT 25-MAR-2003 (revised)

XX DT 20-APR-1995 (first entry)

XX DE Merlin exon 12 splice acceptor site.

XX KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;

XX KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;

XX KW neurofibromatosis; merlin; moesin-erzin-radixin-like protein; D22S28;

XX KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;

XX KW merlin-associated tumour; D22S1; posterior capsular lens opacity;

XX KW deafness; balance disorder; paralysis; ss.

XX OS Homo sapiens.

XX PN EP613945-A2.

XX PD 07-SEP-1994.

XX PF 25-FEB-1994; 94EP-00301367.

XX PR 25-FEB-1993; 93US-00022034.

XX PR 04-MAR-1993; 93US-00026063.

XX PR 19-AUG-1993; 93US-00108808.

XX PR 22-DEC-1993; 93US-00171718.

XX PA (GCHO ) GEN HOSPITAL CORP.

XX PI Trofatter JA, Maccollin MM, Gusella JF;

XX WPI; 1994-272992/34.

XX DR The tumour suppressor gene merlin - for treatment and diagnosis of

XX PT tumours and neurofibromatosis (NF2).

XX PS Example 6; Page 26; 86pp; English.

XX CC The sequences given in AAQ71078-109 represent the splice donor and

XX CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-

XX CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2

XX CC "gene" has been shown by linkage studies to be assigned to chromosome 22.

XX CC The missing or mutated gene in NF2 patients has been shown to be the

XX CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-

XX CC like protein), which possesses tumour suppressor activity, and whose

XX CC tumour suppressor activity is mediated by inter- actions with the

XX CC cytoskeleton. The merlin gene is found on chromosome 22 between the known

XX CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene

XX CC is either lost or mutated. A mutant merlin protein may be encoded by a

XX CC gene in which a mutation of A to T at the first position of the codon

XX CC encoding amino acid 220 causes the substitution of Tyr for Asn. The

XX CC merlin gene may be used in gene therapy for the treatment of a merlin-

XX CC associated tumour or NF2, or for prevention of schwannoma, meningioma,

XX CC posterior capsular lens opacities, deafness or hearing loss, balance

XX CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 10 BP; 1 A; 5 C; 2 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAGGG 5  
 |||||  
 Db 7 GAGGG 3

RESULT 6  
 AAQ64610/c  
 ID AAQ64610 standard; cDNA; 10 BP.  
 XX  
 AC AAQ64610;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 15-DEC-1994 (first entry)  
 XX  
 DE Alzheimer's/Parkinsons mitochondrial DNA mutation detection.  
 XX  
 KW Mitochondrial DNA mutation; associated with Alzheimer's;  
 KW Parkinson's disease; mismatch primers; PCR; amplification;  
 KW polymerase chain reaction; ss.  
 OS Homo sapiens.  
 XX  
 PN W09409162-A1.  
 XX  
 PD 28-APR-1994.  
 XX  
 PF 20-OCT-1993; 93WO-US010072.  
 XX  
 PR 20-OCT-1992; 92US-00963723.  
 XX  
 PA (UYEM-) UNIV EMORY SCHOOL MEDICINE.  
 XX  
 PI Wallace DC;  
 XX  
 DR WPI; 1994-151346/18.  
 XX  
 PT Detection of mitochondrial DNA mutation associated with Alzheimer's  
 PT disease and/or Parkinson's disease - for diagnosing or predicting a pre-  
 PT disposition to Alzheimer's disease and/or Parkinson's disease in a  
 PT patient.  
 XX  
 PS Disclosure; Page 36; 83pp; English.  
 XX  
 CC A 12S(956-965) insertion mutation harbours a novel 12S rRNA gene  
 CC insertion. Direct sequence analysis revealed that the insertion consisted  
 CC of approximately five cytosines within AAQ64610. This mitochondrial DNA  
 CC mutation is associated with Alzheimer's and/or Parkinson's diseases. The  
 CC detection of the mutations is useful for diagnosing or predicting a pre-  
 CC disposition to either of the diseases. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 XX  
 SQ Sequence 10 BP; 0 A; 9 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAGGG 5  
 |||||  
 Db 7 GAGGG 3

RESULT 7  
 AAQ88295/c  
 ID AAQ88295 standard; DNA; 10 BP.  
 XX  
 AC AAQ88295;  
 XX  
 DT 12-DEC-1995 (first entry)

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAGGG 5  
 |||||  
 Db 7 GAGGG 3

RESULT 8  
 AAQ88289  
 ID AAQ88289 standard; DNA; 10 BP.  
 XX  
 AC AAQ88289;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 12-DEC-1995 (first entry)  
 XX  
 DE 5'-target sequence 3 for detection of fruit species by PCR.  
 XX  
 KW Polymerase chain reaction amplification; fruit juice; fruit pulp;  
 KW species detection; apple; orange; grapefruit; RAPD technique; ss.  
 XX  
 OS Citrus.  
 XX  
 PN FR2711143-A1.  
 XX  
 PD 21-APR-1995.  
 XX  
 PF 13-OCT-1994; 94FR-00012235.  
 XX  
 PR 13-OCT-1993; 93GB-00021113.  
 XX  
 PA (UKAG-) UK MIN AGRIC FISHERIES & FOOD.  
 XX  
 PI Lindsey K, Twell D;  
 XX  
 DR WPI; 1995-157154/21.  
 XX  
 PT Identifying species, variety etc. of fruits by PCR amplification - then  
 PT comparing products with standards, also new test kits, primers and  
 PT hybridisation probes, partic. to detect fraudulent use in food prodn.  
 XX  
 PS Claim 8; Page 17; 20pp; French.  
 XX  
 CC Primers have been identified which give useful results for identification  
 CC of genus, species or variety of fruits (see AAQ88293-Q88298);  
 CC amplification profiles are established using several of the primers,  
 CC which are complementary to regions (see AAQ88287-Q88292) at the 5'-end of  
 CC the target sequences which are amplified. Using the primers it was  
 CC possible to distinguish between e.g. different varieties of Navel oranges  
 CC and also between "red" apples and "Granny Smith" apples  
 XX  
 SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GAGGG 5  
 |||||  
 Db 8 GAGGG 4

RESULT 9  
 AAQ88295/c  
 ID AAQ88295 standard; DNA; 10 BP.  
 XX  
 AC AAQ88295;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 12-DEC-1995 (first entry)  
 XX  
 DE 5'-target sequence 3 for detection of fruit species by PCR.  
 XX  
 KW Polymerase chain reaction amplification; fruit juice; fruit pulp;  
 KW species detection; apple; orange; grapefruit; RAPD technique; ss.  
 XX  
 OS Citrus.  
 XX  
 PN FR2711143-A1.  
 XX  
 PD 21-APR-1995.  
 XX  
 PF 13-OCT-1994; 94FR-00012235.  
 XX  
 PR 13-OCT-1993; 93GB-00021113.  
 XX  
 PA (UKAG-) UK MIN AGRIC FISHERIES & FOOD.  
 XX  
 PI Lindsey K, Twell D;  
 XX  
 DR WPI; 1995-157154/21.  
 XX  
 PT Identifying species, variety etc. of fruits by PCR amplification - then  
 PT comparing products with standards, also new test kits, primers and  
 PT hybridisation probes, partic. to detect fraudulent use in food prodn.  
 XX  
 PS Claim 8; Page 17; 20pp; French.  
 XX  
 CC Primers have been identified which give useful results for identification  
 CC of genus, species or variety of fruits (see AAQ88293-Q88298);  
 CC amplification profiles are established using several of the primers,  
 CC which are complementary to regions (see AAQ88287-Q88292) at the 5'-end of  
 CC the target sequences which are amplified. Using the primers it was  
 CC possible to distinguish between e.g. different varieties of Navel oranges  
 CC and also between "red" apples and "Granny Smith" apples  
 XX  
 SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

PI Lindsey K, Twell D;  
 XX WPI; 1995-157154/21.  
 XX Identifying species, variety etc. of fruits by PCR amplification - then  
 PT comparing products with standards, also new test kits, primers and  
 PT hybridisation probes, partic. to detect fraudulent use in food prodn.  
 XX  
 XX Claim 7; Page 17; 20pp; French.  
 XX  
 CC Primers have been identified which give useful results for identification  
 CC of genus, species or variety of fruits (see AAQ8293-Q88298);  
 CC amplification profiles are established using several of the primers,  
 CC which are complementary to regions (see AAQ8287-Q88292) at the 5'-end of  
 CC the target sequences which are amplified. Using the primers it was  
 CC possible to distinguish between e.g. different varieties of Navel oranges  
 CC and also between "red" apples and "Granny Smith" apples. (Updated on 27-  
 CC AUG-2003 to correct OS field.)  
 XX  
 XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GAGGG 5  
 Db 3 GAGGG 7  
 |||||  
 RESULT 9  
 AAQ81904/C  
 ID AAQ81904 standard; RNA; 10 BP.  
 XX  
 AC AAQ81904;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 08-SEP-1995 (first entry)  
 XX  
 DE Interferon-gamma binding oligonucleotide 34.  
 XX  
 XX Interferon gamma; IFN-gamma; inhibition; binding; immunomodulation;  
 KW septic shock; rheumatoid arthritis; HIV infection; ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO950529-A1.  
 PN  
 XX 05-JAN-1995.  
 PD  
 XX 17-JUN-1994; 94WO-US006897.  
 PF  
 XX 18-JUN-1993; 93US-00079677.  
 PR  
 XX 17-MAR-1994; 94US-00210222.  
 XX  
 XX (PHAR-) PHARMAGENICS INC.  
 PA  
 XX Coppola GR, Beutel BA, Bertelsen AH;  
 PI  
 XX WPI; 1995-051993/07.  
 DR  
 XX Oligo-nucleotide(s) which bind to interferon-gamma - used for modulating,  
 PT inhibiting or enhancing the activity or function of interferon-gamma.  
 XX  
 XX Claim 4; Page 32; 43pp; English.  
 PS  
 XX Oligonucleotides which bind to interferon-gamma are useful for  
 CC modulating, inhibiting or enhancing the activity or function of the IFN.  
 CC Particularly, they are useful for treatment of septic shock, rheumatoid  
 CC arthritis and HIV infection. Preferred oligonucleotides are given in  
 CC AAQ81894-Q81909 and AAQ81913-Q81932; esp. the oligo- nucleotides comprise  
 CC at least one of the sequences AAGTUG, UGANGCUC, GCACGNC, AAQ81903 or  
 CC AAQ81904. (Updated on 25-MAR-2003 to correct PN field.)

XX  
 SQ Sequence 10 BP; 1 A; 6 C; 2 G; 0 T; 1 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GAGGG 5  
 Db 9 GAGGG 5  
 |||||  
 RESULT 10  
 AAT05374/C  
 ID AAT05374 standard; DNA; 10 BP.  
 XX  
 AC AAT05374;  
 XX  
 DT 04-JUN-1996 (first entry)  
 XX  
 DE Setoria tritici RAPD primer OPE-6.  
 XX  
 KW Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;  
 KW pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR;  
 KW Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;  
 KW internal transcribed region; strain; capture; colourimetric assay;  
 KW isolate; development; population; random amplified polymorphic DNA; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9529260-A2.  
 PN  
 XX 02-NOV-1995.  
 PD  
 XX 19-APR-1995; 95WO-US004712.  
 PF  
 XX 25-APR-1994; 94US-00233608.  
 PR  
 XX (CIBA ) CIBA GEIGY AG.  
 PA  
 XX Ligon JM, Beck JJ;  
 PI  
 XX WPI; 1995-383005/49.  
 DR  
 XX DNA encoding intervening transcribed sequence - used for detection of  
 PT plant fungal pathogens.  
 XX  
 XX Claim 9; Page 16; 65pp; English.  
 PS  
 XX A novel method for the detection of plant pathogenic strains of fungi  
 CC e.g. Septoria nodorum, S.tritici, Pseudocercospora herpotrichoides,  
 CC Mycosphaerella fijiensis, M.musicola or Fusarium spp. involves the PCR  
 CC amplification of sequences found in the internal transcribed region (ITS)  
 CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93  
 CC and AAT05357-72. These primers are derived from the ITS sequences of  
 CC these fungi (AAT05394-T05404 and AAQ94398) and are strain specific. The  
 CC amplification products of the reactions using these primers can be used  
 CC with the capture primers AAT05378-93 in colourimetric assays. The primers  
 CC and ITS DNAs can be used for the detection of specific fungal pathogens  
 CC isolates and in monitoring disease development in plant populations. The  
 CC primers AAT05373-7 were obtained from purchased random amplified  
 CC polymorphic DNA (RAPD) primer libraries and used to PCR amplify ITS  
 CC sequences in conjunction with the primers AAQ94390-3. This primer  
 CC amplified a 1.0 kb region from S.tritici  
 XX  
 XX Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GAGGG 5  
 |||||

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Db      10 GAGGG 6

RESULT 11
AAT45290/c
ID AAT45290 standard; DNA; 10 BP.
XX
AC AAT45290;
XX
DT 06-FEB-1997 (first entry)
XX
DE Gypsy moth FS-2 RAPD primer.
XX
KW Gypsy moth; Lymantria dispar; Asian; North American; European; genotype;
KW assay; RAPD primer; FS-2 fragment; diagnostic marker;
KW randomly amplified polymorphic DNAs; ss.
XX
OS Synthetic.
XX
FN US5571672-A.
XX
PD 05-NOV-1996.
XX
PF 20-SEP-1994; 94US-00308894.
XX
PR 20-SEP-1994; 94US-00308894.
XX
PA (USDA ) US SEC OF AGRIC.
XX
PI Garner KJ, Slavicek JM, Schreiber DE;
XX WPI; 1996-505395/50.
XX
PT Genotype assay for gypsy moth strains - to differentiate between Asian
PT and North American/European strains using specific primers to produce
PT diagnostic PCR amplification prods.
XX
PS Claim 1; Col 19; 17pp; English.
XX
CC Three RAPD (randomly amplified polymorphic DNAs) primers, designated
CC primers FS-1, FS-2 and FS-3, have been identified that generate
CC diagnostic fragment markers from gypsy moth (Lymantria dispar) DNA.
CC Comparison of marker size, e.g. by gel electrophoresis, allows the Asian
CC strain to be distinguished from the North American/European strain. RAPD
CC primers are 10 bp primers that are designed to be used individually, as
CC opposed to the usual primer pair; they can prime both ends of a
CC diagnostic fragment. The present sequence is that of primer FS-2 which
CC generates a fragment of 800 bp from North American/European moths that is
CC absent in control Asian moths
XX
SQ Sequence 10 BP; 2 A; 5 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 8 GAGGG 4

RESULT 12
AAT98848
ID AAT98848 standard; DNA; 10 BP.
XX
AC AAT98848;
XX
DT 20-MAR-1998 (first entry)
XX
DE Binding site BSN6 identified using the method of the invention.
XX
KW Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.

XX OS Synthetic.
XX PN WO9727330-A1.
XX PD 31-JUL-1997.
XX PF 24-JAN-1997; 97WO-US001230.
XX PR 24-JAN-1996; 96US-00590571.
XX PA (UYVA ) UNIV YALE.
XX PI Weissman SM, Kulkarni P, Nallur GN;
XX DR WPI; 1997-393714/36.
XX
PT Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 19; 52pp; English.
XX
CC This sequence represents a binding site identified using the method of
CC the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 5 GAGGG 9

RESULT 13
AAX83301
ID AAX83301 standard; DNA; 10 BP.
XX
AC AAX83301;
XX
DT 31-AUG-1999 (first entry)
XX
DE Breast cancer tumour specific cDNA isolation primer #16.
XX
KW Breast cancer; tumour; gene expression; genome; diagnosis; mammal;
KW human endogenous retrovirus; vaccine; primer; PCR; amplification; ss.
XX
OS Synthetic.
XX OS Homo sapiens.
XX PN WO9725426-A2.
XX PD 17-JUL-1997.
XX PF 10-JAN-1997; 97WO-US000485.

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XX PR 11-JAN-1996; 96US-00585392.
XX PR 20-AUG-1996; 96US-00700014.
XX PA (CORI-) CORIXA CORP.
XX PI Frudakis TN, Smith JM, Reed SG;
XX XX
XX DR WPI; 1997-372865/34.
XX XX
XX PT Breast cancer-related DNA from retrovirus antigen (s) - useful for
XX PT diagnosis and treatment of breast cancer.
XX XX
XX PS Example 1; Page 103; 221pp; English.
XX CC Primers AAX83286-X83329 were used to PCR amplify breast cancer tumour
XX CC specific clones (AAX83201-X83285 and AAX83331-X83415) which are expressed
XX CC from a genomic region containing a human endogenous retrovirus
XX CC (AAX83330). Detection of the clone sequences allows determination of the
XX CC presence of breast cancer in a mammal. Progression of breast cancer can
XX CC be monitored by detecting the level of clone expression. Polypeptides
XX CC encoded by the clones can be used in vaccines to inhibit or prevent
XX CC breast cancer
XX XX
XX SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;
      Query Match 100.0%; Score 5; DB 2; Length 10;
      Best Local Similarity 100.0%; Pred. No. 1.8e+06;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGG 5
Db 3 GAGGG 7
      |||||
      3 GAGGG 7

RESULT 14
AAV62568/c
ID AAV62568 standard; DNA; 10 BP.
AC AAV62568;
XX XX
XX DT 17-DEC-1998 (first entry)
XX XX
XX DE Septoria tritici species specific RAPD primer OPE-6.
XX XX
XX KW Internal transcribed spacer; ITS; ribosomal RNA; Fusarium avenaceum;
XX KW Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
XX KW Septoria avenae; Microdochium nivale; Fusarium poae; fungal pathogen;
XX KW random amplified polymorphic DNA; PCR; nucleic acid detection; RAPD;
XX KW PCR primer; ss.
XX XX
XX OS Synthetic.
XX OS Mycosphaerella graminicola.
XX XX
XX PN US5814453-A.
XX XX
XX PD 29-SEP-1998.
XX XX
XX PF 02-JUL-1997; 97US-00887480.
XX XX
XX PR 19-APR-1995; 95WO-US004712.
XX PR 15-OCT-1996; 96US-00722187.
XX XX
XX PA (NOVS ) NOVARTIS FINANCE CORP.
XX XX
XX PI Beck JU;
XX XX
XX DR WPI; 1998-541745/46.
XX XX
XX PT DNA isolated from fungal RNA, and its internal transcribed spacer
XX PT sequence - used for detecting fungal pathogens in plant tissue.
XX XX
XX PS Example 7; Col 19; 56pp; English.

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XX CC Sequences AAV62567 to AAV62571 represent random amplified polymorphic DNA
XX CC (RAPD) primers used in the course of the invention for detection of
XX CC Septoria species. The invention provides a DNA molecule isolated from the
XX CC ribosomal RNA gene region of a fungal pathogen, where the DNA molecule
XX CC consists of an internal transcribed spacer (ITS) sequence selected from
XX CC ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
XX CC moniliforme, Septoria avenae or Microdochium nivale. A method for
XX CC detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.
XX CC avenaceum and M. nivale isolates is also provided which comprises
XX CC isolating DNA from a plant leaf infected with at least one of the above
XX CC pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
XX CC PCR using specific primers from within these sequences. The pathogen(s)
XX CC are detected by visualising the amplified part of the ITS sequence
XX SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;
      Query Match 100.0%; Score 5; DB 2; Length 10;
      Best Local Similarity 100.0%; Pred. No. 1.8e+06;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGG 5
Db 10 GAGGG 6
      |||||
      10 GAGGG 6

RESULT 15
AAV47256
ID AAV47256 standard; DNA; 10 BP.
XX XX
XX AC AAV47256;
XX XX
XX DT 10-NOV-1998 (first entry)
XX XX
XX DE Antisense oligonucleotide 756, targeting adenosine A1 receptor.
XX XX
XX KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;
XX KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;
XX KW allergy; emphysema; cystic fibrosis; ss.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX FH Key Location/Qualifiers
XX FT modified_base 1..10
XX FT /*tag= a
XX FT /note= "contains phosphorothioate internucleotide
XX FT linkages"
XX PN WO9823294-A1.
XX XX
XX PD 04-JUN-1998.
XX XX
XX PF 26-NOV-1997; 97WO-US022017.
XX XX
XX PR 26-NOV-1996; 96US-00757024.
XX XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX XX
XX PI Nyce JW;
XX XX
XX DR WPI; 1998-322464/28.
XX XX
XX PT Treating respiratory disease with antisense sequences directed against
XX PT adenosine or bradykinin receptors - with localised delivery to the
XX PT respiratory system, suitable for long term treatment of asthma, adult
XX PT respiratory distress syndrome etc.
XX XX
XX PS Claim 12; Page 8-24; 47pp; English.
XX XX
XX CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the
XX CC human adenosine A1 receptor, the design of which required the secondary
XX CC structure of this targets mRNA. The adenosine receptor mRNA secondary

```

CC structure was both analysed and used to construct antisense  
 CC oligonucleotides containing a phosphorothioate backbone. Once the  
 CC antisense molecules are created they can be used to target their  
 CC predetermined target, thus causing the gene product to decrease. The  
 CC antisense oligonucleotides were targeted to specific mRNA regions  
 CC containing either a junction between the intron and exon, or where they  
 CC may overlap the initiation codon. The receptor is a member of the G-  
 CC protein coupled family of cell surface receptors that have 7-  
 CC transmembrane segments. These oligonucleotides can be used to treat or  
 CC prevent conditions associated with bronchoconstriction and/or lung  
 CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
 CC allergy, emphysema and cystic fibrosis  
 XX  
 SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 DB 1 GAGGG 5  
 RESULT 16  
 AAV47215  
 ID AAV47215 standard; DNA; 10 BP.  
 AC AAV47215;  
 DT 10-NOV-1998 (first entry)  
 DE Antisense oligonucleotide 715, targeting adenosine A1 receptor.  
 KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
 KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
 KW allergy; emphysema; cystic fibrosis; ss.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..10  
 FT /tag= a  
 FT /note= "contains phosphorothioate internucleotide  
 linkages"  
 XX  
 PN WO9823294-A1.  
 PD 04-JUN-1998.  
 PF 26-NOV-1997; 97WO-US022017.  
 PR 26-NOV-1996; 96US-00757024.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 DR WPI; 1998-322464/28.  
 XX  
 PT Treating respiratory disease with antisense sequences directed against  
 PT adenosine or bradykinin receptors - with localised delivery to the  
 PT respiratory system, suitable for long term treatment of asthma, adult  
 PT respiratory distress syndrome etc.  
 XX  
 PS Claim 12; Page 8-24; 47pp; English.  
 XX  
 CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
 CC human adenosine A1 receptor, the design of which required the secondary  
 CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
 CC structure was both analysed and used to construct antisense  
 CC oligonucleotides containing a phosphorothioate backbone. Once the  
 CC antisense molecules are created they can be used to target their  
 CC predetermined target, thus causing the gene product to decrease. The

CC antisense molecules are created they can be used to target their  
 CC predetermined target, thus causing the gene product to decrease. The  
 CC antisense oligonucleotides were targeted to specific mRNA regions  
 CC containing either a junction between the intron and exon, or where they  
 CC may overlap the initiation codon. The receptor is a member of the G-  
 CC protein coupled family of cell surface receptors that have 7-  
 CC transmembrane segments. These oligonucleotides can be used to treat or  
 CC prevent conditions associated with bronchoconstriction and/or lung  
 CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
 CC allergy, emphysema and cystic fibrosis  
 XX  
 SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 DB 3 GAGGG 7  
 RESULT 17  
 AAV47236  
 ID AAV47236 standard; DNA; 10 BP.  
 AC AAV47236;  
 DT 10-NOV-1998 (first entry)  
 DE Antisense oligonucleotide 736, targeting adenosine A1 receptor.  
 KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
 KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
 KW allergy; emphysema; cystic fibrosis; ss.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..10  
 FT /tag= a  
 FT /note= "contains phosphorothioate internucleotide  
 linkages"  
 XX  
 PN WO9823294-A1.  
 PD 04-JUN-1998.  
 PF 26-NOV-1997; 97WO-US022017.  
 PR 26-NOV-1996; 96US-00757024.  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 DR WPI; 1998-322464/28.  
 XX  
 PT Treating respiratory disease with antisense sequences directed against  
 PT adenosine or bradykinin receptors - with localised delivery to the  
 PT respiratory system, suitable for long term treatment of asthma, adult  
 PT respiratory distress syndrome etc.  
 XX  
 PS Claim 12; Page 8-24; 47pp; English.  
 XX  
 CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
 CC human adenosine A1 receptor, the design of which required the secondary  
 CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
 CC structure was both analysed and used to construct antisense  
 CC oligonucleotides containing a phosphorothioate backbone. Once the  
 CC antisense molecules are created they can be used to target their  
 CC predetermined target, thus causing the gene product to decrease. The

CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they  
CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-  
CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung  
CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis  
XX  
SQ Sequence 10 BP; 1 A; 2 C; 7 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGGG 5  
Db 2 GAGGG 6  
|||||  
  
RESULT 18  
AAV47170  
ID AAV47170 standard; DNA; 10 BP.  
XX  
AC AAV47170;  
XX  
DT 10-NOV-1998 (first entry)  
XX  
DE Antisense oligonucleotide 670, targeting adenosine A1 receptor.  
XX  
KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
KW allergy; emphysema; cystic fibrosis; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..10  
FT /\*tag= a  
FT /note= "contains phosphorothioate internucleotide  
FT linkages"  
XX  
FN WO9823294-A1.  
XX  
PD 04-JUN-1998.  
XX  
PF 26-NOV-1997; 97WO-US022017.  
XX  
PR 26-NOV-1996; 96US-00757024.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 1998-322464/28.  
XX  
PT Treating respiratory disease with antisense sequences directed against  
PT adenosine or bradykinin receptors - with localised delivery to the  
PT respiratory system, suitable for long term treatment of asthma, adult  
PT respiratory distress syndrome etc.  
XX  
PS Claim 12; Page 8-24; 47pp; English.  
XX  
CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
CC human adenosine A1 receptor, the design of which required the secondary  
CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The  
CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they

CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-  
CC transmembrane segments. These oligonucleotides can be used to treat or  
CC prevent conditions associated with bronchoconstriction and/or lung  
CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
CC allergy, emphysema and cystic fibrosis  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGGG 5  
Db 5 GAGGG 9  
|||||  
  
RESULT 19  
AAV47193  
ID AAV47193 standard; DNA; 10 BP.  
XX  
AC AAV47193;  
XX  
DT 10-NOV-1998 (first entry)  
XX  
DE Antisense oligonucleotide 693, targeting adenosine A1 receptor.  
XX  
KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
KW allergy; emphysema; cystic fibrosis; ss.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..10  
FT /\*tag= a  
FT /note= "contains phosphorothioate internucleotide  
FT linkages"  
XX  
FN WO9823294-A1.  
XX  
PD 04-JUN-1998.  
XX  
PF 26-NOV-1997; 97WO-US022017.  
XX  
PR 26-NOV-1996; 96US-00757024.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 1998-322464/28.  
XX  
PT Treating respiratory disease with antisense sequences directed against  
PT adenosine or bradykinin receptors - with localised delivery to the  
PT respiratory system, suitable for long term treatment of asthma, adult  
PT respiratory distress syndrome etc.  
XX  
PS Claim 12; Page 8-24; 47pp; English.  
XX  
CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
CC human adenosine A1 receptor, the design of which required the secondary  
CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
CC structure was both analysed and used to construct antisense  
CC oligonucleotides containing a phosphorothioate backbone. Once the  
CC antisense molecules are created they can be used to target their  
CC predetermined target, thus causing the gene product to decrease. The  
CC antisense oligonucleotides were targeted to specific mRNA regions  
CC containing either a junction between the intron and exon, or where they  
CC may overlap the initiation codon. The receptor is a member of the G-  
CC protein coupled family of cell surface receptors that have 7-



CC transmembrane segments. These oligonucleotides can be used to treat or  
 CC prevent conditions associated with bronchoconstriction and/or lung  
 CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
 CC allergy, emphysema and cystic fibrosis  
 XX  
 SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 |||||  
 Db 4 GAGGG 8

RESULT 20  
 AAV47146  
 ID AAV47146 standard; DNA; 10 BP.  
 XX  
 AC AAV47146;  
 XX  
 DT 10-NOV-1998 (first entry)  
 XX  
 DE Antisense oligonucleotide 646, targeting adenosine A1 receptor.  
 XX  
 KW Secondary structure; mRNA; phosphorothioate backbone; G-protein;  
 KW bronchoconstriction; lung inflammation; asthma; pulmonary disease;  
 KW allergy; emphysema; cystic fibrosis; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT modified\_base 1..10  
 FT /tag= a  
 FT /note= "contains phosphorothioate internucleotide  
 FT linkages"  
 XX  
 FN WO9823294-A1.  
 XX  
 PD 04-JUN-1998.  
 XX  
 PP 26-NOV-1997; 97WO-US022017.  
 XX  
 PR 26-NOV-1996; 96US-00757024.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 XX  
 PS WPI; 1998-322464/28.  
 XX  
 DR Treating respiratory disease with antisense sequences directed against  
 XX adenosine or bradykinin receptors - with localised delivery to the  
 XX respiratory system, suitable for long term treatment of asthma, adult  
 XX respiratory distress syndrome etc.  
 XX  
 PS Claim 12; Page 8-24; 47pp; English.  
 XX  
 CC Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the  
 CC human adenosine A1 receptor, the design of which required the secondary  
 CC structure of this targets mRNA. The adenosine receptor mRNA secondary  
 CC structure was both analysed and used to construct antisense  
 CC oligonucleotides containing a phosphorothioate backbone. Once the  
 CC antisense molecules are created they can be used to target their  
 CC predetermined target, thus causing the gene product to decrease. The  
 CC antisense oligonucleotides were targeted to specific mRNA regions  
 CC containing either a junction between the intron and exon, or where they  
 CC may overlap the initiation codon. The receptor is a member of the G-  
 CC protein coupled family of cell surface receptors that have 7-  
 CC transmembrane segments. These oligonucleotides can be used to treat or  
 CC prevent conditions associated with bronchoconstriction and/or lung

CC inflammation in humans or other animals e.g. asthma, pulmonary disease,  
 CC allergy, emphysema and cystic fibrosis  
 XX  
 SQ Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 |||||  
 Db 6 GAGGG 10

RESULT 21  
 AAV20923  
 ID AAV20923 standard; DNA; 10 BP.  
 XX  
 AC AAV20923;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 07-JUL-1998 (first entry)  
 XX  
 DE Aloc specific universal PCR primer OPAB-01.  
 XX  
 KW Aloc; detection; identification; amplification; PCR primer; antioxidant;  
 KW differentiation; anti-tumour; anti-diabetic; tyrosine inhibiting; ss.  
 XX  
 OS Synthetic.  
 OS Aloc.  
 XX  
 FN WO9804741-A1.  
 XX  
 PD 05-FEB-1998.  
 XX  
 PF 24-JUL-1997; 97WO-US013001.  
 XX  
 PR 26-JUL-1996; 96US-0022611P.  
 XX  
 PA (UNIV-) UNIVERA PHARM INC.  
 XX  
 PI Toothman P;  
 XX  
 PS WPI; 1998-159152/14.  
 XX  
 DR Detection and assay of Aloc - by extraction of DNA from a sample and  
 XX amplification by polymerase chain reaction using primers specific for  
 XX Aloc.  
 PS Claim 3; Page 15; 37pp; English.  
 XX  
 CC The present sequence represents an Aloc specific universal PCR primer  
 CC from the present invention. The present invention describes a method for  
 CC identifying Aloc using polymerase chain reaction (PCR). The method  
 CC comprises: (a) extracting DNA from a sample containing Aloc; (b)  
 CC amplifying the DNA using PCR, and (c) comparing the sequence of the  
 CC amplified DNA obtained from PCR with the sequence of DNA obtained from a  
 CC known sample of Aloc. Also described are: (1) a nucleotide sequence  
 CC comprising sequences given in the specification or a fragment; (2) a  
 CC method for differentiating between different species of Aloc comprising:  
 CC (a) extracting DNA from an unknown sample containing Aloc, and (b)  
 CC amplifying the DNA by PCR using primers specific for a particular species  
 CC of Aloc, and (3) a method for determining the amount of Aloc present in a  
 CC mixture comprising: (a) extracting DNA from an unknown sample with  
 CC internal controls for recovery of DNA, and (b) simultaneous amplification  
 CC of DNA with primers specific to a particular Aloc species and  
 CC amplification of non-homologous DNA added to a sample to internally  
 CC quantify the amplification. The methods can be used for detecting and  
 CC assaying Aloc in samples and for differentiating between different  
 CC species of Aloc. The Aloc compounds have diverse biological activities,  
 CC including anti-tumour activity, anti-acid activity, anti-diabetic  
 CC activity, tyrosine inhibiting activity and antioxidant activity. (Updated  
 CC on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 |||||  
 Db 2 GAGGG 6

RESULT 22  
 AAV45390  
 ID AAV45390 standard; DNA; 10 BP.  
 XX AC AAV45390;  
 XX 11-JAN-1999 (first entry)  
 DT Mouse CD3-epsilon enhancer binding site for Ikaros.  
 DE Ikaros; mIK; transcription factor; mouse; lymphocyte;  
 KW cell differentiation; T cell; cancer; immunodeficiency;  
 KW Alzheimer's disease; therapy; diagnosis; CD3-epsilon; enhancer; ss.  
 XX Mus sp.  
 OS CA2194256-A.  
 PN 05-MAR-1998.  
 PD 02-JAN-1997; 97CA-02194256.  
 PF 05-SEP-1996; 96US-00711417.  
 PR (GEHO ) GEN HOSPITAL CORP.  
 PA Georgopoulos K;  
 PI WPI; 1998-378292/33.  
 DR New nucleic acid encoding Ikaros protein involved in early  
 PT differentiation of lymphocytes - existing in several isoforms, and  
 PT related products used to treat e.g. immune diseases or cancer and to  
 PT control cell differentiation.  
 XX Disclosure; Page 38; 159pp; English.

XX This oligonucleotide from the mouse CD3-epsilon gene enhancer was  
 CC identified as a potential high affinity binding site for Ikaros proteins  
 CC (see AAW0963-71). It partially includes the core motif GGGAA found in  
 CC consensus recognition sequences for murine Ikaros isoforms mIK-1, mIK-2  
 CC and mIK-3 (see AAV52830-32). High affinity binding sites for Ikaros have  
 CC been found in enhancer and promoter regions of the regulatory domains of  
 CC the TCR antigen complex, the CD3 genes, the SL3 and HIV long terminal  
 CC repeat and in the regulatory domains of other T cell restricted antigens  
 CC (see AAV45358-402) by gel retardation assay. Ikaros is involved in early  
 CC differentiation of lymphocytes. The invention provides Ikaros nucleic  
 CC acids (see AAV42805-11 and AAV42840) and polypeptides, vectors and host  
 CC cells. These are used to treat T and B cell diseases, to control  
 CC expression of heterologous genes placed under control of an Ikaros-  
 CC responsive element, to treat nervous system diseases and to modulate cell  
 CC division, amplification or differentiation, especially in haematopoietic  
 CC cells

XX SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 |||||

Db 1 GAGGG 5  
 |||||

RESULT 23  
 AAV67001  
 ID AAV67001 standard; cDNA; 10 BP.  
 XX AC AAV67001;  
 XX 14-JAN-1999 (first entry)  
 DT CD3-epsilon enhancer oligonucleotide #3.  
 DE CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;  
 KW differentiation marker; immune system; corpus striatum; AIDS;  
 KW Alzheimer's disease; ss.  
 XX Mus sp.  
 OS Synthetic.  
 OS US5824770-A.  
 PN 20-OCT-1998.  
 PD 05-JUN-1995; 95US-00465590.  
 PF 14-SEP-1992; 92US-00946233.  
 PR 14-SEP-1993; 93US-00121438.  
 PR 02-MAY-1994; 94US-00238212.  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA Georgopoulos K;  
 PI WPI; 1998-582621/49.  
 DR Ikaros poly:peptide(s) - useful for treating disorders of immune system  
 PT or corpus striatum.  
 PT Disclosure; Col 27; 111pp; English.

XX The present invention describes a purified peptide having at least one of  
 CC the following properties: (a) it stimulates transcription of a DNA  
 CC sequence under the control of a delta A element, an NFkB element or an  
 CC Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of  
 CC Ikaros binding oligonucleotide consensus sequence; (c) it competitively inhibits the binding of a  
 CC a delta A element, an NFkB element or an Ikaros binding oligonucleotide  
 CC consensus sequence; (d) it competitively inhibits the binding of a  
 CC element or an Ikaros binding oligonucleotide consensus sequence; (e) it  
 CC competitively inhibits Ikaros binding to Ikaros responsive elements; or  
 CC that they stimulate gene transcription under the control of delta A  
 CC elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to  
 CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,  
 CC competitively inhibit binding of naturally occurring Ikaros isoforms to  
 CC delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,  
 CC competitively inhibit Ikaros binding to Ikaros-responsive elements and/or  
 CC inhibit protein-protein interactions of transcriptional complexes with  
 CC naturally occurring Ikaros isoforms, can be used to treat immune system  
 CC disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.  
 CC Alzheimer's disease. AAV66975 to AAV67118 represent oligonucleotides  
 CC given in the present invention

XX SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 |||||

```

Db      1 GAGGG 5

RESULT 24
AAV69060
ID AAV69060 standard; DNA; 10 BP.
XX
AC AAV69060;
XX
DT 22-JAN-1999 (first entry)
XX
DE Human breast tumour cDNA PCR primer #16.
XX
KW Human; breast cancer; breast tumour tissue; diagnosis; treatment;
KW vaccine; epitope; endogenous; retroviral element; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
FN WO9845328-A2.
XX
PD 15-OCT-1998.
XX
PF 09-APR-1998; 98WO-US006939.
XX
PR 09-APR-1997; 97US-00838762.
XX
PR 11-DEC-1997; 97US-00991789.
XX
PA (CORI-) CORIXA CORP.
XX
PI Frudakis TN, Smith JM, Reed SG;
XX
DR WPI; 1998-557473/47.
XX
PT New DNA sequences isolated from endogenous human retroviral element - and
PT related vectors, transformed cells, proteins and antibodies, useful for
PT diagnosis, treatment and prevention of breast cancer.
XX
PS Example 1; Page 69; 173pp; English.
XX
CC The present sequence represents a PCR primer for human breast tumour cDNA
CC nucleotide sequences. The present invention describes nucleotide
CC sequences which encode human breast tumour specific polypeptides.
CC Detection or measurement of human breast tumour specific polypeptides and
CC nucleotide sequences, or the corresponding RNA in a sample, is used for
CC diagnosis and monitoring of breast cancer. Human breast tumour specific
CC polypeptides and nucleotide sequences, and the vectors containing the
CC DNAs, are also useful in vaccines for inhibiting development (for
CC prevention or therapy) of breast cancer. The polypeptides may also be
CC used to raise monoclonal antibodies, used as immunoassay reagents
XX
SQ Sequence 10 BP; 4 A; 1 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db |||||
3 GAGGG 7

RESULT 25
AAV35962
ID AAV35962 standard; DNA; 10 BP.
XX
AC AAV35962;
XX
DT 26-AUG-1998 (first entry)
XX
DE Primer used in RAPD assay of the invention.
XX
KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;

Db      1 GAGGG 5

RESULT 26
AAV35969/c
ID AAV35969 standard; DNA; 10 BP.
XX
AC AAV35969;
XX
DT 26-AUG-1998 (first entry)
XX
DE Primer used in RAPD assay of the invention.
XX
KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
OS Synthetic.
OS Sus sp.
XX
FN WO9815837-A1.
XX
PD 16-APR-1998.
XX
PF 07-OCT-1997; 97WO-GB002741.
XX
PR 07-OCT-1996; 96GB-00020904.
PR 18-FEB-1997; 97GB-00003350.
PR 20-MAR-1997; 97GB-00005796.
PR 09-SEP-1997; 97GB-00019002.
XX
PA (MEAT-) MEAT & LIVESTOCK COMMISSION.
XX
PI Maltin CA, Steven J, Warkup CC;
XX
DR WPI; 1998-240968/21.
XX
PT Assay for alleles or muscle fibre composition characteristic of Duroc
PT type pigs - comprises determination of genotype or muscle fibre
PT properties, used to identify animals for breeding programs and to assess
PT meat quality.
XX
PS Example 3; Page 33; 56pp; English.
XX
CC PCR primers AAV35877-996 were used in a rapid amplification of
CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay
CC is used to determine if an animal has an allele for, or muscle fibre
CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce
CC meat of superior quality (particularly tenderness) but are normally less
CC efficient feed converters and fatter than other types. The assay
CC comprises analysing a tissue sample to determine if the genotype
CC comprises the allele, and genetic features typical of animals with Duroc-
CC type MFC are present. The method is used to select animals that have
CC Duroc characteristics for use in breeding programmes (to develop the
CC animals with Duroc pig characteristics), and to assess meat quality
XX
SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db |||||
6 GAGGG 10

RESULT 26
AAV35969/c
ID AAV35969 standard; DNA; 10 BP.
XX
AC AAV35969;
XX
DT 26-AUG-1998 (first entry)
XX
DE Primer used in RAPD assay of the invention.
XX
KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
OS Synthetic.
OS Sus sp.
XX
FN WO9815837-A1.
XX
PD 16-APR-1998.
XX
PF 07-OCT-1997; 97WO-GB002741.

```

muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.

Synthetic.  
Sus sp.

WO9815837-A1.

16-APR-1998.

07-OCT-1997; 97WO-GB002741.

07-OCT-1996; 96GB-00020904.

18-FEB-1997; 97GB-00003350.

20-MAR-1997; 97GB-00005796.

09-SEP-1997; 97GB-00019002.

(MEAT-) MEAT & LIVESTOCK COMMISSION.

Maltin CA, Steven J, Warkup CC;

WPI; 1998-240968/21.

Assay for alleles or muscle fibre composition characteristic of Duroc type pigs - comprises determination of genotype or muscle fibre properties, used to identify animals for breeding programs and to assess meat quality.

Example 3; Page 33; 56pp; English.

PCR primers AAV35877-996 were used in a rapid amplification of polymorphic DNA (RAPD) reaction in the assay of the invention. This assay is used to determine if an animal has an allele for, or muscle fibre composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce meat of superior quality (particularly tenderness) but are normally less efficient feed converters and fatter than other types. The assay comprises analysing a tissue sample to determine if the genotype comprises the allele, and genetic features typical of animals with Duroc-type MFC are present. The method is used to select animals that have Duroc characteristics for use in breeding programmes (to develop the animals with Duroc pig characteristics), and to assess meat quality

Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db |||||

6 GAGGG 10

RESULT 26

AAV35969/c

ID AAV35969 standard; DNA; 10 BP.

XX

AC AAV35969;

XX

DT 26-AUG-1998 (first entry)

XX

DE

XX

XX

KW

KW

XX

OS

OS

Sus sp.

XX

FN

WO9815837-A1.

XX

PD

16-APR-1998.

XX

PF

07-OCT-1997; 97WO-GB002741.



CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay  
 CC is used to determine if an animal has an allele for, or muscle fibre  
 CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce  
 CC meat of superior quality (particularly tenderness) but are normally less  
 CC efficient feed converters and fatter than other types. The assay  
 CC comprises analysing a tissue sample to determine if the genotype  
 CC comprises the allele, and genetic features typical of animals with Duroc-  
 CC type MFC are present. The method is used to select animals that have  
 CC Duroc characteristics for use in breeding programmes (to develop the  
 CC animals with Duroc pig characteristics), and to assess meat quality  
 SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
 |||||  
 Db 5 GAGGG 1

RESULT 29  
 AAX60193/c  
 ID AAX60193 standard; DNA; 10 BP.  
 XX AC  
 XX AAX60193;  
 XX AC

DT 10-AUG-1999 (first entry)

DE Pyrimidinone derivative of the invention.

XX Pyrimidinone derivative; labeled binding partner; diagnostic assay;  
 KW antisense; transfection complex; primer; probe; ss.  
 XX Synthetic.

XX WO9924452-A2.

XX 20-MAY-1999.

XX 30-OCT-1998; 98WO-US023119.

XX 07-NOV-1997; 97US-00966392.

XX 10-NOV-1997; 97US-00966875.

XX (ISIS-) ISIS PHARM INC.

XX Lin K, Matteucci MD;

XX WPI; 1999-370671/31.

PT Composition comprising pyrimidinone derivatives for diagnostic and  
 PT analytical labels.

PS Example 4; Page 87; 10pp; English.

XX The specification describes pyrimidinone derivatives. These derivatives  
 CC are used as labeled binding partners, particularly as labels for  
 CC diagnostic, analytical and therapeutic applications. The derivatives are  
 CC used as detectable labels for diagnostic assays, to enhance diagnostic  
 CC assays that use oligonucleotides and to improve potency of  
 CC oligonucleotides as antisense reagents that affect gene expression by  
 CC altering intracellular metabolism of complementary RNA sequences encoding  
 CC a target gene. They are also used in transfection complexes to deliver  
 CC oligonucleotides into cell cytoplasm and in PCR e.g. as primers, and  
 CC ligase chain reaction (LCR) e.g. as probes. The derivatives have  
 CC increased affinity and specificity for their complementary sequences and  
 CC facilitate PCR and LCR processes. The present sequence represents a  
 CC pyrimidinone derivative of the invention

XX Sequence 10 BP; 0 A; 6 C; 0 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
 |||||  
 Db 8 GAGGG 4

RESULT 30  
 AAV08397  
 ID AAV08397 standard; DNA; 10 BP.  
 XX AC  
 XX AAV08397;

DT 01-MAR-1999 (first entry)

DE Fsh16 antisense oligonucleotide.

XX Bipolar affective disorder; BAD; fsh16 gene; human;  
 KW neuropsychiatric disorder; schizophrenia; mood disorder;  
 KW attention deficit disorder; schizoaffective disorder;  
 KW unipolar affective disorder; depression; therapy; antisense; ss.

XX Synthetic.

XX Homo sapiens.

XX WO9842726-A1.

XX 01-OCT-1998.

XX 27-MAR-1998; 98WO-US006210.

XX 27-MAR-1997; 97US-00828009.

XX (MILL-) MILLENNIUM PHARM INC.

XX (REGC) UNIV CALIFORNIA.

XX Chen H, Freimer NB;

XX WPI; 1999-045133/04.

XX New isolated human fsh16 gene - used to develop products for treating  
 PT neuropsychiatric disorders, e.g. schizophrenia, attention deficit  
 PT disorder or bipolar affective disorder.

PS Disclosure; Page 55; 91pp; English.

XX Oligonucleotides (see AAV08397-402) are provided that comprise antisense  
 CC molecules complementary to the human fsh16 gene (see AAV08396). This gene  
 CC has been shown to be associated with neuropsychiatric disorders. The  
 CC antisense oligonucleotides can be used to suppress translation of  
 CC endogenous fsh16 mRNAs, and hence to ameliorate a fsh16 disorder or a  
 CC neuropsychiatric disorder such as schizophrenia, attention deficit  
 CC disorder, a schizoaffective disorder, unipolar disorders, or bipolar  
 CC affective disorders, e.g. severe bipolar affective (mood) disorder,  
 CC bipolar affective (mood) disorder with hypomania and major depression, or  
 CC schizoaffective disorder manic type

XX Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
 |||||  
 Db 2 GAGGG 6

RESULT 31  
 AAV81846/c  
 ID AAV81846 standard; DNA; 10 BP.

XX AAV81846;  
 XX AC  
 XX DT  
 XX 11-MAR-1999 (first entry)  
 XX DE  
 XX Human interleukin-1 forward primer OPG20.  
 XX KW  
 XX Human; cardiovascular disease; atherosclerosis; ischaemia; restenosis;  
 KW reperfusion; hypertension; arterial inflammation; diagnosis; rchds28;  
 KW primer; ss.  
 XX KW  
 XX Synthetic.  
 OS Homo sapiens.  
 XX OS  
 XX US5849578-A.  
 XX PN  
 XX 15-DEC-1998.  
 XX PD  
 XX 15-MAR-1996; 96US-00616844.  
 XX PF  
 XX 10-FEB-1995; 95US-00386844.  
 XX PR  
 XX 07-JUN-1995; 95US-00458873.  
 XX PR  
 XX 09-FEB-1996; 96US-00599634.  
 XX PR  
 XX (MILL-) MILLENNIUM PHARM INC.  
 XX PA  
 XX Falb DA;  
 XX PI  
 XX WPI; 1999-069743/06.  
 XX DR  
 XX DNA encoding rchds28 polypeptide - associated with cardiovascular  
 PT disease.  
 PT PT  
 XX PS  
 XX Example; Col 99; 122pp; English.  
 XX PS  
 XX The present invention describes rchds28 protein. A method has been  
 CC developed for producing the rchds28 gene product. The present invention  
 CC also describes methods and compositions for the treatment and diagnosis  
 CC of cardiovascular diseases, including: atherosclerosis; ischaemia;  
 CC restenosis; reperfusion; hypertension; and arterial inflammation. The  
 CC present sequence represents a primer used in an example from the present  
 CC invention  
 CC CC  
 XX SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 Db 8 GAGGG 4  
 |||||  
 |||||  
 RESULT 32  
 AAX53570  
 ID AAX53570 standard; DNA; 10 BP.  
 XX AC  
 XX AAX53570;  
 XX AC  
 XX 05-JUL-1999 (first entry)  
 XX DT  
 XX Human adenosine A1 receptor antisense oligonucleotide fragment.  
 XX DE  
 XX Antisense oligonucleotide; multiple target; antisense treatment;  
 KW impaired respiration; inflammation; lung disease;  
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;  
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

KW prostate cancer; ss.  
 XX Synthetic.  
 XX OS  
 XX WO9913886-A1.  
 XX PN  
 XX 25-MAR-1999.  
 XX PD  
 XX 17-SEP-1998; 98WO-US019419.  
 XX PF  
 XX 17-SEP-1997; 97US-0059160P.  
 XX PR  
 XX 09-JUN-1998; 98US-00093972.  
 XX PR  
 XX (UYEC-) UNIV EAST CAROLINA.  
 XX PA  
 XX Nyce JW;  
 XX PI  
 XX WPI; 1999-229400/19.  
 XX DR  
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 PT vasoconstriction.  
 PT PT  
 XX PS  
 XX Disclosure; Page 38; 120pp; English.  
 XX PS  
 XX The specification describes antisense oligonucleotides (AAX52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
 CC end and the juxta-section between coding and non-coding regions and all  
 CC segments of RNAs encoding proteins associated with one or more diseases,  
 CC conditions or mixtures. The antisense oligonucleotides may be derived  
 CC from sequences AAX55180-271. These multiple target oligonucleotides  
 CC (specifically AAX55180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 XX CC  
 XX SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 Db 4 GAGGG 8  
 |||||  
 |||||  
 RESULT 33  
 AAX53547  
 ID AAX53547 standard; DNA; 10 BP.  
 XX AC  
 XX AAX53547;  
 XX AC  
 XX 05-JUL-1999 (first entry)  
 XX DT  
 XX Human adenosine A1 receptor antisense oligonucleotide fragment.  
 XX DE  
 XX Antisense oligonucleotide; multiple target; antisense treatment;  
 KW impaired respiration; inflammation; lung disease;  
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;  
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;

KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 XX prostate cancer; ss.  
 OS Synthetic.  
 XX WO9913886-A1.  
 PN 25-MAR-1999.  
 XX 17-SEP-1998; 98WO-US019419.  
 PF 17-SEP-1997; 97US-0059160P.  
 PR 09-JUN-1998; 98US-00033972.  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA Nyce JW;  
 PI WPI; 1999-229400/19.  
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 DR vasoconstriction.  
 XX Disclosure; Page 37; 120pp; English.  
 PS The specification describes antisense oligonucleotides (AA52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
 CC end and the juxta-section between coding and non-coding regions and all  
 CC segments of RNAs encoding proteins associated with one or more diseases,  
 CC conditions or mixtures. The antisense oligonucleotides may be derived  
 CC from sequences AAX55272-74. These multiple target oligonucleotides  
 CC (specifically AAX55180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 XX Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 Db 5 GAGGG 9  
 RESULT 34  
 AAX53633  
 ID AAX53633 standard; DNA; 10 BP.  
 AC AAX53633;  
 XX 05-JUL-1999 (first entry)  
 DT Human adenosine A1 receptor antisense oligonucleotide fragment.  
 DE Antisense oligonucleotide; multiple target; antisense treatment;  
 KW impaired respiration; inflammation; lung disease;  
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;

KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 KW prostate cancer; ss.  
 XX Synthetic.  
 XX WO9913886-A1.  
 PN 25-MAR-1999.  
 XX 17-SEP-1998; 98WO-US019419.  
 PF 17-SEP-1997; 97US-0059160P.  
 PR 09-JUN-1998; 98US-00033972.  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA Nyce JW;  
 PI WPI; 1999-229400/19.  
 XX New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 DR vasoconstriction.  
 XX Disclosure; Page 39; 120pp; English.  
 PS The specification describes antisense oligonucleotides (AA52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-  
 CC end and the juxta-section between coding and non-coding regions and all  
 CC segments of RNAs encoding proteins associated with one or more diseases,  
 CC conditions or mixtures. The antisense oligonucleotides may be derived  
 CC from sequences AAX55272-74. These multiple target oligonucleotides  
 CC (specifically AAX55180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 XX Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 Db 1 GAGGG 5  
 RESULT 35  
 AAX53592  
 ID AAX53592 standard; DNA; 10 BP.  
 AC AAX53592;  
 XX 05-JUL-1999 (first entry)  
 DT Human adenosine A1 receptor antisense oligonucleotide fragment.  
 DE Antisense oligonucleotide; multiple target; antisense treatment;  
 KW impaired respiration; inflammation; lung disease;  
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;

KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;  
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 KW prostate cancer; ss.  
 OS Synthetic.  
 XX  
 XX WO9913886-A1.  
 XX  
 XX PD 25-MAR-1999.  
 XX  
 XX PF 17-SEP-1998; 98WO-US019419.  
 XX  
 XX PR 17-SEP-1997; 97US-0059160P.  
 XX  
 XX PR 09-JUN-1998; 98US-00093972.  
 XX  
 XX PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 XX PI Nyce JW;  
 XX  
 XX DR WPI; 1999-229400/19.  
 XX  
 XX PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 PT vasoconstriction.  
 XX  
 XX PS Disclosure; Page 38; 120pp; English.  
 XX  
 CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'  
 CC -end and the juxta-section between coding and non-coding regions and all  
 CC segments of RNAs encoding proteins associated with one or more diseases,  
 CC conditions or mixtures. The antisense oligonucleotides may be derived  
 CC from sequences AAX5272-74. These multiple target oligonucleotides  
 CC (specifically AAX5180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 XX  
 SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 Db 3 GAGGG 7  
 RESULT 36  
 AAX53613  
 ID AAX53613 standard; DNA; 10 BP.  
 XX  
 AC AAX53613;  
 XX  
 XX 05-JUL-1999 (first entry)  
 DT  
 XX Human adenosine A1 receptor antisense oligonucleotide fragment.  
 DE  
 XX Antisense oligonucleotide; multiple target; antisense treatment;  
 KW

KW impaired respiration; inflammation; lung disease;  
 KW pulmonary vasoconstriction; inflammation; allergic rhinitis;  
 KW acute asthma; allergy; asthma; impeded respiration;  
 KW respiratory distress syndrome; pain; cystic fibrosis;  
 KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;  
 KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;  
 KW colon cancer; breast cancer; lung cancer; pancreatic cancer;  
 KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;  
 KW prostate cancer; ss.  
 XX  
 XX OS Synthetic.  
 XX  
 XX PN WO9913886-A1.  
 XX  
 XX PD 25-MAR-1999.  
 XX  
 XX PF 17-SEP-1998; 98WO-US019419.  
 XX  
 XX PR 17-SEP-1997; 97US-0059160P.  
 XX  
 XX PR 09-JUN-1998; 98US-00093972.  
 XX  
 XX PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 XX PI Nyce JW;  
 XX  
 XX DR WPI; 1999-229400/19.  
 XX  
 XX PT New antisense oligonucleotides used in treatment of, e.g. pulmonary  
 PT vasoconstriction.  
 XX  
 XX PS Disclosure; Page 39; 120pp; English.  
 XX  
 CC The specification describes antisense oligonucleotides (AAX52869-X55271)  
 CC directed against at least 2 mRNAs selected from target genes, coding and  
 CC non-coding regions of RNAs corresponding to target genes, gene initiation  
 CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'  
 CC -end and the juxta-section between coding and non-coding regions and all  
 CC segments of RNAs encoding proteins associated with one or more diseases,  
 CC conditions or mixtures. The antisense oligonucleotides may be derived  
 CC from sequences AAX5272-74. These multiple target oligonucleotides  
 CC (specifically AAX5180-271) can be used for the antisense treatment of  
 CC diseases and conditions. Typical diseases and conditions are those  
 CC associated with impaired respiration and inflammation, including lung  
 CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,  
 CC acute asthma, allergies, asthma, impeded respiration, respiratory  
 CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,  
 CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary  
 CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.  
 CC colon cancer, breast cancer, lung cancer, pancreatic cancer,  
 CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as  
 CC well as all types of cancers which may metastasize or have metastasized  
 CC to the lungs, including breast and prostate cancer  
 XX  
 SQ Sequence 10 BP; 1 A; 2 C; 7 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 Db 2 GAGGG 6  
 RESULT 37  
 AAX53523  
 ID AAX53523 standard; DNA; 10 BP.  
 XX  
 AC AAX53523;  
 XX  
 XX 05-JUL-1999 (first entry)  
 DT  
 XX Human adenosine A1 receptor antisense oligonucleotide fragment.  
 DE





XX 19-JAN-1999.  
XX 22-DEC-1993; 93US-00173489.  
XX 29-OCT-1992; 92US-00968436.  
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX Hepburn AG, Wang C;  
XX WPI; 1999-130384/11.  
XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX Disclosure; Col 19-20; 168pp; English.  
XX The present sequence represents a potential triple-helix forming region.  
CC It can be used to demonstrate the assay of the invention. The assay  
CC comprises adding a sample containing double-stranded DNA test sequences,  
CC e.g. containing the present sequence, to an aqueous medium containing at  
CC least one complex of anchor DNA, attached to a solid support, and  
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
CC designed to form a triple-strand structure with part of the test  
CC sequence. Triplex formation results in displacement of the reporter DNA  
CC which is detected as an indication of the presence of the DNA test  
CC sequence. The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus  
XX Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
DB 8 GAGGG 4  
RESULT 40  
AA14901/C  
ID AA14901 standard; DNA; 10 BP.  
XX AA14901;  
XX 24-MAR-1999 (first entry)  
XX Triple helix third strand of 23S rRNA gene nucleotides 149-158.  
XX Triplex formation; DNA detection; triple helix; identification; bacteria;  
KW oncogene; virus; ss.  
XX Synthetic.  
OS Clostridium pasteurianum.  
XX US5861244-A.  
XX 19-JAN-1999.  
XX 22-DEC-1993; 93US-00173489.  
XX 29-OCT-1992; 92US-00968436.  
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX Hepburn AG, Wang C;  
XX WPI; 1999-130384/11.  
XX

XX 19-JAN-1999.  
XX 22-DEC-1993; 93US-00173489.  
XX 29-OCT-1992; 92US-00968436.  
XX (PROF-) PROFILE DIAGNOSTIC SCI INC.  
XX Hepburn AG, Wang C;  
XX WPI; 1999-130384/11.  
XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX Disclosure; Col 23-24; 168pp; English.  
XX The present sequence represents a polynucleotide that is able to form a  
CC triple helix with a double stranded sequence. Cytosine bases in the  
CC present can be replaced with 5-methylcytosine for increased triplex  
CC stability. The present sequence is used in the assay of the invention,  
CC where it can be part of the anchor DNA or reporter DNA sequence. The  
CC assay comprises adding a sample containing double-stranded DNA test  
CC sequences to an aqueous medium containing at least one complex of anchor  
CC DNA, attached to a solid support, and reporter DNA, where either a part  
CC of the anchor DNA or reporter DNA is designed to form a triple-strand  
CC structure with part of the test sequence. Triplex formation results in  
CC displacement of the reporter DNA which is detected as an indication of  
CC the presence of the DNA test sequence. The method is used to detect DNA  
CC sequences, particularly for identification of bacteria (by detecting  
CC genes for ribosomal RNA) in clinical samples, but also detection of  
CC oncogenes and Hepatitis B virus  
XX Sequence 10 BP; 0 A; 5 C; 0 G; 5 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
DB 9 GAGGG 5  
RESULT 41  
AA149477  
ID AA149477 standard; DNA; 10 BP.  
XX AA149477;  
XX 21-MAY-1999 (first entry)  
XX Human senescence factor p23 primer SEQ ID NO:19.  
XX Human; senescence factor; p23; cancer; persistent inflammation;  
KW proliferative disorder; degenerative disorder; primer; ss.  
XX Synthetic.  
OS Homo sapiens.  
XX WO9907893-A1.  
XX 18-FEB-1999.  
XX 05-AUG-1998; 98WO-US016343.  
XX 08-AUG-1997; 97US-00908873.  
XX (UNIW ) UNIV WASHINGTON.  
XX Swisselhelm K, Hosier S, Kubbies M;  
XX WPI; 1999-167454/14.  
XX Newly isolated nucleic acid molecule (designated p23) encoding a p23  
PT polypeptide - useful for inducing a senescence phenotype in a cell.  
XX Example 1; Page 19; 4pp; English.  
XX The present invention describes human senescence factor p23. An  
CC expression vector for p23 is useful for inducing a senescent phenotype in  
CC a cell (preferably eukaryotic). This may help in regulating diseases,  
CC

CC including cancer, persistent inflammation, and various proliferative and  
 CC degenerative disorders. These transgenic cells are useful in gene therapy  
 CC for treating cancer, particularly where antisense oligonucleotides are  
 CC useful for blocking normal or mutant p23 expression in cancer cells or  
 CC other proliferating cells. Transgenic cells are also useful for producing  
 CC the p23 polypeptide in large quantities. The antibodies are useful for  
 CC raising antiserum against p23, and for identifying senescent cells in  
 CC culture and tissue biopsies. The p23 polynucleotides are useful for  
 CC modulating or altering p23 activity in a cell, and for identifying and  
 CC isolating the whole gene encoding p23, and variants of p23. Assays based  
 CC on p23 elements, which detect p23 levels and activity are useful as  
 CC diagnostic markers for staging tumours, determining prognosis, and/or  
 CC predicting therapeutic success. These elements also provide an assay for  
 CC detecting chromosomal rearrangements in chromosome 3 in a human cell. The  
 CC isolation of the p23 polynucleotide permits the manipulation of malignant  
 CC growth in cancer. The present sequence represents a primer used in an  
 CC example from the present invention

XX  
 SQ Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 DB 2 GAGGG 6  
 |||||

RESULT 42  
 AAX26259/C  
 ID AAX26259 standard; DNA; 10 BP.  
 AC AAX26259;  
 XX  
 DT 24-MAY-1999 (first entry)  
 XX  
 DE Forward primer OPG20.  
 XX  
 KW Fingerprinting gene; rchd502; transmembrane protein; cardiovascular;  
 KW fingerprint/target gene; up-regulated; endothelial cell; shear-stress;  
 KW atherosclerosis; ischemia; reperfusion; hypertension; restenosis; human;  
 KW PCR primer; 58.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN US5882925-A.  
 XX  
 PD 16-MAR-1999.  
 XX  
 PF 09-FEB-1996; 96US-00599654.  
 XX  
 PR 10-FEB-1995; 95US-00386844.  
 PR 07-JUN-1995; 95US-00485573.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 PI Faib DA;  
 XX  
 DR WPI; 1999-214071/18.  
 XX  
 PT New polynucleotides consisting of residues 1-1929 of the rchd502 gene -  
 PT are differentially expressed in cardiovascular disease states, and can  
 PT therefore be used to treat and diagnose cardiovascular diseases.  
 XX  
 PS Disclosure; Col 10; 121pp; English.  
 XX  
 CC The invention relates to a rchd502 target/fingerprint gene encoding a  
 CC transmembrane protein. The invention provides cDNAs contained in plasmids  
 CC pFCHD502SP (ATCC 69981) and pFCHD502S7 (ATCC 69982) that encode the  
 CC rchd502 polypeptide, and are differentially expressed in cardiovascular  
 CC disease states. Cultured genetically engineered host cell containing the

CC rchd502 polynucleotides in operative association with a nucleotide  
 CC regulatory element are used for producing a polypeptide rchd502 gene  
 CC product. Identifying that the fingerprint/target gene rchd502 is  
 CC differentially expressed (up-regulated) by endothelial cells subjected to  
 CC shear-stress, provides a tool for the diagnosis and treatment of  
 CC cardiovascular disease e.g. atherosclerosis, ischemia/reperfusion,  
 CC hypertension, restenosis. The fingerprint gene is useful for testing the  
 CC efficacy of candidate drugs in basic research and in clinical trials and  
 CC or imaging of a diseased cardiovascular tissue. The gene may also be used  
 CC in screening for ligands of target gene product receptor domains, as well  
 CC as antagonists of the ligand-receptor interaction

XX  
 SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 DB 8 GAGGG 4  
 |||||

RESULT 43  
 AAX86215/C  
 ID AAX86215 standard; DNA; 10 BP.  
 XX  
 AC AAX86215;  
 XX  
 DT 22-SEP-1999 (first entry)  
 XX  
 DE SAGE tag used to identify transcripts which are enhanced by p53.  
 XX  
 KW p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;  
 KW neoplastic; p53 binding site; PIG-3 promoter; SAGE tag; 88.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9914356-A2.  
 XX  
 PD 25-MAR-1999.  
 XX  
 PF 17-SEP-1998; 98WO-US019300.  
 XX  
 PR 17-SEP-1997; 97US-0059153P.  
 PR 30-MAR-1998; 98US-0079817P.  
 XX  
 PA (UJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Vogelstein B, Kinzler KW, Polyak K;  
 XX  
 DR WPI; 1999-443793/37.  
 XX  
 PT Use of p53 transcription tags to determine p53 status in, e.g. cancer  
 PT diagnosis.  
 XX  
 PS Claim 1; Page 26; 73pp; English.  
 XX  
 CC The specification describes the use of p53 transcription tags for  
 CC developing products to determine p53 status, to diagnose cancer and to  
 CC evaluate cytotoxicity or carcinogenicity of a test agent. A method for  
 CC diagnosing cancer or determining p53 status in a sample suspected for  
 CC being neoplastic comprises comparing the level of transcription of an RNA  
 CC transcript in a first sample (s1) of a first tissue (t1) to the level of  
 CC transcription of the transcript in a second sample (s2) of a second  
 CC tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal  
 CC human tissue (of the same type) and the transcript is identified by a tag  
 CC ; and categorizing s1 as neoplastic or as having a mutant p53 when  
 CC transcription is found to be the same or lower in the first, than in s2.  
 CC The methods and products can be used to determine p53 status, to diagnose  
 CC cancer and to evaluate cytotoxicity or carcinogenicity of a test agent.  
 CC AAX86201-33 represent SAGE tags used to identify transcripts which are  
 CC enhanced by p53

```
XX
SQ Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 5 GAGGG 1

RESULT 44
AAx86246
ID AAx86246 standard; DNA; 10 BP.
XX
XX AC AAx86246;
XX
DT 22-SEP-1999 (first entry)
XX
DE SAGE tag used to identify transcripts which are decreased by p53.
XX
KW p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;
KW neoplastic; p53 binding site; PIG-3 promoter; SAGE tag; ss.
XX
XX OS Homo sapiens.
XX
XX FN WO9914356-A2.
XX
XX PD 25-MAR-1999.
XX
XX PF 17-SEP-1998; 98WO-US019300.
XX
XX PR 17-SEP-1997; 97US-0059153P.
XX
XX PR 30-MAR-1998; 98US-0079817P.
XX
XX PA (UVOJO ) UNIV JOHNS HOPKINS.
XX
XX PI Vogelstein B, Kinzler KW, Polyak K;
XX
XX DR WPI; 1999-443793/37.
XX
XX PF Use of p53 transcription tags to determine p53 status in, e.g. cancer
XX diagnosis.
XX
XX PS Claim 2; Page 29; 73pp; English.
XX
XX CC The specification describes the use of p53 transcription tags for
XX developing products to determine p53 status, to diagnose cancer and to
XX evaluate cytotoxicity or carcinogenicity of a test agent. A method for
XX diagnosing cancer or determining p53 status in a sample suspected for
XX being neoplastic comprises comparing the level of transcription of an RNA
XX transcript in a first sample (s1) of a first tissue (t1) to the level of
XX transcription of the transcript in a second sample (s2) of a second
XX tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal
XX human tissue (of the same type) and the transcript is identified by a tag
XX ; and categorizing s1 as neoplastic or as having a mutant p53 when in
XX CC transcription is found to be the same or lower in the first, than in s2.
XX CC The methods and products can be used to determine p53 status, to diagnose
XX cancer and to evaluate cytotoxicity or carcinogenicity of a test agent.
XX CC AAx86233-64 represent SAGE tags used to identify transcripts which are
XX decreased by p53
XX
XX SQ Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 1 GAGGG 5

RESULT 45
AAx86255
ID AAx86255 standard; DNA; 10 BP.
XX
XX AC AAx86255;
XX
DT 22-SEP-1999 (first entry)
XX
DE SAGE tag used to identify transcripts which are decreased by p53.
XX
KW p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;
KW neoplastic; p53 binding site; PIG-3 promoter; SAGE tag; ss.
XX
XX OS Homo sapiens.
XX
XX FN WO9914356-A2.
XX
XX PD 25-MAR-1999.
XX
XX PF 17-SEP-1998; 98WO-US019300.
XX
XX PR 17-SEP-1997; 97US-0059153P.
XX
XX PR 30-MAR-1998; 98US-0079817P.
XX
XX PA (UVOJO ) UNIV JOHNS HOPKINS.
XX
XX PI Vogelstein B, Kinzler KW, Polyak K;
XX
XX DR WPI; 1999-443793/37.
XX
XX PF Use of p53 transcription tags to determine p53 status in, e.g. cancer
XX diagnosis.
XX
XX PS Claim 2; Page 30; 73pp; English.
XX
XX CC The specification describes the use of p53 transcription tags for
XX developing products to determine p53 status, to diagnose cancer and to
XX evaluate cytotoxicity or carcinogenicity of a test agent. A method for
XX diagnosing cancer or determining p53 status in a sample suspected for
XX being neoplastic comprises comparing the level of transcription of an RNA
XX transcript in a first sample (s1) of a first tissue (t1) to the level of
XX transcription of the transcript in a second sample (s2) of a second
XX tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal
XX human tissue (of the same type) and the transcript is identified by a tag
XX ; and categorizing s1 as neoplastic or as having a mutant p53 when in
XX CC transcription is found to be the same or lower in the first, than in s2.
XX CC The methods and products can be used to determine p53 status, to diagnose
XX cancer and to evaluate cytotoxicity or carcinogenicity of a test agent.
XX CC AAx86233-64 represent SAGE tags used to identify transcripts which are
XX decreased by p53
XX
XX SQ Sequence 10 BP; 4 A; 0 C; 4 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 2 GAGGG 6

RESULT 46
AAA33056
ID AAA33056 standard; DNA; 10 BP.
XX
XX AC AAA33056;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:745.
XX
```

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200009525-A2.  
 XX  
 XX 24-FEB-2000.  
 XX  
 XX 03-AUG-1999; 99WO-US017712.  
 XX  
 XX 03-AUG-1998; 98US-0095212P.  
 XX  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA  
 XX Nyce JW;  
 XX  
 XX WPI; 2000-205971/18.  
 XX  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 PS Claim 18; Page 359; 1343pp; English.  
 XX  
 XX The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impaired respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA3392) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 XX listing  
 XX  
 SQ Sequence 10 BP; 1 A; 2 C; 7 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 |||||  
 DB 2 GAGGG 6  
 RESULT 47  
 AAA33076  
 XX AAA33076 standard; DNA; 10 BP.  
 XX

AC AAA33076;  
 XX  
 DT 28-JUL-2000 (first entry)  
 XX  
 DE Low adenosine antisense oligonucleotide SEQ ID NO:765.  
 XX  
 KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;  
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200009525-A2.  
 XX  
 XX 24-FEB-2000.  
 XX  
 XX 03-AUG-1999; 99WO-US017712.  
 XX  
 XX 03-AUG-1998; 98US-0095212P.  
 XX  
 XX (UYEC-) UNIV EAST CAROLINA.  
 PA  
 XX Nyce JW;  
 XX  
 XX WPI; 2000-205971/18.  
 XX  
 XX New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 PS Claim 18; Page 362; 1343pp; English.  
 XX  
 XX The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impaired respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA3392) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 XX listing  
 XX  
 SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GAGGG 5  
 |||||  
 DB 1 GAGGG 5

Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 48
AAA32966
ID AAA32966 standard; DNA; 10 BP.
XX
XX
AC AAA32966;
XX
DT 28-JUL-2000 (first entry)
XX
DE Low adenosine antisense oligonucleotide SEQ ID NO:655.
XX
XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
XX WO200009525-A2.
XX
XX 24-FEB-2000.
XX
XX 03-AUG-1999; 99WO-US017712.
XX
XX 03-AUG-1998; 98US-0095212P.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 2000-205971/18.
XX
XX New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Claim 18; Page 349; 1343pp; English.
XX
XX The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 185, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
XX listing
XX
SQ Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 3; Length 10;

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Query Match 100.0%; Score 5; DB 3; Length 10;

CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
Db 3 GAGGG 7  
RESULT 50  
ID AAA33013 standard; DNA; 10 BP.  
XX  
XX  
AC AAA33013;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Low adenosine antisense oligonucleotide SEQ ID NO:702.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
PI Nyce JW;  
XX  
XX WPI; 2000-205971/18.  
XX  
XX New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Claim 18; Page 354; 1343pp; English.  
XX  
XX The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impaired respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the

CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GAGGG 5  
Db 4 GAGGG 8  
Search completed: January 7, 2005, 07:11:56  
Job time : 262.4 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 04:56:02 ; Search time 2222.4 Seconds  
(without alignments)  
81.983 Million cell updates/sec

Title: GAGGG

Perfect score: 5

Sequence: 1 gaggg 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 156772

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST1:

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hc:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gest1:\*

9: gb\_gest2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	5	100.0	10	6	CF323895
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5	5	100.0	11	4	BM395228
6	5	100.0	11	4	CF304450
7	5	100.0	11	6	CF322692
8	5	100.0	11	6	CF323154
9	5	100.0	11	8	BH129987
10	5	100.0	11	9	AJ589163
11	5	100.0	11	9	CL437735
12	5	100.0	11	9	CL657848
13	5	100.0	12	4	BG925521
14	5	100.0	12	6	CF306837
15	5	100.0	12	8	BH129328
16	5	100.0	12	9	AJ587286
17	5	100.0	12	9	AJ600549
18	5	100.0	13	1	AJ647701
19	5	100.0	13	1	AJ667961
20	5	100.0	13	5	BQ589768
21	5	100.0	13	6	CF306647
22	5	100.0	14	5	BQ588202
23	5	100.0	14	5	BQ590450
24	5	100.0	14	5	BQ593808

c	25	5	100.0	14	5	BQ605961
c	26	5	100.0	14	9	AJ588060
c	27	5	100.0	15	6	CF303956
c	28	5	100.0	15	6	CF304766
c	29	5	100.0	15	9	AJ599339
c	30	5	100.0	16	1	AA968729
c	31	5	100.0	16	1	AJ075064
c	32	5	100.0	16	1	AJ094839
c	33	5	100.0	16	1	AJ560058
c	34	5	100.0	16	1	AJ564678
c	35	5	100.0	16	1	AJ569544
c	36	5	100.0	16	4	BM394080
c	37	5	100.0	16	6	CF303743
c	38	5	100.0	16	6	CF305660
c	39	5	100.0	16	6	CF323664
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c	41	5	100.0	16	9	AJ595160
c	42	5	100.0	17	1	AJ666397
c	43	5	100.0	17	2	AW248940
c	44	5	100.0	17	4	BG896889
c	45	5	100.0	17	4	BG926068
c	46	5	100.0	17	5	BQ789989
c	47	5	100.0	17	9	AJ587432
c	48	5	100.0	17	9	AJ595555
c	49	5	100.0	17	9	AJ599163
c	50	5	100.0	17	9	CL436788
c	51	5	100.0	18	1	AJ648240
c	52	5	100.0	18	2	AW250267
c	53	5	100.0	18	4	BG896958
c	54	5	100.0	18	4	BG925569
c	55	5	100.0	18	4	BM397132
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c	61	5	100.0	19	1	AJ251781
c	62	5	100.0	19	1	AJ360784
c	63	5	100.0	19	1	AJ570374
c	64	5	100.0	19	1	AJ648553
c	65	5	100.0	19	1	AJ696833
c	66	5	100.0	19	1	AJ649246
c	67	5	100.0	19	1	AJ679811
c	68	5	100.0	19	4	BG896949
c	69	5	100.0	19	5	BQ593604
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c	76	5	100.0	19	8	AJ324165
c	77	5	100.0	19	8	AJ324945
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c	81	5	100.0	19	8	AJ418201
c	82	5	100.0	19	8	AJ420252
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c	85	5	100.0	19	8	AJ447414
c	86	5	100.0	19	8	AJ471573
c	87	5	100.0	19	8	AJ480415
c	88	5	100.0	19	8	AJ494890
c	89	5	100.0	19	8	AJ505490
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c	97	5	100.0	19	8	AJ636812

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CF304766	ABF1--05-
AJ599339	Arabidops
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AJ075064	ou61g11.x
AJ094839	ga22c08.x
AJ560058	tq38h11.x
AJ564678	tq78g03.x
AJ569544	to28d10.x
BM394080	50072-2.1
CF303743	ABF1--03-
CF305660	HDAL--01-
CF323664	HDN--04-H
AJ587352	Arabidops
AJ595160	Arabidops
AJ666397	AJ666397
AW248940	2822481.5
BG896889	HOA58-1-G
BG926068	HNC23-1-E
BQ789989	hage005AB
AJ587432	Arabidops
AJ595555	Arabidops
AJ599163	Arabidops
CL436788	PST3832-N
AJ648240	AJ648240
AW250267	2821151.5
BG896958	HOA59-1-D
BG925569	HNC5-1-E2
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CA850820	D06H05.H0
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CF323060	HDN--02-N
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AJ360784	qx98g07.x
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AJ345792	TM0080G12
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AJ418201	TM0194M12
AJ420252	TM0198G01
AJ432757	TM0218L14
AJ447248	TM0244H23
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AJ480415	TM0301K24
AJ494890	TM0330N19
AJ505490	TM0346N08
AJ508355	TM0350O13
AJ510143	TM0354E21
AJ512762	TM0358M04
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AJ5297219	TM0411K23
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c 103	5	100.0	19	8	A2783420	A2783420	2M0025D07
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c 105	5	100.0	19	8	A2794440	A2794440	2M0048A15
c 106	5	100.0	19	8	A2809734	A2809734	2M0073D19
c 107	5	100.0	19	8	A2827092	A2827092	2M0103M18
c 108	5	100.0	19	8	A2842379	A2842379	2M0140N17
c 109	5	100.0	19	8	A2854718	A2854718	2M0158N23
c 110	5	100.0	19	8	A2977338	A2977338	2M0253P10
c 111	5	100.0	19	9	AJ587161	AJ587161	Arabidops
c 112	5	100.0	19	9	AJ587166	AJ587166	Arabidops
c 113	5	100.0	19	9	AJ587167	AJ587167	Arabidops
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c 117	5	100.0	19	9	CL657902	CL657902	PR1012A_D
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c 119	5	100.0	20	1	AJ696560	AJ696560	AJ696560
c 120	5	100.0	20	1	AJ696560	AJ696560	AJ696560
c 121	5	100.0	20	1	AJ798166	AJ798166	AJ798166
c 122	5	100.0	20	2	AW250737	AW250737	hag002aB
c 123	5	100.0	20	5	BQ789787	BQ789787	hag002aB
c 124	5	100.0	20	6	C21208	C21208	HUMG000223
c 125	5	100.0	20	6	CF293092	CF293092	3ODGS--02
c 126	5	100.0	20	6	CF293747	CF293747	3ODGS--03
c 127	5	100.0	20	6	CF306120	CF306120	HDA1--02-
c 128	5	100.0	20	6	CF306620	CF306620	HDA1--04-
c 129	5	100.0	20	6	CF327699	CF327699	NAC1--02-
c 130	5	100.0	20	7	CF921149	CF921149	smtrRwv3-
c 131	5	100.0	20	7	CF932153	CF932153	SPI-A4 (P6
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c 133	5	100.0	20	7	CO785157	CO785157	BL282C_H0
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c 155	5	100.0	20	8	A2659755	A2659755	1M0537F22
c 156	5	100.0	20	8	A2662459	A2662459	1M0541N02
c 157	5	100.0	20	8	A2665090	A2665090	1M0545P17
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c 178	5	100.0	20	9	CL661389	CL661389	PR10139c
c 179	5	100.0	20	9	CL661719	CL661719	PR10136_E
c 180	5	100.0	20	9	CL670850	CL670850	PR10163a_E
c 181	5	100.0	20	9	CL687844	CL687844	PR10147d-
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c 183	5	100.0	20	9	AG197313	AG197313	Pan trogl
c 184	5	100.0	20	9	AG203409	AG203409	Pan trogl
c 185	5	100.0	20	9	AG203984	AG203984	Pan trogl
c 186	5	100.0	20	1	AJ646946	AJ646946	AJ646946
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c 195	5	100.0	21	6	CF325365	CF325365	JMT1--03-
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c 198	5	100.0	21	8	AZ325878	AZ325878	1M0048D18
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c 203	5	100.0	21	8	AZ405406	AZ405406	1M0174P08
c 204	5	100.0	21	8	AZ440229	AZ440229	1M0233N10
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c 208	5	100.0	21	8	AZ472401	AZ472401	1M0287C07
c 209	5	100.0	21	8	AZ476392	AZ476392	1M0295F12
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c 211	5	100.0	21	8	AZ482019	AZ482019	1M0306I17
c 212	5	100.0	21	8	AZ486694	AZ486694	1M0314F22
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c 215	5	100.0	21	8	AZ596349	AZ596349	1M0409K03
c 216	5	100.0	21	8	AZ653464	AZ653464	1M0527G11
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c 218	5	100.0	21	8	AZ662168	AZ662168	1M0541B12
c 219	5	100.0	21	8	AZ769086	AZ769086	1M0569G22
c 220	5	100.0	21	8	AZ770188	AZ770188	1M0571A12
c 221	5	100.0	21	8	AZ780316	AZ780316	2M0017L02
c 222	5	100.0	21	8	AZ781467	AZ781467	2M0019F23
c 223	5	100.0	21	8	AZ785173	AZ785173	2M0028G19
c 224	5	100.0	21	8	AZ785704	AZ785704	2M0029C21
c 225	5	100.0	21	8	AZ785825	AZ785825	2M0030G05
c 226	5	100.0	21	8	AZ794033	AZ794033	2M0047D12
c 227	5	100.0	21	8	AZ794301	AZ794301	2M0048G05
c 228	5	100.0	21	8	AZ806282	AZ806282	2M0068A15
c 229	5	100.0	21	8	AZ808542	AZ808542	2M0072E10
c 230	5	100.0	21	8	AZ820567	AZ820567	2M0092B19
c 231	5	100.0	21	8	AZ821784	AZ821784	2M0094N09
c 232	5	100.0	21	8	AZ826252	AZ826252	2M0101C23
c 233	5	100.0	21	8	AZ829064	AZ829064	2M0106A01
c 234	5	100.0	21	8	AZ829277	AZ829277	2M0106A24
c 235	5	100.0	21	8	AZ836049	AZ836049	2M0130E11
c 236	5	100.0	21	8	AZ843343	AZ843343	2M0142K10
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c 238	5	100.0	21	8	AZ850337	AZ850337	2M0152H11
c 239	5	100.0	21	8	AZ853378	AZ853378	2M0156J01
c 240	5	100.0	21	8	AZ857175	AZ857175	2M0184B13
c 241	5	100.0	21	8	AZ8955804	AZ8955804	2M0222L03
c 242	5	100.0	21	8	AZ960531	AZ960531	2M0228C11
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C 246	5	100.0	21	8	AZ991107	2M0275E08	C 319	5	100.0	22	8	AZ644887	1M0510G05
C 247	5	100.0	21	9	AI601344	Arabidops	C 320	5	100.0	22	8	AZ645874	1M0525K24
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C 256	5	100.0	22	1	AA911591	cd9b007.8	C 329	5	100.0	22	8	AZ809838	2M0074G04
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C 261	5	100.0	22	1	AI039313	ox36b04.8	C 334	5	100.0	22	8	AZ871408	2M0184E16
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C 284	5	100.0	22	1	AJ806746	AJ806746	C 357	5	100.0	22	8	AZ875902	2M0192D07
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C 330	5	100.0	23	8	A2621487	AZ621487	1M0454A17	463	5	100.0	24	8	AZ823931	AZ823931	2M0098F17
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C 332	5	100.0	23	8	A2647317	AZ647317	1M0513F14	465	5	100.0	24	8	AZ832930	AZ832930	2M0113J10
C 333	5	100.0	23	8	A2659712	AZ659712	1M0537J18	466	5	100.0	24	8	AZ848167	AZ848167	2M0149C11
C 334	5	100.0	23	8	A2660131	AZ660131	1M0538H03	467	5	100.0	24	8	AZ861819	AZ861819	2M0168L12
C 335	5	100.0	23	8	A2660176	AZ660176	1M0538A12	468	5	100.0	24	8	AZ861955	AZ861955	2M0169D02
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C 337	5	100.0	23	8	A2665777	AZ665777	1M0547G23	470	5	100.0	24	8	AZ936903	AZ936903	2M0193E20
C 338	5	100.0	23	8	A2666452	AZ666452	1M0548A07	C 471	5	100.0	24	8	AZ983288	AZ983288	2M0264G23
C 339	5	100.0	23	8	A2763749	AZ763749	1M0559B19	472	5	100.0	24	8	BH000494	BH000494	2M0288H21
C 400	5	100.0	23	8	A2766246	AZ766246	1M0563J08	C 473	5	100.0	24	9	AJ587189	AJ587189	Arbidops
C 401	5	100.0	23	8	A2766803	AZ766803	1M0564B12	C 474	5	100.0	24	9	TA114B01P	TA114B01P	AL462593 T. brucei
C 402	5	100.0	23	8	A2767581	AZ767581	1M0566A19	475	5	100.0	24	9	TA115B03Q	TA115B03Q	AL463750 T. brucei
C 403	5	100.0	23	8	A2771291	AZ771291	1M0573A23	476	5	100.0	24	9	TA115E01P	TA115E01P	AL462835 T. brucei
C 404	5	100.0	23	8	A2775223	AZ775223	2M0007I20	C 477	5	100.0	24	9	TA178F08P	TA178F08P	AL474698 T. brucei
C 405	5	100.0	23	8	A2780543	AZ780543	2M0018C03	478	5	100.0	24	9	TA185C06P	TA185C06P	AL474052 T. brucei
C 406	5	100.0	23	8	A2784767	AZ784767	2M0027F17	C 479	5	100.0	24	9	TA87G04P	TA87G04P	AL461242 T. brucei
C 407	5	100.0	23	8	A2785027	AZ785027	2M0028H03	480	5	100.0	24	9	CL653351	CL653351	PR1011Bb
C 408	5	100.0	23	8	A2789956	AZ789956	2M0038L05	481	5	100.0	24	9	CL653505	CL653505	PR1011Bd
C 409	5	100.0	23	8	A2790388	AZ790388	2M0038E22	482	5	100.0	24	9	CL692392	CL692392	PR10158d
C 410	5	100.0	23	8	A2799237	AZ799237	2M0056P24	C 483	5	100.0	24	9	AG193471	AG193471	Pan trogl
C 411	5	100.0	23	8	A2800080	AZ800080	2M0057I22	484	5	100.0	25	1	AA878831	AA878831	of83f10.s
C 412	5	100.0	23	8	A2800632	AZ800632	2M0058E17	485	5	100.0	25	1	AA909239	AA909239	ol08d04.s
C 413	5	100.0	23	8	A2806508	AZ806508	2M0068P05	486	5	100.0	25	1	AA927233	AA927233	om17c03.s
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C 415	5	100.0	23	8	A2807263	AZ807263	2M0070C02	488	5	100.0	25	1	AA931670	AA931670	om03b01.s
C 416	5	100.0	23	8	A2808123	AZ808123	2M0071C01	489	5	100.0	25	1	AA936737	AA936737	om159f10.s
C 417	5	100.0	23	8	A2842845	AZ842845	2M0141A06	C 490	5	100.0	25	1	AA994478	AA994478	om17e09.s
C 418	5	100.0	23	8	A2862305	AZ862305	2M0169N22	C 491	5	100.0	25	1	AI023012	AI023012	ow57f01.s
C 419	5	100.0	23	8	A2871545	AZ871545	2M0184A04	C 492	5	100.0	25	1	AI123486	AI123486	ga01e11.x
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C 421	5	100.0	23	8	A2968672	AZ968672	2M0241B09	C 494	5	100.0	25	1	AI264778	AI264778	qx56h03.x
C 422	5	100.0	23	9	AJ587346	AJ587346	Arbidops	495	5	100.0	25	1	AI299118	AI299118	qn14g07.x
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C 424	5	100.0	23	9	TA121H10Q	TA121H10Q	T. brucei	C 497	5	100.0	25	1	AI339004	AI339004	qq44n01.x
C 425	5	100.0	23	9	TA175H02P	TA175H02P	T. brucei	498	5	100.0	25	1	AI344221	AI344221	tc02h03.x
C 426	5	100.0	23	9	TA178H03P	TA178H03P	T. brucei	C 499	5	100.0	25	1	AI363940	AI363940	qw34b12.x
C 427	5	100.0	23	9	TA208C04P	TA208C04P	T. brucei	C 500	5	100.0	25	1	AI416870	AI416870	sa19b03.x
C 428	5	100.0	23	9	TA266D03P	TA266D03P	T. brucei								
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C 433	5	100.0	23	9	AG202994	AG202994	Pan trogl								
C 434	5	100.0	24	1	AJ656826	AJ656826	HMA59-1-C								
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C 437	5	100.0	24	6	CF322725	CF322725	HDN--01-O								
C 438	5	100.0	24	6	CF324811	CF324811	JMT1--01-								
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C 441	5	100.0	24	8	AZ335328	AZ335328	1M006SC13								
C 442	5	100.0	24	8	AZ379773	AZ379773	1M0135H09								
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C 460	5	100.0	24	8	AZ814317	AZ814317	2M0082C12								
C 461	5	100.0	24	8	AZ820006	AZ820006	2M0091P19								
C 462	5	100.0	24	8	AZ822664	AZ822664	2M0096A07								

RESULT 1

CF305881

LOCUS

HDAL--02-A07.gi OSHDAC1-overexpressing transgenic rice lambda phage

CDNA library I (HDAl) Oryza sativa (japonica cultivar-group) cDNA

clone HDAl--02-A07, mRNA sequence.

CF305881

CF305881.1

GI:33677642

EST.

ORIGIN

Oryza sativa (japonica cultivar-group)

Source

Oryza sativa (japonica cultivar-group)

Keywords

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

Version

1 (bases 1 to 10)

Keywords

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Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

Features

source

1. 10

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDAL--02-A07"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
phage cDNA library I (HDAL)"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2:  
XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
was inserted into lambda Uni-ZAP XR vector at 5' end with  
EcoRI and 3' end with XhoI site. mRNA was derived from  
rice Histone Deacetylase overexpression line."

## ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

## RESULT 2

CF323895 10 bp mRNA linear EST 18-AUG-2003  
LOCUS HDN--05-A22.g1 OSHDA1-overexpressing transgenic rice lambda phage  
DEFINITION cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA  
clone HDN--05-A22, mRNA sequence.

ACCESSION CF323895  
VERSION CF323895.1 GI:33796055  
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source  
1..10  
Location/Qualifiers  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="HDN--05-A22"  
/tissue\_type="callus"  
/dev\_stage="proliferated callus on 2N6 media for 2 weeks"  
/lab\_host="E.coli SOLR"  
/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
phage cDNA library II (HDN)"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at  
5' end with EcoRI and 3' end with XhoI site. mRNA was  
derived from rice Histone Deacetylase overexpression  
line."

## ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

## RESULT 3

## LOCUS

CF325441 10 bp mRNA linear EST 18-AUG-2003  
DEFINITION JMT1--03-D24.g1 AtJMT-overexpressing transgenic rice lambda phage  
clone JMT1--03-D24, mRNA sequence.

ACCESSION CF325441  
VERSION CF325441.1 GI:33799167  
KEYWORDS EST.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.

## REFERENCE

AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

## FEATURES

source  
1..10  
Location/Qualifiers  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="JMT1--03-D24"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="AtJMT-overexpressing transgenic rice lambda  
phage cDNA library (JMT1)"  
/note="Vector: pBluescript SK(+); Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at 5'  
end with EcoRI and 3' end with XhoI site. mRNA was  
prepared from Arabidopsis Jasmonate Carboxyl  
methyltransferase overexpression line."

## ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

## RESULT 4

## LOCUS

AJ657108 11 bp mRNA linear EST 28-JUN-2004  
DEFINITION AJ657108 KN277 Sus scrofa cDNA clone C0005196\_K06, mRNA sequence.

ACCESSION AJ657108  
VERSION AJ657108.1 GI:49341140  
KEYWORDS EST.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 11)

## REFERENCE

AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.  
TITLE Development of cDNA and EST resources for studying reproduction and

```

embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13P Normalised library constructed
from pooled early embryos, from 8- cell stage to blastocysts.
Clones available from UK Centre for Functional Genomics in Farm
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
www.argenomics.org.

FEATURES
    source
    1..11
    /organism="Sus scrofa"
    /mol_type="mRNA"
    /db_xref="taxon:9823"
    /clone="C0005196.K06"
    /tissue_type="embryo"
    /clone_lib="K0277"
    /note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2:
    NotI; Single pass sequencing. Normalised library
    constructed from pooled early embryos, from 8-cell stage
    to blastocysts."

ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 5 GAGGG 9

RESULT 5
BM395228/c
LOCUS      BM395228
DEFINITION 50072-2-8-B05.r1 Chilcoat/Turkewitz cDNA (large fraction)
VERSION    BM395228
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE  1 (bases 1 to 11)
            Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
            EST from Tetrahymena thermophila, strain CU428.1, growing cells
            Unpublished (2002)
            Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.

FEATURES
    source
    1..11
    /organism="Tetrahymena thermophila"
    /mol_type="mRNA"
    /strain="CU428.1"
    /db_xref="taxon:5911"
    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
    /note="Vector: BlueScript2 SK+; Details on library
    preparation can be found in Chilcoat and Turkewitz (2001)
    Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

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```

Query Match      100.0%; Score 5; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 11 GAGGG 7

RESULT 6
CF304450
LOCUS      CF304450
DEFINITION ABF1--05-A03.g1 ABF3-overexpressing transgenic rice lambda phage
            cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
            clone ABF1--05-A03, mRNA sequence.
ACCESSION  CF304450
VERSION     CF304450.1 GI:33676211
KEYWORDS   EST.
SOURCE     Oryza sativa (japonica cultivar-group)
            Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 11)
            Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
            Large-scale Sequencing Analysis of Rice ESTs
            Unpublished (2003)
            Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, Myongji University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
    1..11
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /cultivar="Nackdong"
    /db_xref="taxon:39947"
    /clone="ABF1--05-A03"
    /tissue_type="leaf"
    /dev_stage="14 days after germination"
    /lab_host="E.coli SOLR"
    /clone_lib="ABF3-overexpressing transgenic rice lambda
    phage cDNA library (ABF1)"
    /note="Vector: pBlueScript SK(+); Site_1: EcoRI; Site_2:
    XhoI; Leaf was dried for 2hrs. cDNA was inserted into
    lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
    with XhoI site. mRNA was prepared from ABA-responsive
    element binding transcription factor 3 overexpression
    line."

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 5 GAGGG 9

RESULT 7
CF322692
LOCUS      CF322692
DEFINITION HDN--01-M19.g1 OsHDAC1-overexpressing transgenic rice lambda phage
            cDNA library II (HDN) Oryza sativa (japonica cultivar-group) cDNA
            clone HDN--01-M19, mRNA sequence.
ACCESSION  CF322692
VERSION     CF322692.1 GI:33793616

ORIGIN

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KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 (bases 1 to 11)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES source
1..11
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN--01-M19"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
|||||
Db 5 GAGGG 9

RESULT 8
CF323154 11 bp mRNA linear EST 18-AUG-2003
LOCUS HDN--03-B04.g1 OshDAC1-overexpressing transgenic rice lambda phage
DEFINITION cDNA library II (HDN) Oryza sativa (japonica cultivar-group) CDNA
clone HDN--03-B04, mRNA sequence.
ACCESSION CF323154
VERSION CF323154.1 GI:33794534
KEYWORDS EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 (bases 1 to 11)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongui University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers

FEATURES source
1..11
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDN--03-B04"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library II (HDN)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
|||||
Db 5 GAGGG 9

RESULT 9
BH129987/c 11 bp DNA linear GSS 23-JUL-2001
LOCUS BH129987
DEFINITION G-6e3.f Maize Random Small-insert Genomic Library Zea mays genomic
clone G-6e3 both, genomic survey sequence.
ACCESSION BH129987
VERSION BH129987.1 GI:14998894
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
1 (bases 1 to 11)
AUTHORS Meyers,B.C., Tingey,S.V. and Morgante,M.
TITLE Abundance, distribution and transcriptional activity of repetitive
elements in the maize genome
JOURNAL Genome Res. 11 (10), 1660-1676 (2001)
MEDLINE 21475670
PUBMED 11591643
COMMENT Contact: Morgante M
Suite 200
Dupont Genomics
PO Box 6104, Newark, DE 19714-6104, USA
Tel: 302 631 2638
Fax: 302 631 2607
Email: Michele.morgante@usa.dupont.com
Sequences were trimmed to include only high quality bases; forward
and reverse reads were assembled when significant overlaps were
detected.
Seg primer: M13univ
Class: shotgun.
Location/Qualifiers

FEATURES source
1..11
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="G-6e3"
/sex="hermaphrodite"
/tissue_type="leaf"
/cell_type="Young leaf"
/dev_stage="seedling"
/clone_lib="Maize Random Small-insert Genomic Library"
/notes="Vector: pCR-Script; Total genomic DNA was
nebulized; ends were polished with Pfu polymerase and the

```

fragments cloned into pCR-Script."

ORIGIN  
Query Match 100.0%; Score 5; DB 8; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 7 GAGGG 3

RESULT 10  
AJ589163/c  
LOCUS  
DEFINITION  
AJ589163  
Arabidopsis thaliana T-DNA flanking sequence, left border, clone  
545D12, genomic survey sequence.

ACCESSION  
AJ589163  
VERSION  
GSS; left border; T-DNA flanking sequence.  
KEYWORDS  
Arabidopsis thaliana (thale cress)  
SOURCE  
Arabidopsis thaliana

ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE  
1  
AUTHORS  
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,  
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,  
Leplintec, L., Caboche, M., and Lecharny, A.

TITLE  
T-DNA integration into the Arabidopsis genome depends on sequences  
of pre-insertion sites

JOURNAL  
EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE  
22363535  
PubMed  
12446565

REFERENCE  
2 (bases 1 to 11)  
AUTHORS  
Balzerque, S.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue  
Gaston Cremieux, 91057 Evry cedex, FRANCE  
COMMENT  
PCR was performed on DNA from transformants of Arabidopsis thaliana  
plants from INRA (Versailles). The DNA fragment (s) resulting from  
the PCR were directly sequenced from the left or the right border  
to determine the genomic sequence flanking the insertion. T-DNA  
derived sequences were removed. Information to order the  
corresponding mutant line and a link to a database providing a  
graphical display of the insertion site are available at  
http://dbgap.versailles.inra.fr/publiclines/. This sequence has  
been generated in the framework of the French plant genomics  
program 'Genoplante' (http://www.genoplante.com and  
http://genoplante-info.infobiogen.fr).

FEATURES  
source  
1..11  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="Wassillewskija"  
/db\_xref="taxon:3702"  
/clone="545D12"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature  
1..11  
/note="T-DNA flanking sequence  
left border"

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 7 GAGGG 3

RESULT 11

CL437735/c  
LOCUS  
DEFINITION  
PST6197-NR-Seq MICB1 Mus musculus genomic clone PST6197-NR-Seq  
similar to Dncl1, genomic survey sequence.

ACCESSION  
CL437735  
VERSION  
CL437735.1 GI:45573647  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)

ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
Hicks, G.G.  
1 (bases 1 to 11)  
www.Escells.ca  
Unpublished (2002)  
Contact: Hicks GG  
Mammalian Functional Genomics Centre  
Manitoba Institute of Cell Biology, University of Manitoba  
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada  
Tel: 204 787 2133  
Fax: 204 787 2190  
Email: hicksgg@cc.umanitoba.ca

REFERENCE  
1  
AUTHORS  
UNNeoSV1 gene trap. Tag generated by plasmid rescue. Additional  
sequence information and target gene cloning can be generated. ES  
cell line harboring insertion mutation of target gene is available.  
Sequence analysis available from  
http://140.193.242.7/esdb/public\_search\_frame.php?PST=PST6197-NR.Se

Q  
Class: Gene Trap.  
Location/Qualifiers  
1..11  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="129 sv"  
/db\_xref="taxon:10090"  
/clone="PST6197-NR-Seq"  
/sex="Male"  
/cell\_type="Embryonic stem cell"  
/cell\_line="D3H (J1 subclone)"  
/clone\_lib="MICB1"  
/note="Vector: U3NeoSV1"

FEATURES  
source  
1..11  
Query Match 100.0%; Score 5; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 5 GAGGG 1

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 5 GAGGG 1

RESULT 12  
CL657848/c  
LOCUS  
DEFINITION  
PRI012c\_H02 - PRI012c.B21 (11) Mixed stage foamid library of P.  
pacificus var. California Pristionchus pacificus genomic, genomic  
survey sequence.

ACCESSION  
CL657848  
VERSION  
CL657848.1 GI:50139878  
KEYWORDS  
GSS.  
SOURCE  
Pristionchus pacificus  
Pristionchus pacificus  
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.

REFERENCE  
1 (bases 1 to 11)  
AUTHORS  
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.  
AppADB: an AcedB database for the nematode satellite organism  
Pristionchus pacificus  
Nucleic Acids Res. 32 (1), D421-D422 (2004)  
Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology

Qy 1 GAGGG 5  
|||||  
Db 5 GAGGG 1

ORIGIN  
Query Match 100.0%; Score 5; DB 9; Length 11;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 5 GAGGG 1



Spannstr. 37-39, Tuebingen D-72076, Germany  
 Tel: 00497071601371  
 Fax: 00497071601498  
 Email: raf.sommer@uebingen.mpg.de  
 This library was generated at Caltech, Pasadena, USA and end  
 sequenced at Vancouver, Canada.  
 Seq primer: 17  
 Class: fosmid ends.

# FEATURES

Location/Qualifiers  
 1..11  
 /organism="Pristionchus pacificus"  
 /mol\_type="genomic DNA"  
 /strain="California"  
 /db\_xref="taxon:54126"  
 /clone\_lib="Mixed stage fosmid library of P. pacificus  
 var. California"  
 /note="Vector: pEpifos-5 Fosmid vector"

## ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 7 GAGGG 3

## RESULT 13

BG925521/c  
 LOCUS 12 bp mRNA linear EST 06-NOV-2001  
 DEFINITION HNC5-1-D3.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA  
 sequence.

ACCESSION BG925521

VERSION BG925521.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,  
 Sathie,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and  
 Lark,M.W.

TITLE Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries  
 JOURNAL Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 MEDLINE 21482651  
 PUBMED 11597177

## COMMENT

Contact: Sanjay Kumar  
 UW2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar-1@gsk.com  
 Seq primer: 17

# FEATURES

Location/Qualifiers  
 1..12  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
 Directional"

## ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 11 GAGGG 7

## RESULT 14

CF306837

LOCUS

DEFINITION

CF306837

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..12

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clones="HDAL-04-P19"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_hosts="E.coli SOLR"

/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
 phage cDNA library 1 (HDAL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
 was inserted into lambda Uni-ZAP XR vector at 5' end with  
 EcoRI and 3' end with XhoI site. mRNA was derived from  
 rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 5 GAGGG 9

RESULT 15

LOCUS

DEFINITION

BH129328

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..12

/organism="Maize Random Small-insert Genomic Library Zea mays genomic  
 clone G-5a10 both, genomic survey sequence."

ORIGIN

Query Match 100.0%; Score 5; DB 12 bp DNA linear GSS 23-JUL-2001

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 5 GAGGG 9

RESULT 15

LOCUS

DEFINITION

BH129328

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..12

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nackdong"

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/clones="HDAL-04-P19"

/tissue\_type="callus"

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/lab\_hosts="E.coli SOLR"

/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
 phage cDNA library 1 (HDAL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
 was inserted into lambda Uni-ZAP XR vector at 5' end with  
 EcoRI and 3' end with XhoI site. mRNA was derived from  
 rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 5 GAGGG 9

RESULT 15

LOCUS

DEFINITION

BH129328

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..12

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

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/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_hosts="E.coli SOLR"

/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
 was inserted into lambda Uni-ZAP XR vector at 5' end with  
 EcoRI and 3' end with XhoI site. mRNA was derived from  
 rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 5 GAGGG 9

RESULT 15

LOCUS

DEFINITION

BH129328

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..12

/organism="Oryza sativa (japonica cultivar-group)"

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/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
 phage cDNA library 1 (HDAL)"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
 was inserted into lambda Uni-ZAP XR vector at 5' end with  
 EcoRI and 3' end with XhoI site. mRNA was derived from  
 rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 5 GAGGG 9

RESULT 15

LOCUS

DEFINITION

BH129328

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

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/organism="Oryza sativa (japonica cultivar-group)"

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/cultivar="Nackdong"

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/tissue\_type="callus"

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/lab\_hosts="E.coli SOLR"

/clone\_lib="OSHDA1-overexpressing transgenic rice lambda  
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/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
 XhoI; Callus was treated with ABA(20um) for 1hour. cDNA  
 was inserted into lambda Uni-ZAP XR vector at 5' end with  
 EcoRI and 3' end with XhoI site. mRNA was derived from  
 rice Histone Deacetylase overexpression line."

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 12;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 5 GAGGG 9

RESULT 15

LOCUS

DEFINITION

BH129328

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

1..12

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/cultivar="Nackdong"

/db\_xref="taxon:39947"

/clones="HDAL-04-P19"

/tissue\_type="callus"

/dev\_stage="proliferated callus on 2N6 media for 2 weeks"

/lab\_hosts="E.coli SOLR"

/clone\_lib="OSHDA1-overexpressing transgenic rice lambda

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REFERENCE
AUTHORS      Meyers, B.C., Tingey, S.V. and Morgante, M.
TITLE        Abundance, distribution and transcriptional activity of repetitive
              elements in the maize genome
JOURNAL      Genome Res. 11 (10), 1660-1676 (2001)
MEDLINE      21475670
PUBMED       11591643
COMMENT      Suite 200
              Dupont Genomics
              PO Box 6104, Newark, DE 19714-6104, USA
              Tel: 302 631 2638
              Fax: 302 631 2607
              Email: Michele.morgante@usa.dupont.com
              Sequences were trimmed to include only high quality bases; forward
              and reverse reads were assembled when significant overlaps were
              detected.
              Seq primer: M13univ
              Class: shotgun.
FEATURES     source
              Location/Qualifiers
                1..12
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
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                /sex="hermaphrodite"
                /tissue_type="leaf"
                /cell_type="Young leaf"
                /dev_stage="seedling"
                /clone_lib="Maize Random Small-insert Genomic Library"
                /note="Vector: PCR-Script; Total genomic DNA was
              nebulized; ends were polished with Pfu polymerase and the
              fragments cloned into PCR-Script."
ORIGIN
Query Match      100.0%; Score 5; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
    |||||
Db 4 GAGGG 8

RESULT 16
AJ587286/c
LOCUS      AJ587286
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
258G07, genomic survey sequence.
ACCESSION  AJ587286
VERSION     AJ587286.1 GI:37936875
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepintec, B., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
2363535
PUBMED      12446565
REFERENCE    2 (bases 1 to 12)
            Balzerque, S.
            Direct Submission
            Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment (s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
            Location/Qualifiers
              1..12
              /organism="Arabidopsis thaliana"

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```

plants from INRA (Versailles). The DNA fragment (s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
            Location/Qualifiers
              1..12
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              /db_xref="taxon:3702"
              /clone="258G07"
              /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
              1..12
              /note="T-DNA flanking sequence
              left border"
ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
    |||||
Db 8 GAGGG 4

RESULT 17
AJ600549
LOCUS      AJ600549
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone
508F08, genomic survey sequence.
ACCESSION  AJ600549
VERSION     AJ600549.1 GI:37950177
KEYWORDS    GSS; right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepintec, B., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
2363535
PUBMED      12446565
REFERENCE    2 (bases 1 to 12)
            Balzerque, S.
            Direct Submission
            Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment (s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
            Location/Qualifiers
              1..12
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/note="T-DNA flanking sequence
right border"

ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 3 GAGGG 7

RESULT 18
AJ647701/c
LOCUS
DEFINITION AJ647701 CSEQRAN19 Sus scrofa cDNA clone C0003260_G16, mRNA
sequence.
ACCESSION AJ647701
VERSION AJ647701.1 GI:49324546
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 13)
AUTHORS Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
TITLE Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.
JOURNAL Contact: Anderson SI
COMMENT Genomics and Bioinformatics
Roslin Institute

FEATURES
source
1..13
location/Qualifiers
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000044_G09"
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NotI; Single pass sequencing. Normalised library
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 8 GAGGG 12

RESULT 20
BQ589768/c
LOCUS
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CDNA clone 024-020-D03-SP6 MP1Z-ADIS-024-storage root Beta vulgaris
sequence.
ACCESSION BQ589768
VERSION BQ589768.1 GI:26119351
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 13)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

```

```

Email: weishaa@mpiz-koeln.mpg.de
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Location/Qualifiers
1. .13
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/mol_type="mRNA"
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line)"
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/clone_lib="MPIZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
source
ORIGIN
Query Match 100.0%; Score 5; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
|||||
Db 5 GAGGG 9

RESULT 22
BQ588202/c
LOCUS
DEFINITION BQ588202 14 bp mRNA linear EST 06-DEC-2002
024-009-104 5-PRIME, mRNA sequence.
ACCESSION BQ588202
VERSION BQ588202.1 GI:26117785
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 14)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
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Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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/db_xref="taxon:161934"
/clone="024-009-I04"
/tissue_type="leaf"
/lab_host="EMDH108"
/clone_lib="MPIZ-ADIS-024-leaf"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

FEATURES
source
ORIGIN
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 20 row: D column: 03
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:190356"
/db_xref="taxon:161934"
/clone="024-020-D03"
/tissue_type="storage root"
/lab_host="EMDH108"
/clone_lib="MPIZ-ADIS-024-storage root"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

FEATURES
source
ORIGIN
Query Match 100.0%; Score 5; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
|||||
Db 5 GAGGG 1

RESULT 21
CF306647
LOCUS
DEFINITION HDAl--04-H13-g1 OSHDAC1-overexpressing transgenic rice lambda phage
cDNA library I (HDAl) Oryza sativa (japonica cultivar-group) cDNA
clone HDAl--04-H13, mRNA sequence.
ACCESSION CF306647
VERSION CF306647.1 GI:33678408
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.
Location/Qualifiers
1. .13
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="HDAl--04-H13"
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/dev_stages="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"

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Query Match 100.0%; Score 5; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 |||||  
 Db 10 GAGGG 6

RESULT 23  
 BQ590450  
 LOCUS  
 DEFINITION E012839-024-019-A07-SP6 MP1Z-ADIS-024-storage root Beta vulgaris  
 CDNA clone 024-019-A07 5-PRIME, mRNA sequence.

ACCESSION BQ590450  
 VERSION BQ590450.1 GI:26120033  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 REFERENCE 1 (bases 1 to 14)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698

COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
 Plate: 19 row: A column: 07  
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES  
 Location/Qualifiers  
 1..14  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:189667"  
 /db\_xref="taxon:161934"  
 /db\_xref="GABI:193044"  
 /clone="024-019-A07"  
 /tissue\_type="storage root"  
 /lab\_host="EMDH108"  
 /clone\_lib="MP1Z-ADIS-024-storage root"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinzellbener Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 |||||  
 Db 9 GAGGG 13

RESULT 24  
 BQ593808/c  
 LOCUS  
 DEFINITION

ACCESSION BQ593808  
 VERSION BQ593808.1 GI:26123391  
 KEYWORDS EST.  
 SOURCE Beta vulgaris  
 ORGANISM Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 14)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698

COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
 Plate: 26 row: O column: 07  
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES  
 Location/Qualifiers  
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 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
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 /db\_xref="GABI:193044"  
 /db\_xref="taxon:161934"  
 /clone="024-026-007"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH108"  
 /clone\_lib="MP1Z-ADIS-024-developing root"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinzellbener Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
 |||||  
 Db 14 GAGGG 10

RESULT 25  
 BQ605961/c  
 LOCUS  
 DEFINITION

ACCESSION BQ605961  
 VERSION BQ605961.1 GI:21555112  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 14)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.

TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL Plant J. 32 (5), 845-857 (2002)  
 MEDLINE 22362189  
 PUBMED 12472698

COMMENT Contact: Weishaar B  
 ADIS DNA core facility at MPIZ  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 14 Std Error: 0.00  
 Plate: 26 row: O column: 07  
 Seq primer: SP6; CATACGATTAGGTGACACTATAG.

FEATURES  
 Location/Qualifiers  
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 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:193044"  
 /db\_xref="taxon:161934"  
 /clone="024-026-007"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH108"  
 /clone\_lib="MP1Z-ADIS-024-developing root"  
 /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinzellbener Saatgut AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

```

ORGANISM      Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Triticum.

REFERENCE
AUTHORS      Clarke,B., Lambrecht,M. and Rhee,S.Y.
TITLE        Arabidopsis genomic information for interpreting wheat EST
              sequences
JOURNAL       Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE       22478026
PUBMED        12590341
COMMENT      Contact: Lambrecht M
              The Arabidopsis Information Resource
              Carnegie Institution of Washington, Dept. of Plant Biology
              260 Panama Street, Stanford, CA 94305, USA
              Tel: 1 650 325 1521 x 251
              Fax: 1 650 325 3748
              Email: rhee@acoma.stanford.edu.

FEATURES
source
1. .14
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wyuana"
/db_xref="taxon:4565"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/clone_lib="wheat EST endosperm library"

ORIGIN
Query Match      100.0%; Score 5; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
    |||||
Db 10 GAGGG 6

RESULT 26
AJ588060/c
LOCUS          Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION     526B05, genomic survey sequence.
ACCESSION      AJ588060.1 GI:37937684
VERSION        GSS; left border; T-DNA flanking sequence.
KEYWORDS       Arabidopsis thaliana (thale cress)
SOURCE         Arabidopsis thaliana
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosoids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
AUTHORS        Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
              Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
              Lepoint,L., Caboche,M. and Lecharny,A.
TITLE          T-DNA integration into the Arabidopsis genome depends on sequences
              of pre-insertion sites
JOURNAL        EMOB Rep. 3 (12), 1152-1157 (2002)
MEDLINE        22363535
PUBMED         12446565
REFERENCE      2 (bases 1 to 14)
AUTHORS        Balzergue,S.
TITLE          Direct Submission
JOURNAL        Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
              Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT        PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at

```

```

http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.inbio.gen.fr).

FEATURES
Location/Qualifiers
1. .14
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassiljewskija"
/db_xref="taxon:3702"
/clone="526B05"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature
1. .14
/notes="T-DNA flanking sequence
left border"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
    |||||
Db 7 GAGGG 3

RESULT 27
CF303956
LOCUS          CF303956 15 bp mRNA linear EST 15-AUG-2003
DEFINITION     ABF1--03-K24, gl ABF3-overexpressing transgenic rice lambda phage
              cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
              clone ABF1--03-K24, mRNA sequence.
ACCESSION      CF303956
VERSION        CF303956.1 GI:33675717
KEYWORDS       EST.
SOURCE         Oryza sativa (japonica cultivar-group)
ORGANISM       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS        Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
              Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE          Large-scale Sequencing Analysis of Rice ESTs
JOURNAL         Unpublished (2003)
COMMENT        Contact: Nahm B.H.
              Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
              of Bioscience and Bioinformatics, Myongui University
              Yongin, Kyeonggi, Korea
              Tel: 82 31 330 6193
              Fax: 82 31 321 6355
              Email: bhnam@ggbio.com, bhnam@bio.myongji.ac.kr.

FEATURES
Location/Qualifiers
1. .15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1--03-K24"
/tissue_type="leaf"
/dev_stage="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage cDNA library (ABF1)"
/notes="vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was dried for 2hrs. cDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 15;

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Best Local Similarity 100.0%; Pred. No. 1.2e+07; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 0;

QY 1 GAGGG 5
Db 5 GAGGG 9

RESULT 28
CF304766
LOCUS
DEFINITION
ABF1--05-006.g1 ABF3-overexpressing transgenic rice lambda phage
CDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA
clone ABF1--05-006, mRNA sequence.
CF304766
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 15)
AUTHORS
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
CONTACT: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bnhahm@bio.com, bnhahm@bio.myongji.ac.kr.
FEATURES
Location/Qualifiers
1..15
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:39947"
/clone="ABF1--05-006"
/tissue_type="leaf"
/dev_stages="14 days after germination"
/lab_host="E.coli SOLR"
/clone_lib="ABF3-overexpressing transgenic rice lambda
phage CDNA library (ABF1)"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Leaf was dried for 2hrs. CDNA was inserted into
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end
with XhoI site. mRNA was prepared from ABA-responsive
element binding transcription factor 3 overexpression
line."
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 4 GAGGG 8

RESULT 29
AJ599339/c
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
485B10, genomic survey sequence.
AJ599339
ACCESSION
VERSION
KEYWORDS
SOURCE
Arabidopsis thaliana
15 bp DNA linear GSS 15-JAN-2004

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
MEDLINE
12446565
PUBMED
2 (bases 1 to 15)
REFERENCE
Balzergue, S.
Direct Submission
TITLE
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
Location/Qualifiers
1..15
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="485B10"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1..15
/misc_feature
/notes="T-DNA flanking sequence
left border"
ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5
Db 5 GAGGG 1

RESULT 30
AA968729
LOCUS
DEFINITION
orf9h11.61 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1601157.
similar to SW:PRPE_HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E
; contains element MSRI repetitive element ;, mRNA sequence.
AA968729
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
REFERENCE
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.

```

cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Insert Length: 514 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:1601157"
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/lab_host="DH10B"
/clone_lib="NCI CGAP GC3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

#### ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 10 GAGGG 14

RESULT 31  
AI075064/c  
LOCUS ou61g11.x1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE:1632356 3'  
DEFINITION similar to TR:Q24348 FIBRILLARIN ;, mRNA sequence.  
ACCESSION AI075064  
VERSION AI075064.1 GI:3399844  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 16)  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert Length: 712 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

#### FEATURES

source

```
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
```

```
/clone="IMAGE:1632356"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Br2"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. This library is the normalized version of
NCI CGAP Br1.1. Library was constructed by Bento Soares
and M. Fatima Bonaldo. "
```

#### ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 12 GAGGG 8

RESULT 32  
AI094839/c  
LOCUS Q222c08.x1 NCI\_CGAP\_Brn23 Homo sapiens cDNA clone IMAGE:1687502 3'  
DEFINITION similar to TR:O00599 O00599 CON1.; contains element MSRI repetitive  
element ;, mRNA sequence.  
ACCESSION AI094839  
VERSION AI094839.1 GI:3433815  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 16)  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute / National Institute of Neurological  
Disorders and Stroke, Brain Tumor Genome Anatomy Project  
(CGAP/BTGAP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
Bonaldo, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 1.  
Location/Qualifiers

#### FEATURES

source

```
1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1687502"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn23"
/note="Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTACCAATCTGAAGGGAGCGCGCATATCTTTTITTTTTTTTTTTT
T 3']; double-stranded cDNA was ligated to Eco RI
```



adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pV73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GAGGG 5  
 Db 8 GAGGG 4

## RESULT 33

AI560058

## LOCUS

DEFINITION tq38h11.x1 NCI CGAP Utl1 Homo sapiens CDNA clone IMAGE:2211141 3'  
 similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RPL5  
 PRECURSOR. ; contains MSRI.t2 MSRI repetitive element ;, mRNA  
 sequence.

## ACCESSION

AI560058

## VERSION

AI560058.1 GI:4510263

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 16)

## AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

## FEATURES

source

1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2211141"  
 /tissue\_type="well-differentiated endometrial  
 adenocarcinoma, 7 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Utl1"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.75 kb. Life Technologies catalog #:  
 11538-014"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GAGGG 5  
 Db 10 GAGGG 14

## RESULT 34

AI564678/c

## LOCUS

## DEFINITION

tq78g03.x1 NCI CGAP Utl1 Homo sapiens CDNA clone IMAGE:2214964 3'  
 similar to TR:Q15214 Q15214 SALIVARY PROLINE-RICH PROTEIN 1  
 ; contains element MSRI repetitive element ;, mRNA sequence.

## ACCESSION

AI564678

## VERSION

AI564678.1 GI:4523135

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 16)

## AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapsb@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1719 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

## FEATURES

source

1..16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2214964"

/tissue\_type="well-differentiated endometrial  
 adenocarcinoma, 7 pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Utl1"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.75 kb. Life Technologies catalog #:  
 11538-014"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.2e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 11 GAGGG 7

## RESULT 35

AI569544/c

## LOCUS

## DEFINITION

tc28d10.x1 NCI CGAP Utl4 Homo sapiens CDNA clone IMAGE:2180371 3'  
 similar to TR:Q18444 Q18444 COSMID C34D4. ; contains MSRI.b2 MSRI  
 repetitive element ;, mRNA sequence.

## ACCESSION

AI569544

## VERSION

AI569544.1 GI:4532918

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 16)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
Insert Length: 1683 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1  
POLYA=No.

# FEATURES

Location/Qualifiers

1..16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2180371"  
/tissue\_type="serous papillary carcinoma, high grade, 2  
pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Ut4"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dr.  
Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

# ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 6 GAGGG 2

# RESULT 36

BM394080 16 bp mRNA linear EST 17-JAN-2002  
LOCUS  
DEFINITION  
50072-2-12-H02.r.1 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.  
ACCESSION  
BM394080  
VERSION  
BM394080.1 GI:18194133  
KEYWORDS  
EST.  
SOURCE  
Tetrahymena thermophila  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE  
1 (bases 1 to 16)  
Turkewitz, A.P., Karter, K.M., Jahn, C., Orlas, E., Kirk, K.E.,  
Frankel, J., and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.

# FEATURES

Location/Qualifiers

source  
1..16  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 7 GAGGG 3

RESULT 37

CF303743 16 bp mRNA linear EST 15-AUG-2003  
LOCUS  
DEFINITION  
ABF1--03-B14.g1 ABF3-overexpressing transgenic rice lambda phage  
cDNA library (ABF1) Oryza sativa (japonica cultivar-group) cDNA  
clone ABF1--03-B14, mRNA sequence.  
ACCESSION  
CF303743  
VERSION  
CF303743.1 GI:33675504  
KEYWORDS  
EST.  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzeae; Oryza.  
REFERENCE  
1 (bases 1 to 16)  
Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.  
Genomics and Genetics Institute, Greengene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Kyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

Location/Qualifiers

1..16  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABF1--03-B14"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="ABF3-overexpressing transgenic rice lambda  
phage cDNA library (ABF1)"  
/note="vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into  
lambda Uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

# ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

```

RESULT 38
CF305660
LOCUS
DEFINITION
  HDAL--01-F18.g1 OshDAC1-overexpressing transgenic rice lambda phage
  cDNA library I (HDAL) Oryza sativa (japonica cultivar-group) cDNA
  clone HDAL--01-F18, mRNA sequence.
ACCESSION
CF305660
VERSION
CF305660.1 GI:33677421
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE
Large-scale Sequencing Analysis of Rice ESTs
JOURNAL
Unpublished (2003)
COMMENT
Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
source
1..16
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39947"
/clone="HDAL--01-F18"
/tissue_type="callus"
/dev_stage="proliferated callus on 2N6 media for 2 weeks"
/lab_host="E.coli SOLR"
/clone_lib="OshDAC1-overexpressing transgenic rice lambda
phage cDNA library I (HDAL)"
/notes="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; cDNA was inserted into lambda Uni-ZAP XR vector at
5' end with EcoRI and 3' end with XhoI site. mRNA was
derived from rice Histone Deacetylase overexpression
line."
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGGG 5
Db 11111
5 GAGGG 9
RESULT 40
AJ587352/c
LOCUS
DEFINITION
  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
  268H05, genomic survey sequence.
ACCESSION
AJ587352
VERSION
AJ587352.1 GI:37936976
KEYWORDS
GSS; left border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
AUTHORS
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepointec,L., Caboche,M. and Lecharny,A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE
22363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 16)
AUTHORS
Balzerque,S.
TITLE
Direct Submision
JOURNAL
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics

```

```

program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
    source
        1..16
        /organism="Arabidopsis thaliana"
        /mol_type="genomic DNA"
        /cultivar="Wassillewskija"
        /db_xref="taxon:3702"
        /clone="266H05"
        /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
    misc_feature
        1..16
        /note="T-DNA flanking sequence
        left border"
ORIGIN
    Query Match      100.0%; Score 5; DB 9; Length 16;
    Best Local Similarity 100.0%; Pred. No. 1.2e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    Qy 1 GAGGG 5
        |||||
    Db 11 GAGGG 7

RESULT 41
AJ595160          16 bp DNA linear GSS 15-JAN-2004
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, left border, clone
412D05, genomic survey sequence.
ACCESSION
AJ595160.1 GI:37944784
VERSION
GSS; left border; T-DNA flanking sequence.
KEYWORDS
Arabidopsis thaliana (thale cress)
SOURCE
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepointec, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE
23363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 16)
Balzerque, S.
Direct Submision
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
1..16
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="412D05"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1..16
/note="T-DNA flanking sequence
left border"
misc_feature

FEATURES
    source
        1..17
        /organism="Sus scrofa"
        /mol_type="mRNA"
        /db_xref="taxon:9823"
        /clone="C0000033 K10"
        /tissue_type="placenta"
        /clone_lib="CSEQRAN09"
        /note="vector: pBluescriptII(KS+); Site_1: EcoRI; Site_2:
        NotI; Single pass sequencing. Normalised library
        constructed from pooled tissue from day 30 placentas."
ORIGIN
    Query Match      100.0%; Score 5; DB 1; Length 17;
    Best Local Similarity 100.0%; Pred. No. 1.2e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    Qy 1 GAGGG 5
        |||||
    Db 10 GAGGG 6

RESULT 43
AW246940          17 bp mRNA linear EST 07-JAN-2000
LOCUS
DEFINITION
2822481.Sprime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2822481 5',
mRNA sequence.
ACCESSION
AW246940
VERSION
AW246940.1 GI:6589933
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```



Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
 |||||  
 Db 7 GAGGG 3

RESULT 46  
 BQ789989/c  
 LOCUS  
 DEFINITION hage005ab12 Heterobasidion annosum - Scots pine infection stage (HAGE) subtraction cDNA library Pinus sylvestris/Heterobasidion annosum mixed EST library cDNA clone hage005ab12, mRNA sequence.  
 BQ789989  
 BQ789989.1 GI:22004951  
 EST.  
 Pinus sylvestris/Heterobasidion annosum mixed EST library  
 SOURCE Pinus sylvestris/Heterobasidion annosum mixed EST library  
 ORGANISM Eukaryota; mixed EST libraries.  
 REFERENCE 1 (bases 1 to 17)  
 AUTHORS Asiegbu,F.O., Nahalkova,J. and Dean,R.A.  
 TITLE Selected Expressed sequence tags of cDNA clones from the interaction of the root rot fungus (Heterobasidion annosum) with seedling roots of Scots pine (Pinus sylvestris)  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Fred O. Asiegbu  
 Dept. of Forest Mycology & Pathology  
 Swedish University of Agriculture, Box 7026,S-750 07, Uppsala, Sweden  
 Tel: +46 18 67 15 98  
 Fax: +46 18 30 92 45  
 Email: Fred.Asiegbu@mykopat.slu.se  
 Seq primer: T7 primer.  
 Location/Qualifiers  
 1..17  
 /organism="Pinus sylvestris/Heterobasidion annosum mixed EST library"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:169015"  
 /clone="hage005ab12"  
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 /clone\_lib="Heterobasidion annosum - Scots pine infection stage (HAGE) subtraction cDNA library"  
 /note="vector: pT-Adv; Site\_1: EcoRI; The subtractive hybridization cDNA library was constructed from scots pine roots infected for 6-days with mycelia of Heterobasidion annosum (FP5)."

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
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 Db 12 GAGGG 8

RESULT 47  
 AJ587432/c  
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 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 277All, genomic survey sequence.  
 AJ587432  
 AJ587432.1 GI:37937056  
 EST.  
 Arabidopsis thaliana  
 SOURCE Arabidopsis thaliana  
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1

AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.  
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
 MEDLINE 22363535  
 PUBMED 12446565  
 REFERENCE 2 (bases 1 to 17)  
 AUTHORS Balzergue,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE  
 COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment (s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobio.gen.fr).

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 /db\_xref="taxon:3702"  
 /clone="277All"  
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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
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 Db 7 GAGGG 3

RESULT 48  
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 LOCUS  
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 419A03, genomic survey sequence.  
 AJ595555  
 AJ595555.1 GI:37945183  
 VERSION GSS; left border; T-DNA flanking sequence.  
 KEYWORDS GSS; left border; T-DNA flanking sequence.  
 SOURCE Arabidopsis thaliana (thale cress)  
 ORGANISM Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1

AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.  
 TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites  
 JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
 MEDLINE 22363535  
 PUBMED 12446565  
 REFERENCE 2 (bases 1 to 17)  
 AUTHORS Balzergue,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of *Arabidopsis thaliana* plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

#### FEATURES

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Location/Qualifiers  
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left border"

#### ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
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Db 7 GAGGG 11

#### RESULT 49

AJ599163  
LOCUS AJ599163 17 bp DNA linear GSS 15-JAN-2004  
DEFINITION *Arabidopsis thaliana* T-DNA flanking sequence, left border, clone 481F12, genomic survey sequence.

ACCESSION AJ599163

VERSION AJ599163.1 GI:37948791

KEYWORDS GSS; left border; T-DNA flanking sequence.

SOURCE *Arabidopsis thaliana* (thale cress)

ORGANISM *Arabidopsis thaliana*

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; *Arabidopsis*.

#### REFERENCE

AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Derose, R., Pelletier, G., Lepointec, L., Caboche, M. and Lecharny, A.  
T-DNA integration into the *Arabidopsis* genome depends on sequences of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)  
MEDLINE 22363535  
PUBMED 12446565

REFERENCE 2 (bases 1 to 17)

AUTHORS Balzerque, S.

TITLE Direct Submission

JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue

Gaston Cremieux, 91057 Evry cedex, FRANCE  
PCR was performed on DNA from transformants of *Arabidopsis thaliana* plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).

#### FEATURES

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/cultivar="Wassillewskija"  
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/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature  
1. .17  
/note="T-DNA flanking sequence  
left border"

#### ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

#### RESULT 50

CL436788  
LOCUS CL436788 17 bp DNA linear GSS 18-MAR-2004  
DEFINITION PST3832-NL.Seq MICB1 *Mus musculus* genomic clone PST3832-NL.Seq, genomic survey sequence.

ACCESSION CL436788

VERSION CL436788.1 GI:45571937

KEYWORDS GSS.

SOURCE *Mus musculus* (house mouse)

ORGANISM *Mus musculus*

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; *Mus*.  
Hicks, G.G.

REFERENCE 1 (bases 1 to 17)

AUTHORS www.EScells.ca

TITLE Unpublished (2002)

JOURNAL Contact: Hicks GG

COMMENT Mammalian Functional Genomics Centre

Manitoba Institute of Cell Biology, University of Manitoba

ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada

Tel: 204 787 2133

Fax: 204 787 2130

Email: [hicksgg@cc.umanitoba.ca](mailto:hicksgg@cc.umanitoba.ca)

UNNeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from [http://140.193.242.7/esdb/public\\_search\\_frame.php?PST=PST3832-NL.Se](http://140.193.242.7/esdb/public_search_frame.php?PST=PST3832-NL.Se)

#### FEATURES

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/cell\_line="D3H (J1 subclone)"  
/clone\_lib="MICB1"  
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#### ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 11 GAGGG 15

Search completed: January 7, 2005, 11:00:56  
Job time : 2250.4 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 05:37:38 ; Search time 58 Seconds

(without alignments)  
61.275 Million cell updates/sec

Title: GAGGG

Perfect score: 5

Sequence: 1 gaggg 5

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 896372

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*

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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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8	5	100.0	10	1	US-08-233-608-43
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13	5	100.0	10	1	US-08-171-718-40
14	5	100.0	10	1	US-08-171-718-41
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24	5	100.0	10	2	US-08-590-571-29
25	5	100.0	10	2	US-08-485-778-42
26	5	100.0	10	2	US-08-599-654-20
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29	5	100.0	10	2	US-09-721-777-4
30	5	100.0	10	2	US-07-704-288C-5
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c 31	5	100.0	10	3	US-08-899-786-9	Sequence 9, Appl
c 32	5	100.0	10	3	US-08-520-550A-42	Sequence 42, Appl
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c 38	5	100.0	10	3	US-08-757-024-678	Sequence 678, Appl
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c 54	5	100.0	10	3	US-09-580-517-11	Sequence 11, Appl
c 55	5	100.0	10	3	US-09-062-451-102	Sequence 102, Appl
c 56	5	100.0	10	3	US-08-327-874A-8	Sequence 8, Appl
c 57	5	100.0	10	3	US-08-327-874A-8	Sequence 8, Appl
c 58	5	100.0	10	4	US-09-598-326-102	Sequence 102, Appl
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c 76	5	100.0	10	5	PCT-US94-09700-8	Sequence 8, Appl
c 77	5	100.0	10	5	PCT-US95-04712-43	Sequence 43, Appl
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c 80	5	100.0	11	1	US-08-401-512-18	Sequence 18, Appl
c 81	5	100.0	11	1	US-08-258-261B-15	Sequence 15, Appl
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c 84	5	100.0	11	1	US-08-456-837-16	Sequence 16, Appl
c 85	5	100.0	11	1	US-08-457-342-15	Sequence 15, Appl
c 86	5	100.0	11	1	US-08-457-342-16	Sequence 16, Appl
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c 90	5	100.0	11	1	US-08-357-396-12	Sequence 12, Appl
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c 399 5 100.0 14 4 US-09-904-420A-5 Sequence 5, Appli
c 400 5 100.0 14 4 US-09-688-990-1 Sequence 1, Appli
c 401 5 100.0 14 4 US-10-059-877-14 Sequence 14, Appl
c 402 5 100.0 14 4 US-10-059-877-18 Sequence 18, Appl
c 403 5 100.0 14 5 PCT-US92-06685-2 Sequence 2, Appli
c 404 5 100.0 14 6 5214136-8 Patent No. 5214136
c 405 5 100.0 14 6 5214136-11 Patent No. 5214136
c 406 5 100.0 14 6 5214136-13 Patent No. 5214136
c 407 5 100.0 14 6 5214136-16 Patent No. 5214136
c 408 5 100.0 14 6 5258288-11 Patent No. 5258288
c 409 5 100.0 14 6 5258288-12 Patent No. 5258288
c 410 5 100.0 14 6 5486603-1 Patent No. 5486603
c 411 5 100.0 14 6 5486603-2 Patent No. 5486603
c 412 5 100.0 15 1 US-08-237-233-4 Sequence 4, Appli
c 413 5 100.0 15 1 US-08-156-020-13 Sequence 13, Appl
c 414 5 100.0 15 1 US-08-105-483-273 Sequence 273, App
c 415 5 100.0 15 1 US-07-909-383-5 Sequence 5, Appli
c 416 5 100.0 15 1 US-08-170-095B-13 Sequence 13, Appl
c 417 5 100.0 15 1 US-08-170-095B-14 Sequence 14, Appl
c 418 5 100.0 15 1 US-08-050-073-364 Sequence 264, App
c 419 5 100.0 15 1 US-08-452-156A-2 Sequence 2, Appli
c 420 5 100.0 15 1 US-08-452-196A-8 Sequence 8, Appli
c 421 5 100.0 15 1 US-08-137-701-18 Sequence 18, Appl
c 422 5 100.0 15 1 US-08-182-968A-3 Sequence 3, Appli
c 423 5 100.0 15 1 US-08-182-968A-31 Sequence 31, Appl
c 424 5 100.0 15 1 US-08-182-968A-35 Sequence 35, Appl
c 425 5 100.0 15 1 US-08-182-968A-36 Sequence 36, Appl
c 426 5 100.0 15 1 US-08-182-968A-45 Sequence 45, Appl
c 427 5 100.0 15 1 US-08-182-968A-121 Sequence 121, App
c 428 5 100.0 15 1 US-08-182-968A-162 Sequence 162, App
c 429 5 100.0 15 1 US-08-182-968A-163 Sequence 163, App
c 430 5 100.0 15 1 US-08-182-968A-164 Sequence 164, App
c 431 5 100.0 15 1 US-08-182-968A-248 Sequence 248, App
c 432 5 100.0 15 1 US-08-182-968A-249 Sequence 249, App
c 433 5 100.0 15 1 US-08-182-968A-321 Sequence 321, App
c 434 5 100.0 15 1 US-08-182-968A-363 Sequence 363, App
c 435 5 100.0 15 1 US-08-182-968A-364 Sequence 364, App
c 436 5 100.0 15 1 US-08-182-968A-365 Sequence 365, App
c 437 5 100.0 15 1 US-08-182-968A-381 Sequence 381, App
c 438 5 100.0 15 1 US-08-182-968A-382 Sequence 382, App
c 439 5 100.0 15 1 US-08-182-968A-396 Sequence 396, App
c 440 5 100.0 15 1 US-08-319-492B-100 Sequence 100, App
c 441 5 100.0 15 1 US-08-319-492B-101 Sequence 101, App
c 442 5 100.0 15 1 US-08-319-492B-101 Sequence 101, App
c 443 5 100.0 15 1 US-08-319-492B-435 Sequence 435, App
c 444 5 100.0 15 1 US-08-319-492B-436 Sequence 436, App
c 445 5 100.0 15 1 US-08-319-492B-437 Sequence 437, App
c 446 5 100.0 15 1 US-08-434-503-50 Sequence 50, Appli
c 447 5 100.0 15 1 US-08-241-372-8 Sequence 8, Appli
c 448 5 100.0 15 1 US-08-241-372-9 Sequence 9, Appli
c 449 5 100.0 15 1 US-08-381-097A-20 Sequence 20, Appl
c 450 5 100.0 15 1 US-08-373-124A-87 Sequence 87, Appl
c 451 5 100.0 15 1 US-08-291-932A-10 Sequence 10, Appl
c 452 5 100.0 15 1 US-08-291-932A-11 Sequence 11, Appl
c 453 5 100.0 15 1 US-08-291-932A-12 Sequence 12, Appl
c 454 5 100.0 15 1 US-08-291-932A-13 Sequence 13, Appl
c 455 5 100.0 15 1 US-08-291-932A-14 Sequence 14, Appl
c 456 5 100.0 15 1 US-08-291-932A-15 Sequence 15, Appl
c 457 5 100.0 15 1 US-08-291-932A-32 Sequence 32, Appl
c 458 5 100.0 15 1 US-08-291-932A-88 Sequence 88, Appl
c 459 5 100.0 15 1 US-08-291-932A-92 Sequence 92, Appl
c 460 5 100.0 15 1 US-08-291-932A-123 Sequence 123, App
c 461 5 100.0 15 1 US-08-291-932A-152 Sequence 152, App
c 462 5 100.0 15 1 US-08-291-932A-188 Sequence 188, App
c 463 5 100.0 15 1 US-08-291-932A-199 Sequence 199, App
c 464 5 100.0 15 1 US-08-291-932A-200 Sequence 200, App
c 465 5 100.0 15 1 US-08-291-932A-201 Sequence 201, App
c 466 5 100.0 15 1 US-08-291-932A-202 Sequence 202, App
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c 466 5 100.0 15 1 US-08-291-932A-221 Sequence 221, App
c 467 5 100.0 15 1 US-08-291-932A-222 Sequence 222, App
c 468 5 100.0 15 1 US-08-291-932A-242 Sequence 242, App
c 469 5 100.0 15 1 US-08-291-932A-296 Sequence 296, App
c 470 5 100.0 15 1 US-08-291-932A-312 Sequence 312, App
c 471 5 100.0 15 1 US-08-291-932A-347 Sequence 347, App
c 472 5 100.0 15 1 US-08-291-932A-357 Sequence 357, App
c 473 5 100.0 15 1 US-08-291-932A-358 Sequence 358, App
c 474 5 100.0 15 1 US-08-386-579-15 Sequence 15, Appl
c 475 5 100.0 15 1 US-08-396-866-13 Sequence 13, Appl
c 476 5 100.0 15 1 US-08-396-866-14 Sequence 14, Appl
c 477 5 100.0 15 1 US-08-580-242-5 Sequence 5, Appli
c 478 5 100.0 15 1 US-08-580-242-9 Sequence 9, Appli
c 479 5 100.0 15 1 US-08-462-305-10 Sequence 10, Appl
c 480 5 100.0 15 1 US-08-462-305-41 Sequence 41, Appl
c 481 5 100.0 15 1 US-08-462-305-42 Sequence 42, Appl
c 482 5 100.0 15 1 US-08-363-240A-117 Sequence 117, App
c 483 5 100.0 15 1 US-08-363-240A-118 Sequence 118, App
c 484 5 100.0 15 1 US-08-363-240A-118 Sequence 118, App
c 485 5 100.0 15 1 US-08-363-240A-215 Sequence 215, App
c 486 5 100.0 15 1 US-08-363-240A-523 Sequence 523, App
c 487 5 100.0 15 1 US-08-363-240A-644 Sequence 644, App
c 488 5 100.0 15 1 US-08-363-240A-645 Sequence 645, App
c 489 5 100.0 15 1 US-08-363-240A-646 Sequence 646, App
c 490 5 100.0 15 1 US-08-363-240A-736 Sequence 736, App
c 491 5 100.0 15 1 US-08-651-835A-2 Sequence 2, Appli
c 492 5 100.0 15 1 US-08-686-116A-19 Sequence 19, Appl
c 493 5 100.0 15 1 US-08-686-116A-20 Sequence 20, Appl
c 494 5 100.0 15 1 US-08-686-116A-23 Sequence 23, Appl
c 495 5 100.0 15 1 US-08-686-116A-24 Sequence 24, Appl
c 496 5 100.0 15 1 US-08-685-484-19 Sequence 19, Appl
c 497 5 100.0 15 1 US-08-685-484-20 Sequence 20, Appl
c 498 5 100.0 15 1 US-08-685-484-23 Sequence 23, Appl
c 499 5 100.0 15 1 US-08-685-484-24 Sequence 24, Appl
c 500 5 100.0 15 1 US-08-847-108-19 Sequence 19, Appl
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## ALIGNMENTS

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RESULT 1
US-09-263-790-24
; Sequence 24, Application US/09263790
; Patent No. Ppl2997
; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: OPT 04 Primer - Used to develop the unique RAPD profiles of the
; OTHER INFORMATION: plant Jal Pallavi
US-09-263-790-24
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Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 1 GAGGG 5
Db 5 GAGGG 9
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RESULT 2
US-09-721-777-4
; Sequence 4, Application US/09721777
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; Patent No. PPI3279  
; GENERAL INFORMATION:  
; APPLICANT: Khanuja, Suman Preet Singh  
; APPLICANT: Kumar, Sushil  
; APPLICANT: Shasany, Ajit Kumar  
; APPLICANT: Dhawan, Sunita  
; APPLICANT: Darokar, Mahendra Pandurang  
; APPLICANT: Nagvi, Ali Arif  
; APPLICANT: Dhawan, Om Parkash  
; APPLICANT: Singh, Anil Kumar  
; APPLICANT: Patra, Nirmal Kumar  
; APPLICANT: Bahl, Janak Raj  
; APPLICANT: Bansal, Ram Prakash  
; TITLE OF INVENTION: Mint Plant Named Saksham  
; FILE REFERENCE: 033166-002  
; CURRENT APPLICATION NUMBER: US/09/721,777  
; CURRENT FILING DATE: 2000-11-27  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: OPT primer  
US-09-721-777-4

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 5 GAGGG 9

RESULT 3  
US-07-704-288C-5/c  
; Sequence 5, Application US/07704288C  
; Patent No. 5399680  
; GENERAL INFORMATION:  
; APPLICANT: LAMB, CHRISTOPHER J.  
; APPLICANT: ZHU, QUN  
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY  
; TITLE OF INVENTION: ELEMENTS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER, BRUGGEMANN & CLARK  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: United States  
; ZIP: 90071-2921  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/704,288C  
; FILING DATE: 22-MAY-1991  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P31 8899  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 546-4737  
; TELEFAX: (619) 546-9392  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs

; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
US-07-704-288C-5

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 5 GAGGG 1

RESULT 4  
US-07-963-723A-3/c  
; Sequence 3, Application US/07963723A  
; Patent No. 5494794  
; GENERAL INFORMATION:  
; APPLICANT: Wallace, Douglas C.  
; TITLE OF INVENTION: Detection of Mitochondrial DNA Mutations  
; TITLE OF INVENTION: Associated with Alzheimer's Disease and Parkinson's  
; TITLE OF INVENTION: Disease  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Needle & Rosenberg, P.C.  
; STREET: 133 Carnegie Way, N.W., Suite 400  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: U.S.A.  
; ZIP: 30301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/963,723A  
; FILING DATE: 19921020  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perryman, David G.  
; REGISTRATION NUMBER: 33,438  
; REFERENCE/DOCKET NUMBER: 0510.027  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 688-0770  
; TELEFAX: (404) 688-9880  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-07-963-723A-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 7 GAGGG 3

RESULT 5  
US-08-049-283A-28/c  
; Sequence 28, Application US/08049283A  
; Patent No. 5502176  
; GENERAL INFORMATION:  
; APPLICANT: Tenen, Daniel G.  
; APPLICANT: Pahl, Heike L.

;; APPLICANT: Burn, Timothy C.  
;; TITLE OF INVENTION: Cell Specific Promoter and Uses Thereof  
;; NUMBER OF SEQUENCES: 34  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
;; STREET: Two Militia Drive  
;; CITY: Lexington  
;; STATE: Massachusetts  
;; COUNTRY: USA  
;; ZIP: 02173  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/049,283A  
;; FILING DATE: 14-APR-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/020,465  
;; FILING DATE: 19-FEB-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 07/837,776  
;; FILING DATE: 13-FEB-1992  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Brook, David E.  
;; REGISTRATION NUMBER: 22,592  
;; REFERENCE/DOCKET NUMBER: BIH91-03'A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (617) 861-6240  
;; TELEFAX: (617) 861-9540  
;; INFORMATION FOR SEQ ID NO: 28:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-049-283A-28  
  
Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGGG 5  
Db 9 GAGGG 5

RESULT 6  
US-08-308-894-6/c  
; Sequence 6, Application US/08308894  
; Patent No. 5571672  
; GENERAL INFORMATION:  
; APPLICANT: Slavicek, James M.  
; APPLICANT: Garner, Karen J.  
; APPLICANT: Schreiber, David E.  
; TITLE OF INVENTION: GYPSY MOTH GENOTYPE ASSAY  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: USDA - Forest Products Laboratory  
; STREET: One Gifford Pinchot Drive  
; CITY: Madison  
; STATE: WI  
; COUNTRY: U.S.A.  
; ZIP: 53705-2398  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/308,894  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Stockhausen, Janet I.  
;; REGISTRATION NUMBER: 34,256  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (608) 231-9502  
;; TELEFAX: (608) 231-9508  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: oligonucleotide  
US-08-308-894-6  
  
Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGGG 5  
Db 8 GAGGG 4

RESULT 7  
US-08-330-123A-11/c  
; Sequence 11, Application US/08330123A  
; Patent No. 5583016  
; GENERAL INFORMATION:  
; APPLICANT: VILLEPONTTEAU, Bryant  
; APPLICANT: FENG, Junli  
; APPLICANT: FUNK, Walter  
; APPLICANT: ANDREWS, William H.  
; TITLE OF INVENTION: HUMAN TELOMERASE  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,123A  
; FILING DATE: 27-OCT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 15389-000810  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA

US-08-330-123A-11

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 9 GAGGG 5

## RESULT 8

US-08-233-608-43/c

; Sequence 43, Application US/08233608

; Patent No. 5585238

; GENERAL INFORMATION:

; APPLICANT: Ligon, James M

; APPLICANT: Beck, James J

; TITLE OF INVENTION: Detection of Fungal Pathogens Using the

; TITLE OF INVENTION: Polymerase Chain Reaction

; NUMBER OF SEQUENCES: 49

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ciba-Geigy Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: NY

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/233,608

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Spruill, W. Murray

; REGISTRATION NUMBER: 32,943

; REFERENCE/DOCKET NUMBER: CGC 1739

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-541-8615

; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: Other nucleic acid

; DESCRIPTION: Oligonucleotide primer OPE-6

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-08-233-608-43

Query Match

Best Local Similarity 100.0%; Score 5; DB 1; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 10 GAGGG 6

## RESULT 9

US-08-210-222-34/c

; Sequence 34, Application US/08210222

; Patent No. 5599917

; GENERAL INFORMATION:

; APPLICANT: Coppola, George R.

; APPLICANT: Beutel, Bruce A.

; APPLICANT: Bertelsen, Arthur H.

; TITLE OF INVENTION: Inhibition of Interferon- with Oligonucleotides  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carella, Byrne, Bain, Gilfillan,

; ADDRESSEE: Cecchi, Stewart &amp; Olstein

; STREET: 6 Becker Farm Road

; CITY: Roseland

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch diskette

; COMPUTER: IBM

; OPERATING SYSTEM: MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/210,222

; FILING DATE: Unassigned

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Herron, Charles J.

; REGISTRATION NUMBER: 28,019

; REFERENCE/DOCKET NUMBER: 23550-114

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201-994-1700

; TELEFAX: 201-994-1744

; INFORMATION FOR SEQ ID NO: 34:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 BASES

; TYPE: NUCLEIC ACID

; STRANDEDNESS: SINGLE

; TOPOLOGY: LINEAR

; HYPOTHETICAL: NO

US-08-210-222-34

Query Match

Best Local Similarity 100.0%; Score 5; DB 1; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 9 GAGGG 5

## RESULT 10

US-07-971-978-18/c

; Sequence 18, Application US/07971978

; Patent No. 5614617

; GENERAL INFORMATION:

; APPLICANT: Cook and Sanghvi

; TITLE OF INVENTION: Nuclease Resistant, Pyrimidine

; TITLE OF INVENTION: Modified Oligonucleotides that Detect and Modulate

; TITLE OF INVENTION: Gene Expression

; NUMBER OF SEQUENCES: 65

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and

; ADDRESSEE: No. 5614617ris

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WordPerfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/971,978

; FILING DATE: February 18, 1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/558,806

;  
; FILING DATE: July 27, 1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Joseph Lucci  
; REGISTRATION NUMBER: 33,307  
; REFERENCE/DOCKET NUMBER: ISIS-0333  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 3  
; OTHER INFORMATION: 6-aza-thymidine substitution  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 4  
; OTHER INFORMATION: 6-aza-thymidine substitution  
; FEATURE:  
; NAME/KEY: Modified-site  
; LOCATION: 9  
; OTHER INFORMATION: 6-aza-thymidine substitution  
; US-07-971-978-18  
  
Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;  
  
Qy 1 GAGGG 5  
Db 10 GAGGG 6  
  
RESULT 11  
US-08-379-259-5/c  
; Sequence 5, Application US/08379259  
; Patent No. 5695939  
; GENERAL INFORMATION:  
; APPLICANT: LAMB, CHRISTOPHER J.  
; APPLICANT: ZHU, QUN  
; TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT  
; TITLE OF INVENTION: DEFENSE REGULATORY  
; TITLE OF INVENTION: ELEMENTS  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK  
; STREET: 444 South Flower Street, Suite 2000  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: United States  
; ZIP: 90071-2921  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/379,259  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/704,288  
; FILING DATE: 22-MAY-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Reiter, Stephen E.  
; REGISTRATION NUMBER: 31,192  
; REFERENCE/DOCKET NUMBER: P31 8899  
; TELECOMMUNICATION INFORMATION:

;  
; TELEPHONE: (619) 546-4737  
; TELEFAX: (619) 546-9392  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; MOLECULE TYPE: DNA (genomic)  
; US-08-379-259-5  
  
Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;  
  
Qy 1 GAGGG 5  
Db 5 GAGGG 1  
  
RESULT 12  
US-08-171-718-38/c  
; Sequence 38, Application US/08171718  
; Patent No. 5707863  
; GENERAL INFORMATION:  
; APPLICANT: Trofatter, James A.  
; APPLICANT: MacCollin, Mia M.  
; APPLICANT: Guseilla, James F.  
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/171,718  
; FILING DATE: 22-DEC-1993  
; CLASSIFICATION: 436  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/108,808  
; FILING DATE: 19-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/022,034  
; FILING DATE: 25-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/026,063  
; FILING DATE: 04-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Anne  
; REGISTRATION NUMBER: 36,463  
; REFERENCE/DOCKET NUMBER: 0609.3850003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-171-718-38  
  
Query Match 100.0%; Score 5; DB 1; Length 10;



Best Local Similarity 100.0%; Pred. No. 2.6e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
 Db 6 GAGGG 2

# RESULT 13

US-08-171-718-40/c  
 ; Sequence 40, Application US/08171718  
 ; Patent No. 5707863  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Trofetter, James A.  
 ; APPLICANT: Maccollin, Mia M.  
 ; APPLICANT: Gusella, James F.  
 ; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
 ; TITLE OF INVENTION: Thereof  
 ; NUMBER OF SEQUENCES: 120  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
 ; STREET: 1100 New York Avenue, N.W., Suite 600  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/171,718  
 ; FILING DATE: 22-DEC-1993  
 ; CLASSIFICATION: 436  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/108,808  
 ; FILING DATE: 19-AUG-1993  
 ; APPLICATION NUMBER: US 08/022,034  
 ; FILING DATE: 25-FEB-1993  
 ; APPLICATION NUMBER: US 08/026,063  
 ; FILING DATE: 04-MAR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Brown, Anne  
 ; REGISTRATION NUMBER: 36,463  
 ; REFERENCE/DOCKET NUMBER: 0609.3850003  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 371-2600  
 ; TELEFAX: (202) 371-2540  
 ; INFORMATION FOR SEQ ID NO: 40:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-171-718-40

Query Match 100.0%; Score 5; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Mismatches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
 Db 7 GAGGG 3

# RESULT 14

US-08-171-718-41  
 ; Sequence 41, Application US/08171718  
 ; Patent No. 5707863  
 ; GENERAL INFORMATION:

; APPLICANT: Trofetter, James A.  
 ; APPLICANT: Maccollin, Mia M.  
 ; APPLICANT: Gusella, James F.  
 ; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
 ; TITLE OF INVENTION: Thereof  
 ; NUMBER OF SEQUENCES: 120  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
 ; STREET: 1100 New York Avenue, N.W., Suite 600  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20005-3934  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/171,718  
 ; FILING DATE: 22-DEC-1993  
 ; CLASSIFICATION: 436  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/108,808  
 ; FILING DATE: 19-AUG-1993  
 ; APPLICATION NUMBER: US 08/022,034  
 ; FILING DATE: 25-FEB-1993  
 ; APPLICATION NUMBER: US 08/026,063  
 ; FILING DATE: 04-MAR-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Brown, Anne  
 ; REGISTRATION NUMBER: 36,463  
 ; REFERENCE/DOCKET NUMBER: 0609.3850003  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202) 371-2600  
 ; TELEFAX: (202) 371-2540  
 ; INFORMATION FOR SEQ ID NO: 41:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-171-718-41

Query Match 100.0%; Score 5; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
 Mismatches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
 Db 3 GAGGG 7

RESULT 15  
 US-08-482-115B-11/c  
 ; Sequence 11, Application US/08482115B  
 ; Patent No. 5776679  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Villeponteau, Bryant  
 ; APPLICANT: Feng, Junli  
 ; APPLICANT: Funk, Walter  
 ; APPLICANT: Andrews, William H.  
 ; TITLE OF INVENTION: Assays for the RNA Component of Human  
 ; TITLE OF INVENTION: Telomerase  
 ; NUMBER OF SEQUENCES: 40  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA

ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,115B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Storella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000830US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-482-115B-11

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 9 GAGGG 5

RESULT 16  
US-08-887-480-43/c  
Sequence 43, Application US/08887480  
Patent No. 581453  
GENERAL INFORMATION:  
APPLICANT: Beck, James J  
TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
OPERATING SYSTEM: Polymerase Chain Reaction  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 581453artis Corporation  
STREET: 520 White Plains Road  
CITY: Tarrytown  
STATE: NY  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/887,480  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/722,187  
FILING DATE: 15-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-541-8587  
TELEFAX: 919-541-8689  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: Oligonucleotide primer OPE-6  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-887-480-43

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 10 GAGGG 6

RESULT 17  
US-08-465-590-35  
Sequence 35, Application US/08465590  
Patent No. 5824770  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, Suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Ascii (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,590  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/238,212  
FILING DATE: 02-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/121,438  
FILING DATE: 14-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/946,233  
FILING DATE: 14-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,695  
REFERENCE/DOCKET NUMBER: MFG-006C2DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-465-590-35

Query Match 100.0%; Score 5; DB 1; Length 10;

```
Best Local Similarity 100.0%; Pred. No. 2.6e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 GAGGG 5
Db 1 GAGGG 5

RESULT 18
US-08-480-994-20/c
; Sequence 20, Application US/08480994
; Patent No. 5834248
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,994
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-033
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-08-480-994-20

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 GAGGG 5
Db 8 GAGGG 4

RESULT 19
US-08-660-678A-11/c
; Sequence 11, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
```

```
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-660-678A-11

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 0;

Qy 1 GAGGG 5
Db 9 GAGGG 5

RESULT 20
US-08-616-844-20/c
; Sequence 20, Application US/08616844
; Patent No. 5849578
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/616,844  
FILING DATE: 15-MAR-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-053  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic oligonucleotide"  
HYPOTHETICAL: NO  
US-08-616-844-20

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 8 GAGGG 4

RESULT 21  
US-08-173-489C-170/c  
Sequence 170, Application US/08173489C  
Patent No. 5861244  
GENERAL INFORMATION:  
APPLICANT: WANG, C. -G.  
APPLICANT: HEPBURN, A. G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10021.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 246-8959  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 199:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
DESCRIPTION: hepatitis B virus adr isolate,  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 170:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 bases  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: third strand derived from Hepatitis B  
DESCRIPTION: isolate ayw sequence region in Seq ID No. 5861344169  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
PUBLICATION INFORMATION:  
RELEVANT RESIDUES IN SEQ ID NO: 170 :FROM 1 TO 10  
US-08-173-489C-170  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 7 GAGGG 3

RESULT 22  
US-08-173-489C-199/c  
Sequence 199, Application US/08173489C  
Patent No. 5861244  
GENERAL INFORMATION:  
APPLICANT: WANG, C. -G.  
APPLICANT: HEPBURN, A. G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10021.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 199:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
DESCRIPTION: hepatitis B virus adr isolate,  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6

ANTI-SENSE: no  
ORIGINAL SOURCE: Hepatitis B virus  
INDIVIDUAL ISOLATE: adr  
PUBLICATION INFORMATION:  
AUTHORS: Fujiyama, A, Miyanochara, A, No. 5861244aki, C,  
Toneyama, T, Ohromo, N, Matsubara, K.  
TITLE: Cloning and structural  
analysis of Hepatitis B virus DNAs subtype adr  
JOURNAL: Nucleic Acids Research  
VOLUME: 11  
PAGES: 4601-4610  
DATE: 1983  
RELEVANT RESIDUES IN SEQ ID NO: 199 :FROM 1 TO 10  
US-08-173-489C-199

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
DB 8 GAGGG 4

RESULT 23  
US-08-173-489C-288/c  
Sequence 288, Application US/08173489C  
Patent No. 5861244  
GENERAL INFORMATION:  
APPLICANT: WANG, C. -G.  
APPLICANT: HEPBURN, A. G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10021

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 288:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 bases  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: third strand derived from C.  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
PUBLICATION INFORMATION:

US-08-173-489C-288  
Sequence 288, Application US/08173489C  
Patent No. 5861244  
GENERAL INFORMATION:  
APPLICANT: WANG, C. -G.  
APPLICANT: HEPBURN, A. G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK  
COUNTRY: USA  
ZIP: 10021

RELEVANT RESIDUES IN SEQ ID NO: 288 :FROM 1 TO 10  
US-08-173-489C-288

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
DB 9 GAGGG 5

RESULT 24  
US-08-590-571-29  
Sequence 29, Application US/08590571  
Patent No. 5861246  
GENERAL INFORMATION:  
APPLICANT: Sherman Weissman and Girish N. Mallur  
TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,571  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-590-571-29

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGGG 5  
DB 5 GAGGG 9

RESULT 25  
US-08-485-778-42/c  
Sequence 42, Application US/08485778  
Patent No. 5876979  
GENERAL INFORMATION:  
APPLICANT: Andrews, William H.  
APPLICANT: Avilion, Ariel Athena  
APPLICANT: Feng, Junli  
APPLICANT: Funk, Walter  
APPLICANT: Greider, Carol  
APPLICANT: Maruenda, Maria Antonia Blasco  
APPLICANT: Villeponteau, Bryant

;; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE  
;; NUMBER OF SEQUENCES: 45  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
;; STREET: Two Militia Drive  
;; CITY: Lexington  
;; STATE: MA  
;; COUNTRY: US  
;; ZIP: 02173  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/485,778  
;; FILING DATE: 07-JE-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/387,524  
;; FILING DATE: 13-FEB-1995  
;; APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/330,123  
;; FILING DATE: 27-OCT-1994  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/272,102  
;; FILING DATE: 07-JUL-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Granahan, Patricia  
;; REGISTRATION NUMBER: 32,227  
;; REFERENCE/DOCKET NUMBER: CSHL94-05A4  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 617-861-6240  
;; TELEFAX: 617-861-9540  
;; INFORMATION FOR SEQ ID NO: 42:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-485-778-42

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||  
Db 9 GAGGG 5

RESULT 26  
US-08-599-654-20/c  
; Sequence 20, Application US/08599654  
; Patent No. 5882925  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/599,654  
;; FILING DATE: 09-FEB-1996  
;; CLASSIFICATION: 800  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/485,573  
;; FILING DATE: 07-JUN-1995  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/386,844  
;; FILING DATE: 10-FEB-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CORUZZI, LAURA A  
;; REGISTRATION NUMBER: 30,742  
;; REFERENCE/DOCKET NUMBER: 7853-041  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
;; DESCRIPTION: /desc = "synthetic oligonucleotide"  
;; HYPOTHETICAL: NO  
;; US-08-599-654-20

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||  
Db 8 GAGGG 4

RESULT 27  
US-08-828-009-4  
; Sequence 4, Application US/08828009  
; Patent No. 5914394  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Hong  
; APPLICANT: Friemer, Nelson, B.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; THE DIAGNOSIS AND TREATMENT OF NEUROPSYCHIATRIC  
; DISORDERS  
; TITLE OF INVENTION: DISORDERS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/828,009  
; FILING DATE: 27-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-070  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-790-9090



```
;
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,573
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; US-08-485-573-20

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 8 GAGGG 4

RESULT 31
US-08-899-786-9
; Sequence 9, Application US/08899786
; Patent No. 6001572
; GENERAL INFORMATION:
; APPLICANT: Toothman, Penelope
; TITLE OF INVENTION: Method of Identifying Aloe Using
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3 1/2 diskette, 1.44 MB
; COMPUTER: IBM pc compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/899,786
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/022,611
```

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;
; FILING DATE: 26-JULY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: UNI.07
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; US-08-899-786-9

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 2 GAGGG 6

RESULT 32
US-08-520-550A-42/c
; Sequence 42, Application US/08520550A
; Patent No. 6013468
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel A.
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria A. B.
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA Component of Telomerase
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/520,550A
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A3B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 42:
```



SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-520-550A-42

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 9 GAGGG 5

RESULT 33  
US-08-944-868A-20/c  
Sequence 20, Application US/08944868A  
Patent No. 6018025  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944:868A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/599,654  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-041  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic oligonucleotide"  
HYPOTHETICAL: NO  
US-08-944-868A-20

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 8 GAGGG 4

RESULT 34  
US-08-944-423A-20/c  
Sequence 20, Application US/08944423A  
Patent No. 6020463  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: WINDOWS 95  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/944,423A  
FILING DATE: 06-OCT-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/599,654  
FILING DATE: 09-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: JUN-07-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: CORUZZI, LAURA A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "synthetic oligonucleotide"  
HYPOTHETICAL: NO  
US-08-944-423A-20

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 8 GAGGG 4

RESULT 35  
US-08-757-024-609  
Sequence 609, Application US/08757024  
Patent No. 6025339  
GENERAL INFORMATION:  
APPLICANT: Nyce, Jonathan W.  
TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
NUMBER OF SEQUENCES: 952  
CORRESPONDENCE ADDRESS:

```
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 609:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-024-609

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 6 GAGGG 10
|||||

RESULT 36
US-08-757-024-633
; Sequence 633, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
```

```
; INFORMATION FOR SEQ ID NO: 633:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-024-633

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 5 GAGGG 9
|||||

RESULT 37
US-08-757-024-656
; Sequence 656, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA
; NUMBER OF SEQUENCES: 952
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON
; STREET: P.O. Drawer 34009
; CITY: Charlotte
; STATE: No. 6025339th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/757,024
; FILING DATE: 26-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5218-41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 656:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-757-024-656

Query Match 100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.6e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 4 GAGGG 8
|||||

RESULT 38
US-08-757-024-678
; Sequence 678, Application US/08757024
; Patent No. 6025339
; GENERAL INFORMATION:
```

; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,024  
; FILING DATE: 26-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5218-41  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 678:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-757-024-678

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 3 GAGGG 7

RESULT 39  
US-08-757-024-699  
; Sequence 699, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,024  
; FILING DATE: 26-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5218-41

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 699:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-757-024-699

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 2 GAGGG 6

RESULT 40  
US-08-757-024-719  
; Sequence 719, Application US/08757024  
; Patent No. 6025339  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: METHOD OF TREATMENT FOR ASTHMA  
; NUMBER OF SEQUENCES: 952  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BELL, SELTZER, PARK & GIBSON  
; STREET: P.O. Drawer 34009  
; CITY: Charlotte  
; STATE: No. 6025339th Carolina  
; COUNTRY: USA  
; ZIP: 28234  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/757,024  
; FILING DATE: 26-NOV-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Sibley, Kenneth D.  
; REGISTRATION NUMBER: 31,665  
; REFERENCE/DOCKET NUMBER: 5218-41  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-881-3140  
; TELEFAX: 919-881-3175  
; TELEX: 575102  
; INFORMATION FOR SEQ ID NO: 719:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-757-024-719

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 1 GAGGG 5

RESULT 41

US-08-925-743-20/c  
; Sequence 20, Application US/08925743  
; Patent No. 6054558  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/925,743  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/485,573  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
US-08-925-743-20  
  
Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGGG 5  
Db 8 GAGGG 4  
  
RESULT 42  
US-08-925-743-20/c  
; Sequence 1, Application US/09075215A  
; Patent No. 6054571  
; GENERAL INFORMATION:  
; APPLICANT: JOLICOEUR, Paul  
; APPLICANT: BALSALOBRE, Aurelio  
; TITLE OF INVENTION: dft-A GENE, DIAGNOSTIC AND  
; THERAPEUTIC USES THEREOF  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swabey Ogilvy Renault  
; STREET: Suite 1600, 1981 McGill College  
; CITY: Montreal  
; STATE: QC  
; COUNTRY: Canada  
; ZIP: H3A 2Y3  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/075,215A  
FILING DATE: 11-MAY-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Ctt, France  
REGISTRATION NUMBER: 37,037  
REFERENCE/DOCKET NUMBER: 13497-4"US" FC/ld  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 514-845-7126  
TELEFAX: 514-288-8389  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-09-075-215A-1  
  
Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGGG 5  
Db 3 GAGGG 7  
  
RESULT 43  
US-08-998-443-11/c  
; Sequence 11, Application US/08998443  
; Patent No. 6054575  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 30  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/998,443  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/660,678  
; FILING DATE: 05-JUN-1996  
; APPLICATION NUMBER: US 08/330,123  
; FILING DATE: 27-OCT-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/272,102  
; FILING DATE: 07-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Storella, John R.

REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000811US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-998-443-11

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 9 GAGGG 5

RESULT 44  
US-08-906-691-19  
Sequence 19, Application US/08906691  
Patent No. 6066452  
GENERAL INFORMATION:  
APPLICANT: Weissman, Sherman M.  
APPLICANT: Nallur, Girish N.  
APPLICANT: Kulkarni, Prakash  
TITLE OF INVENTION: MULTIPLEX SELECTION TECHNIQUE FOR  
IDENTIFYING PROTEIN-BINDING SITES FOR DNA-BINDING PROTEINS  
NUMBER OF SEQUENCES: 50  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 981094  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/906,691  
FILING DATE: 31-JUL-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 6066452tenburg Ph.D., Carol  
REGISTRATION NUMBER: 39,317  
REFERENCE/DOCKET NUMBER: 390036.403C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-906-691-19

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 5 GAGGG 9

RESULT 45  
US-08-478-087-38/c  
Sequence 38, Application US/08478087  
Patent No. 6077685  
GENERAL INFORMATION:  
APPLICANT: Trofatter, James A.  
APPLICANT: Maccollin, Mia M.  
APPLICANT: Gusella, James F.  
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
TITLE OF INVENTION: Thereof  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/478,087  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/171,718  
FILING DATE: 22-DEC-1993  
APPLICATION NUMBER: US 08/108,808  
FILING DATE: 19-AUG-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/022,034  
FILING DATE: 25-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/026,063  
FILING DATE: 04-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Brown, Anne  
REGISTRATION NUMBER: 36,463  
REFERENCE/DOCKET NUMBER: 0609.3850003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-478-087-38

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
|||||  
Db 6 GAGGG 2

RESULT 46  
US-08-478-087-40/c  
Sequence 40, Application US/08478087  
Patent No. 6077685  
GENERAL INFORMATION:  
APPLICANT: Trofatter, James A.  
APPLICANT: Maccollin, Mia M.  
APPLICANT: Gusella, James F.  
TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses

;  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,087  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/171,718  
; FILING DATE: 22-DEC-1993  
; APPLICATION NUMBER: US 08/108,808  
; FILING DATE: 19-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/022,034  
; FILING DATE: 25-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/026,063  
; FILING DATE: 04-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Anne  
; REGISTRATION NUMBER: 36,463  
; REFERENCE/DOCKET NUMBER: 0609.3850003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-478-087-40

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGGG 5  
|||  
Db 7 GAGGG 3

RESULT 47  
US-08-478-087-41  
; Sequence 41, Application US/08478087  
; Patent No. 6077685  
; GENERAL INFORMATION:  
; APPLICANT: Trofatter, James A.  
; APPLICANT: MacCollin, Mia M.  
; APPLICANT: Gusella, James F.  
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses  
; TITLE OF INVENTION: Thereof  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3934  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

;  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,087  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/171,718  
; FILING DATE: 22-DEC-1993  
; APPLICATION NUMBER: US 08/108,808  
; FILING DATE: 19-AUG-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/022,034  
; FILING DATE: 25-FEB-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/026,063  
; FILING DATE: 04-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Brown, Anne  
; REGISTRATION NUMBER: 36,463  
; REFERENCE/DOCKET NUMBER: 0609.3850003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-478-087-41

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GAGGG 5  
|||  
Db 3 GAGGG 7

RESULT 48  
US-08-944-496-20/c  
; Sequence 20, Application US/08944496  
; Patent No. 6124433  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/944,496  
; FILING DATE: 06-OCT-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/599,654  
; FILING DATE: 09-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/386,844  
;; FILING DATE: 10-FEB-1995  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CORUZZI, LAURA A  
;; REGISTRATION NUMBER: 30,742  
;; REFERENCE/DOCKET NUMBER: 7853-104  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 790-9090  
;; TELEFAX: (212) 869-8864  
;; TELEX: 66141 PENNIE  
;; INFORMATION FOR SEQ ID NO: 20:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: other nucleic acid  
;; DESCRIPTION: /desc = "synthetic oligonucleotide"  
;; HYPOTHETICAL: NO  
US-08-944-496-20

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.6e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 8 GAGGG 4

RESULT 49  
US-08-991-789A-102  
; Sequence 102, Application US/08991789A  
; Patent No. 6225054  
; GENERAL INFORMATION:  
; APPLICANT: Fridakis, Tony N.  
; Smith, John M.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF BREAST CANCER  
; NUMBER OF SEQUENCES: 292  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seed IP Law Group  
; STREET: 701 Fifth Avenue, Suite 6300  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION NUMBER: US/08/991,789A  
; FILING DATE: 11-Dec-1997  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Potter, Jane E. R.  
; REGISTRATION NUMBER: 33,332  
; REFERENCE/DOCKET NUMBER: 210121.419C3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206) 622-4900  
; TELEFAX: (206) 682-6031  
; INFORMATION FOR SEQ ID NO: 102:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 102:

US-08-991-789A-102

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 3 GAGGG 7

RESULT 50  
US-08-925-767-20/C  
; Sequence 20, Application US/08925767  
; Patent No. 6225084  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/925,767  
; FILING DATE: 09-SEPT-1997  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-097  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
US-08-925-767-20

Query Match 100.0%; Score 5; DB 3; Length 10;  
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Search completed: January 7, 2005, 11:05:35  
Job time : 63 secs

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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 06:51:47 ; Search time 270.2 Seconds  
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Title: GAGGG

Perfect score: 5

Sequence: 1 gaggg 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 2912722

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 128	5	100.0	11	9	US-09-772-719-81	Sequence 81, Appl	c 201
c 129	5	100.0	11	9	US-09-263-959-505	Sequence 505, App	c 202
c 130	5	100.0	11	9	US-09-263-959-684	Sequence 684, App	c 203
c 131	5	100.0	11	9	US-09-263-959-707	Sequence 707, App	c 204
c 132	5	100.0	11	9	US-09-263-959-737	Sequence 737, App	c 205
c 133	5	100.0	11	9	US-09-263-959-906	Sequence 906, App	c 206
c 134	5	100.0	11	10	US-09-918-715-30	Sequence 30, Appl	c 207
c 135	5	100.0	11	10	US-09-918-715-35	Sequence 35, Appl	c 208
c 136	5	100.0	11	10	US-09-918-715-60	Sequence 60, Appl	c 209
c 137	5	100.0	11	10	US-09-918-715-78	Sequence 78, Appl	c 210
c 138	5	100.0	11	10	US-09-918-715-144	Sequence 144, App	c 211
c 139	5	100.0	11	10	US-09-974-143A-10	Sequence 10, Appl	c 212
c 140	5	100.0	11	10	US-09-918-715-67	Sequence 67, Appl	c 213
c 141	5	100.0	11	10	US-09-249-155-67	Sequence 67, Appl	c 214
c 142	5	100.0	11	10	US-09-249-155-92	Sequence 92, Appl	c 215
c 143	5	100.0	11	10	US-09-249-155-116	Sequence 116, App	c 216
c 144	5	100.0	11	10	US-09-249-155-235	Sequence 235, App	c 217
c 145	5	100.0	11	10	US-09-249-155-251	Sequence 251, App	c 218
c 146	5	100.0	11	10	US-09-967-237-81	Sequence 81, Appl	c 219
c 147	5	100.0	11	10	US-09-093-972C-583	Sequence 583, App	c 220
c 148	5	100.0	11	10	US-09-093-972C-608	Sequence 608, App	c 221
c 149	5	100.0	11	10	US-09-093-972C-632	Sequence 632, App	c 222
c 150	5	100.0	11	10	US-09-093-972C-655	Sequence 655, App	c 223
c 151	5	100.0	11	10	US-09-093-972C-677	Sequence 677, App	c 224
c 152	5	100.0	11	10	US-09-093-972C-698	Sequence 698, App	c 225
c 153	5	100.0	11	10	US-09-093-972C-718	Sequence 718, App	c 226
c 154	5	100.0	11	10	US-09-864-636A-196	Sequence 196, App	c 227
c 155	5	100.0	11	10	US-09-864-636A-715	Sequence 715, App	c 228
c 156	5	100.0	11	10	US-09-864-636A-748	Sequence 748, App	c 229
c 157	5	100.0	11	11	US-09-864-426A-196	Sequence 196, App	

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c 235	5	100.0	11	14	US-10-193-451A-30	Sequence 30, Appl	c 308	5	100.0	11	18	US-10-474-794-35	Sequence 35, Appl
c 236	5	100.0	11	15	US-10-266-138B-22	Sequence 22, Appl	309	5	100.0	11	18	US-10-474-794-60	Sequence 60, Appl
c 237	5	100.0	11	15	US-10-104-025-14	Sequence 14, Appl	c 310	5	100.0	11	18	US-10-474-794-78	Sequence 78, Appl
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c 245	5	100.0	11	15	US-10-084-839-3527	Sequence 3527, Ap	c 318	5	100.0	12	9	US-09-194-842A-44	Sequence 44, Appl
c 246	5	100.0	11	15	US-10-407-637-5	Sequence 5, Appl	319	5	100.0	12	9	US-09-943-458-6	Sequence 6, Appl
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c 248	5	100.0	11	15	US-10-310-677-8	Sequence 8, Appl	321	5	100.0	12	9	US-09-263-959-456	Sequence 456, Appl
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US-10-257-017B-273521  
US-10-257-017B-273556  
US-10-257-017B-273618  
US-10-257-017B-273679  
US-10-257-017B-273755  
US-10-257-017B-273821  
US-10-257-017B-273943  
US-10-257-017B-274001  
US-10-257-017B-274002  
US-10-257-017B-274242  
US-10-257-017B-274362  
US-10-257-017B-274503  
US-10-257-017B-274504  
US-10-257-017B-274507  
US-10-257-017B-274873  
US-10-257-017B-274874  
US-10-257-017B-274884  
US-10-257-017B-274899  
US-10-257-017B-275004  
US-10-257-017B-275005  
US-10-257-017B-275016  
US-10-257-017B-275068  
US-10-257-017B-275214  
US-10-257-017B-275223  
US-10-257-017B-275234  
US-10-257-017B-275649  
US-10-257-017B-275669  
US-10-257-017B-275823  
US-10-257-017B-275882  
US-10-257-017B-275883  
US-10-257-017B-276216  
US-10-257-017B-276247  
US-10-257-017B-306195

RESULT 1  
US-09-057-351-11/c  
; Sequence 11, Application US/09057351  
; Patent No. US20010034439A1  
; GENERAL INFORMATION:  
; APPLICANT: Villeponteau, Bryant  
; APPLICANT: Feng, Junli  
; APPLICANT: Funk, Walter  
; APPLICANT: Andrews, William H.  
; TITLE OF INVENTION: Mammalian Telomerase  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/057,351  
FILING DATE: 08-APR-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/330,123  
FILING DATE: 27-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,802  
FILING DATE: 07-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Scorella, John R.  
REGISTRATION NUMBER: 32,944  
REFERENCE/DOCKET NUMBER: 015389-000821US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-09-057-351-11

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 GAGGG 5  
|||||

Db 9 GAGGG 5

RESULT 2  
US-09-811-286-18  
; Sequence 18, Application US/09811286  
; Patent No. US20010051712A1  
; GENERAL INFORMATION:  
; APPLICANT: Drysdale, Connie M  
; APPLICANT: Judson, Richard S  
; APPLICANT: Liggett, Stephen B  
; APPLICANT: Nandabalan, Krishnan  
; APPLICANT: Stack, Catherine B.  
; APPLICANT: Stephens, J. Claiborne  
; TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes  
; FILE REFERENCE: with drug response  
; FILE REFERENCE: MMH-0303US1  
; CURRENT APPLICATION NUMBER: US/09/811,286  
; CURRENT FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-811-286-18

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 GAGGG 5  
|||||

Db 5 GAGGG 9

RESULT 3  
US-09-796-138-15  
; Sequence 15, Application US/09796138  
; Patent No. US20020031782A1  
; GENERAL INFORMATION:  
; APPLICANT: Waterman, Michael R.  
; APPLICANT: Bellamine, Aouatef  
; APPLICANT: Podust, Larissa M.  
; TITLE OF INVENTION: Mycobacterium tuberculosis CYP51 HIGH RESOLUTION STRUCTURE, POLYPEPTIDES AND THERAPEUTIC AND SCREENING METHODS  
; TITLE OF INVENTION: NUCLEIC ACIDS, AND THERAPEUTIC AND SCREENING METHODS  
; TITLE OF INVENTION: RELATING TO SAME  
; FILE REFERENCE: Attorney Docket No. US20020031782A1 1242-17-2  
; CURRENT APPLICATION NUMBER: US/09/796,138  
; CURRENT FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: 09/345,218  
; PRIOR FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-09-796-138-15

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 GAGGG 5  
|||||

Db 4 GAGGG 8

RESULT 4  
US-09-909-903-15  
; Sequence 15, Application US/09909903  
; Patent No. US20020052031A1  
; GENERAL INFORMATION:  
; APPLICANT: Waterman, Michael R.  
; APPLICANT: Bellamine, Aouatef  
; TITLE OF INVENTION: Mycobacterium tuberculosis CYP51 POLYPEPTIDES AND THERAPEUTIC AND SCREENING METHODS  
; TITLE OF INVENTION: NUCLEIC ACIDS AND THERAPEUTIC AND SCREENING METHODS  
; TITLE OF INVENTION: RELATING TO SAME  
; FILE REFERENCE: Attorney Docket No. US20020052031A1 1242-17  
; CURRENT APPLICATION NUMBER: US/09/909,903  
; CURRENT FILING DATE: 2001-07-20  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 15  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
US-09-909-903-15

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

QY 1 GAGGG 5  
|||||

Db 4 GAGGG 8

RESULT 5  
US-09-154-750A-18/c  
; Sequence 18, Application US/09154750A  
; Publication No. US20020055097A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert

```
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; PRIOR FILING DATE: 1998-09-17
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-18

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 5 GAGGG 1

RESULT 6
US-09-154-750A-49
; Sequence 49, Application US/09154750A
; Publication No. US20020055097A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-49

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 1 GAGGG 5

RESULT 7
US-09-154-750A-58
; Sequence 58, Application US/09154750A
; Publication No. US20020055097A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR FILING DATE: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 58
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-58

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 1 GAGGG 5

RESULT 8
US-09-989-789-92
; Sequence 92, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-92

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 1 GAGGG 5

RESULT 9
US-09-989-789-93
; Sequence 93, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-93
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Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 1 GAGGG 5

## RESULT 10

US-09-989-789-626  
; Sequence 626, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 626  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-626

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 1 GAGGG 5

## RESULT 11

US-09-989-789-1630  
; Sequence 1630, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1630  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1630

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 1 GAGGG 5

## RESULT 12

US-09-989-789-1631

; Sequence 1631, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1631  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1631

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 1 GAGGG 5

## RESULT 13

US-09-989-789-1666  
; Sequence 1666, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1666  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1666

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 2 GAGGG 6

## RESULT 14

US-09-989-789-1674  
; Sequence 1674, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1674  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1674

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
| | | | |  
Db 2 GAGGG 6

RESULT 15  
US-09-989-789-1685  
; Sequence 1685, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1685  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1685

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
| | | | |  
Db 1 GAGGG 5

RESULT 16  
US-09-989-789-1703  
; Sequence 1703, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1703  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1703

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GAGGG 5  
| | | | |  
Db 1 GAGGG 5

RESULT 17  
US-09-989-789-1704  
; Sequence 1704, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1704  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1704

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
| | | | |  
Db 1 GAGGG 5

RESULT 18  
US-09-810-936-102  
; Sequence 102, Application US/09810936  
; Patent No. US20020068285A1  
; GENERAL INFORMATION:  
; APPLICANT: Frudakis, Tony N.  
; APPLICANT: Reed, Steven G.  
; APPLICANT: Smith, John M.  
; APPLICANT: Misher, Linda E.  
; APPLICANT: Dillon, Davin C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Wang, AiJun  
; APPLICANT: Skeiky, Yasir A.W.  
; APPLICANT: Harlocker, Susan L.  
; APPLICANT: Day, Craig H.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; FILE REFERENCE: 210121.419C11  
; CURRENT APPLICATION NUMBER: US/09/810,936  
; CURRENT FILING DATE: 2001-03-16  
; NUMBER OF SEQ ID NOS: 334  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 102  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer for amplification from breast tumor cDNA  
US-09-810-936-102

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5





;  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/970,820  
; FILING DATE: 05-Oct-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-970-820-20  
  
Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGGG 5  
Db 8 GAGGG 4  
  
RESULT 23  
US-09-986-718-20/c  
; Sequence 20, Application US/09986718  
; Patent No. US20020178458A1  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

;  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/986,718  
; FILING DATE: 09-No. US20020178458A1-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/485,573  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-032  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-986-718-20  
  
Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGGG 5  
Db 8 GAGGG 4  
  
RESULT 24  
US-09-971-372A-8  
; Sequence 8, Application US/09971372A  
; Publication No. US20030035814A1  
; GENERAL INFORMATION:  
; APPLICANT: Kawaoka, Yoshihiro  
; APPLICANT: Neumann, Gabriele  
; TITLE OF INVENTION: Recombinant influenza viruses for vaccines and gene  
; TITLE OF INVENTION: therapy  
; FILE REFERENCE: 960296.98130  
; CURRENT APPLICATION NUMBER: US/09/971,372A  
; CURRENT FILING DATE: 2001-10-04  
; PRIOR APPLICATION NUMBER: PCT/US00/09021  
; PRIOR FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: 60/127,912  
; PRIOR FILING DATE: 1999-04-06  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: end of  
; OTHER INFORMATION: restriction enzyme digestion product  
US-09-971-372A-8  
  
Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GAGGG 5  
Db 6 GAGGG 10  
  
RESULT 25  
US-09-990-186-92

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; Sequence 92, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-92

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
Db      1 GAGGG 5

RESULT 26
US-09-990-186-93
; Sequence 93, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-93

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
Db      1 GAGGG 5

RESULT 27
US-09-990-186-626
; Sequence 626, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
```

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; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-626

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
Db      1 GAGGG 5

RESULT 28
US-09-990-186-1630
; Sequence 1630, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-1630

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
Db      1 GAGGG 5

RESULT 29
US-09-990-186-1631
; Sequence 1631, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1631
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-1631

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 1 GAGGG 5

RESULT 30
US-09-990-186-1666
; Sequence 1666, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1666
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
; US-09-990-186-1666

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 2 GAGGG 6

RESULT 31
US-09-990-186-1674
; Sequence 1674, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1674
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
; US-09-990-186-1674

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 2 GAGGG 6

RESULT 32
US-09-990-186-1685
; Sequence 1685, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
; US-09-990-186-1685

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 2 GAGGG 6

RESULT 33
US-09-990-186-1703
; Sequence 1703, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1703
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
; US-09-990-186-1703

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 1 GAGGG 5

RESULT 34
US-09-990-186-1704
; Sequence 1704, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
; US-09-990-186-1704

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
Db 1 GAGGG 5
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-1704

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
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Db 1 GAGGG 5

RESULT 35
US-09-979-593-41/c
; Sequence 41, Application US/09979593
; Publication No. US2003008255A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Klem, Stefanie E
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MMH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 60/201,946
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-41

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
   |||||
Db 1 GAGGG 5

RESULT 36
US-09-979-593-47
; Sequence 47, Application US/09979593
; Publication No. US2003008255A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Klem, Stefanie E
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MMH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 60/201,946
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-979-593-47

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5
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Db 7 GAGGG 3

RESULT 37
US-09-093-972C-609
; Sequence 609, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRUCTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 609:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 609:
US-09-093-972C-609

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GAGGG 5  
Db 6 GAGGG 10

RESULT 38  
US-09-093-972C-633  
; Sequence 633, Application US/09093972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-00672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 633:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 633:  
US-09-093-972C-633  
Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 5 GAGGG 9

RESULT 39  
US-09-093-972C-656  
; Sequence 656, Application US/09093972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-00672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 656:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 656:  
US-09-093-972C-656  
Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-00672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 656:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 656:  
US-09-093-972C-656  
Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 4 GAGGG 8

RESULT 40  
US-09-093-972C-678  
; Sequence 678, Application US/09093972C  
; Publication No. US20030087845A1  
; GENERAL INFORMATION:  
; APPLICANT: Nyce, Jonathan W.  
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION  
; NUMBER OF SEQUENCES: 996  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
; STREET: 7 Clarke Drive  
; CITY: Cranbury  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 08512  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/093,972C  
; FILING DATE: 09-Jun-1998  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 08/757,024  
; FILING DATE: 26-11-1996  
; APPLICATION NUMBER: US 08/472,527  
; FILING DATE: 7-June-1995  
; APPLICATION NUMBER: US 09/016,464  
; FILING DATE: 30-January-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Amzel, Viviana  
; REGISTRATION NUMBER: 30,930  
; REFERENCE/DOCKET NUMBER: EPI-00672  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 609-409-3035  
; TELEFAX: 413-254-9245  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 656:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 656:  
US-09-093-972C-656  
Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/093,972C  
FILING DATE: 09-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 08/757,024  
FILING DATE: 26-11-1996  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 09/016,464  
FILING DATE: 30-January-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-00672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 678:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 678:  
US-09-093-972C-678

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 3 GAGGG 7

RESULT 41  
US-09-093-972C-699  
Sequence 699, Application US/09093972C  
Publication No. US20030087845A1  
GENERAL INFORMATION:  
APPLICANT: Nyce, Jonathan W.  
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
BRONCHOCOSTRUCTION, ALLERGY(IES) & INFLAMMATION  
NUMBER OF SEQUENCES: 996  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
STREET: 7 Clarke Drive  
CITY: Cranbury  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/093,972C  
FILING DATE: 09-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 08/757,024  
FILING DATE: 26-11-1996  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 09/016,464  
FILING DATE: 30-January-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-00672  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 699:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 699:  
US-09-093-972C-699

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5  
Db 2 GAGGG 6

## RESULT 42

US-09-093-972C-719  
Sequence 719, Application US/09093972C  
Publication No. US20030087845A1  
GENERAL INFORMATION:  
APPLICANT: Nyce, Jonathan W.  
TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION  
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH  
BRONCHOCOSTRUCTION, ALLERGY(IES) & INFLAMMATION  
NUMBER OF SEQUENCES: 996  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
STREET: 7 Clarke Drive  
CITY: Cranbury  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/093,972C  
FILING DATE: 09-Jun-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 08/757,024  
FILING DATE: 26-11-1996  
APPLICATION NUMBER: US 08/472,527  
FILING DATE: 7-June-1995  
APPLICATION NUMBER: US 09/016,464  
FILING DATE: 30-January-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930

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; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 605-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 719:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 719:
US-09-093-972C-719

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
        |||||
Db      1 GAGGG 5

RESULT 43
US-09-811-285-18
; Sequence 18, Application US/09811285
; Publication No. US20030091998A1
; GENERAL INFORMATION:
; APPLICANT: Drysdale, Connie M
; APPLICANT: Judson, Richard S
; APPLICANT: Liggett, Stephen B
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: Association of beta2-adrenergic receptor haplotypes
; FILE OF INVENTION: with drug response
; FILE REFERENCE: MMH-0303US2
; CURRENT APPLICATION NUMBER: US/09/811,285
; CURRENT FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-811-285-18

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
        |||||
Db      5 GAGGG 9

RESULT 44
US-09-989-994-92
; Sequence 92, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-92

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
        |||||
Db      1 GAGGG 5

RESULT 45
US-09-989-994-93
; Sequence 93, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 93
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-93

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
        |||||
Db      1 GAGGG 5

RESULT 46
US-09-989-994-626
; Sequence 626, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-626

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAGGG 5
        |||||
Db      1 GAGGG 5
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Db 1 GAGGG 5

## RESULT 47

US-09-989-994-1630  
; Sequence 1630, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1630  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1630

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 1 GAGGG 5

## RESULT 48

US-09-989-994-1631  
; Sequence 1631, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1631  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1631

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 1 GAGGG 5

## RESULT 49

US-09-989-994-1666  
; Sequence 1666, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS

FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1666  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1666

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 2 GAGGG 6

## RESULT 50

US-09-989-994-1674  
; Sequence 1674, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1674  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1674

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGGG 5

Db 2 GAGGG 6

Search completed: January 7, 2005, 11:31:21  
Job time : 274.2 secs

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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GGGAG  
Perfect score: 5  
Sequence: 1 gggag 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_ats.\*
- 12: gb\_sy.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	10	6	A08937 H.sapiens f
C 2	5	100.0	10	6	A08947 A08947 Nucleotide
C 3	5	100.0	10	6	AR029980 AR029980 Sequence
C 4	5	100.0	10	6	AR030011 AR030011 Sequence
C 5	5	100.0	10	6	AR030098 AR030098 Sequence
C 6	5	100.0	10	6	AR030208 AR030208 Sequence
C 7	5	100.0	10	6	AR030218 AR030218 Sequence
C 8	5	100.0	10	6	AR030220 AR030220 Sequence
C 9	5	100.0	10	6	AR030221 AR030221 Sequence
C 10	5	100.0	10	6	AR053555 AR053555 Sequence
C 11	5	100.0	10	6	AR053565 AR053565 Sequence
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C 19	5	100.0	10	6	AR065892 AR065892 Sequence

C 20	5	100.0	10	6	AR070981 AR070981 Sequence
C 21	5	100.0	10	6	AR080364 AR080364 Sequence
C 22	5	100.0	10	6	AR080374 AR080374 Sequence
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C 37	5	100.0	10	6	AR148319 AR148319 Sequence
C 38	5	100.0	10	6	AR148329 AR148329 Sequence
C 39	5	100.0	10	6	AR175394 AR175394 Sequence
C 40	5	100.0	10	6	AR178839 AR178839 Sequence
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C 76	5	100.0	10	6	BD240207 BD240207 Preparati
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C 84	5	100.0	10	6	BD240699 BD240699 Preparati
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C 87	5	100.0	10	6	BD262813 BD262813 Diagnosti
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C 443	5	100.0	11	6	CQ837645	Sequence			
C 444	5	100.0	11	6	CQ837666	Sequence			
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C 454	5	100.0	11	6	CQ837927	Sequence			
C 455	5	100.0	11	6	CQ837936	Sequence			
C 456	5	100.0	11	6	CQ837941	Sequence			
C 457	5	100.0	11	6	CQ837949	Sequence			
C 458	5	100.0	11	6	CQ837957	Sequence			
C 459	5	100.0	11	6	CQ837993	Sequence			
C 460	5	100.0	11	6	CQ838045	Sequence			
C 461	5	100.0	11	6	CQ838052	Sequence			
C 462	5	100.0	11	6	CQ838067	Sequence			
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C 464	5	100.0	11	6	E05323	Anti-sense			
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C 466	5	100.0	11	6	E09846	Primer, 9/1			
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C 468	5	100.0	11	6	I18119	Sequence 35			
C 469	5	100.0	11	6	I46967	Sequence 60			
C 470	5	100.0	11	6	AR202475	Sequence			
C 471	5	100.0	11	6	AR202477	Sequence			
C 472	5	100.0	11	6	AR228387	Sequence			
C 473	5	100.0	11	6	AR241864	Sequence			
C 474	5	100.0	11	6	AR301472	Sequence			
C 475	5	100.0	11	6	AR301557	Sequence			
C 476	5	100.0	11	6	AR301611	Sequence			
C 477	5	100.0	11	6	AR301650	Sequence			
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C 481	5	100.0	11	6	AR301718	Sequence			
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C 492	5	100.0	11	6	AX099004	Sequence			
C 493	5	100.0	11	6	AX099005	Sequence			
C 494	5	100.0	11	6	AX099006	Sequence			
C 495	5	100.0	11	6	AX099043	Sequence			
C 496	5	100.0	11	6	AX099044	Sequence			
C 497	5	100.0	11	6	AX099065	Sequence			
C 498	5	100.0	11	6	AX099066	Sequence			
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C 500	5	100.0	11	6	AX099092	Sequence			
RESULT 1	A08937	10 bp DNA linear PAT 27-AUG-1993							
LOCUS	H.sapiens factor recognition motif in promoter.								
DEFINITION	A08937								
ACCESSION	A08937.1	GI:411846							
VERSION	1	(bases 1 to 10)							
KEYWORDS	Homo sapiens (human)								
SOURCE	Homo sapiens								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.								
TITLE	1 (bases 1 to 10)								
JOURNAL	Taniguchi, T.								
FEATURES	Improvements in and relating to the regulation of gene expression								
source	Patent: Ep 0374503-A 4 27-JUN-1990;								
	Taniguchi, Tadatsugu, Prof. Dr								
	Location/Qualifiers								
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Best Local Similarity	100.0%;				Pred. No. 3.3e+07;				

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Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  GGGAG  5
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Db      10 GGGAG  6

RESULT 2
A08947/c
LOCUS      A08947      10 bp      DNA      linear      PAT 27-AUG-1993
DEFINITION Nucleotide sequence 16 from patent number EP0374503.
ACCESSION  A08947
VERSION    A08947.1  GI:411856
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unidentified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Taniguchi,T.
TITLE      Improvements in and relating to the regulation of gene expression
JOURNAL    Taniguchi, Tadatsugu, Prof. Dr
FEATURES   Location/Qualifiers
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ORIGIN

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Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  GGGAG  5
      |||||
Db      10 GGGAG  6

RESULT 3
AR029980
LOCUS      AR029980      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 169 from patent US 5861244.
ACCESSION  AR029980
VERSION    AR029980.1  GI:5943194
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Wang,C.-G. and Hepburn,A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 169 19-JAN-1999;
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"

ORIGIN

Query Match      100.0%;  Score 5;  DB 6;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 3.3e+07;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  GGGAG  5
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Db      3  GGGAG  7

RESULT 4
AR030011/c
LOCUS      AR030011      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 200 from patent US 5861244.
ACCESSION  AR030011
VERSION    AR030011.1  GI:5943225

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KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Wang,C.-G. and Hepburn,A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 200 19-JAN-1999;
FEATURES   Location/Qualifiers
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ORIGIN

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Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  GGGAG  5
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Db      7  GGGAG  3

RESULT 5
AR030098
LOCUS      AR030098      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 287 from patent US 5861244.
ACCESSION  AR030098
VERSION    AR030098.1  GI:5943312
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Wang,C.-G. and Hepburn,A.G.
TITLE      Genetic sequence assay using DNA triple strand formation
JOURNAL    Patent: US 5861244-A 287 19-JAN-1999;
FEATURES   Location/Qualifiers
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ORIGIN

Query Match      100.0%;  Score 5;  DB 6;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 3.3e+07;
Matches      5;  Conservative      0;  Mismatches      0;  Indels      0;  Gaps      0;

Qy      1  GGGAG  5
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Db      5  GGGAG  9

RESULT 6
AR030208/c
LOCUS      AR030208      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 19 from patent US 5861246.
ACCESSION  AR030208
VERSION    AR030208.1  GI:5943422
KEYWORDS   Unknown.
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Weissman,S.M., Mallur,G.N. and Kulkarni,P.
TITLE      Multiple selection process for binding sites of DNA-binding proteins
JOURNAL    Patent: US 5861246-A 19 19-JAN-1999;
FEATURES   Location/Qualifiers
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ORIGIN

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Query Match 100.0%; Score 5; DB 6; Length 10;  
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Qy 1 GGGAG 5  
Db 9 GGGAG 5

RESULT 7  
AR030218 LOCUS AR030218 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 29 from patent US 5861246.  
ACCESSION AR030218  
VERSION AR030218.1 GI:5943432  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 29 19-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..10  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 3 GGGAG 7

RESULT 8  
AR030220/c LOCUS AR030220 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 31 from patent US 5861246.  
ACCESSION AR030220  
VERSION AR030220.1 GI:5943434  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 31 19-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 9 GGGAG 5

RESULT 9  
AR030221 LOCUS AR030221 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 32 from patent US 5861246.

ACCESSION AR030221  
VERSION AR030221.1 GI:5943435  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 32 19-JAN-1999;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"

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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 10

RESULT 10  
AR053555/c LOCUS AR053555 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 20 from patent US 5834248.  
ACCESSION AR053555  
VERSION AR053555.1 GI:5978417  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.  
TITLE Compositions and methods using rchds34, a gene uregulated by shear stress  
JOURNAL Patent: US 5834248-A 20 10-NOV-1998;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 2

RESULT 11  
AR053565 LOCUS AR053565 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 30 from patent US 5834248.  
ACCESSION AR053565  
VERSION AR053565.1 GI:5978427  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Falb,D.  
TITLE Compositions and methods using rchds34, a gene uregulated by shear stress  
JOURNAL Patent: US 5834248-A 30 10-NOV-1998;  
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Query Match      100.0%; Score 5; DB 6; Length 10;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
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Db 6 GGGAG 10

RESULT 12
AR058463
LOCUS      AR058463      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 40 from patent US 5837832.
ACCESSION AR058463
VERSION   AR058463.1 GI:5984040
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS  Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
          Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE     Arrays of nucleic acid probes on biological chips
JOURNAL   Patent: US 5837832-A 40 17-NOV-1998;
FEATURES  Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
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Db 6 GGGAG 10

RESULT 13
AR058519
LOCUS      AR058519      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 96 from patent US 5837832.
ACCESSION AR058519
VERSION   AR058519.1 GI:5984096
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS  Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
          Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE     Arrays of nucleic acid probes on biological chips
JOURNAL   Patent: US 5837832-A 96 17-NOV-1998;
FEATURES  Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
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Db 5 GGGAG 9

RESULT 14
AR058771/c
LOCUS      AR058771/c    10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 348 from patent US 5837832.
ACCESSION AR058771
VERSION   AR058771.1 GI:5984348
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS  Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
          Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE     Arrays of nucleic acid probes on biological chips
JOURNAL   Patent: US 5837832-A 348 17-NOV-1998;
FEATURES  Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
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Db 7 GGGAG 3

RESULT 15
AR058772/c
LOCUS      AR058772/c    10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 349 from patent US 5837832.
ACCESSION AR058772
VERSION   AR058772.1 GI:5984349
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS  Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
          Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE     Arrays of nucleic acid probes on biological chips
JOURNAL   Patent: US 5837832-A 349 17-NOV-1998;
FEATURES  Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
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Db 8 GGGAG 4

RESULT 16
AR058773/c
LOCUS      AR058773      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 350 from patent US 5837832.
ACCESSION AR058773
VERSION   AR058773.1 GI:5984350
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS  Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
          Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.

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TITLE   Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 350 17-NOV-1998;
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 9 GGGAG 5

RESULT 17
AR058774/c
LOCUS      AR058774      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 351 from patent US 5837832.
ACCESSION  AR058774
VERSION     AR058774.1 GI:5984351
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Chee,M., Cronin,M.T., Fodor,S.P.A., Huang,X.X., Hubbell,E.A.,
           Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE     Arrays of nucleic acid probes on biological chips
JOURNAL   Patent: US 5837832-A 351 17-NOV-1998;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 10 GGGAG 6

RESULT 18
AR065882/c
LOCUS      AR065882      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 20 from patent US 5849578.
ACCESSION  AR065882
VERSION     AR065882.1 GI:5996098
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Falb,D.A.
TITLE     Compositions and methods for the treatment and diagnosis of
           cardiovascular using RCHD528 as a target
JOURNAL   Patent: US 5849578-A 20 15-DEC-1998;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 10 GGGAG 5

TITLE   Arrays of nucleic acid probes on biological chips
JOURNAL Patent: US 5837832-A 350 17-NOV-1998;
FEATURES Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 9 GGGAG 5

RESULT 19
AR065892/c
LOCUS      AR065892      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 30 from patent US 5849578.
ACCESSION  AR065892
VERSION     AR065892.1 GI:5996108
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Falb,D.A.
TITLE     Compositions and methods for the treatment and diagnosis of
           cardiovascular using RCHD528 as a target
JOURNAL   Patent: US 5849578-A 30 15-DEC-1998;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 6 GGGAG 10

RESULT 20
AR070981/c
LOCUS      AR070981      10 bp      DNA      linear      PAT 18-FEB-2000
DEFINITION Sequence 15 from patent US 5908978.
ACCESSION  AR070981
VERSION     AR070981.1 GI:7221869
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Amerson,H.V., Wilcox,P., Sederoff,R.R., Kuhlman,E.George.,
           O'Malley,D.M. and Grattapaglia,D.
TITLE     Methods for within family selection of disease resistance in woody
           perennials using genetic markers
JOURNAL   Patent: US 5908978-A 15 01-JUN-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 10 GGGAG 6

RESULT 21
AR080364/c
LOCUS      AR080364      10 bp      DNA      linear      PAT 31-AUG-2000
DEFINITION Sequence 20 from patent US 5968770.
ACCESSION  AR080364
VERSION     AR080364.1 GI:10007099
KEYWORDS   .
SOURCE     Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.
TITLE Compositions and methods for the treatment and diagnosis of
JOURNAL cardiovascular disease using rchd523 as a target
FEATURES Patent: US 5968770-A 20 19-OCT-1999;
source Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 6 GGGAG 2

RESULT 22
LOCUS AR080374 10 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 30 from patent US 5968770.
ACCESSION AR080374
VERSION AR080374.1 GI:10007109
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Falb,D.A. and Gimbrone,M.A. Jr.
TITLE Compositions and methods for the treatment and diagnosis of
JOURNAL cardiovascular disease using rchd523 as a target
FEATURES Patent: US 5968770-A 30 19-OCT-1999;
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 6 GGGAG 10

RESULT 23
LOCUS AR092689/c 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 5998193.
ACCESSION AR092689
VERSION AR092689.1 GI:10019441
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 1 07-DEC-1999;
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 10 GGGAG 6

RESULT 24
LOCUS AR092690 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 2 from patent US 5998193.
ACCESSION AR092690
VERSION AR092690.1 GI:10019442
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 2 07-DEC-1999;
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 1 GGGAG 5

RESULT 25
LOCUS AR092692 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 4 from patent US 5998193.
ACCESSION AR092692
VERSION AR092692.1 GI:10019444
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 4 07-DEC-1999;
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 1 GGGAG 5

RESULT 26
LOCUS AR092697 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 9 from patent US 5998193.

```

```
ACCESSION AR092697
VERSION AR092697.1 GI:10019449
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese, P., Stapper, M. and Perriman, R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 9 07-DEC-1999;
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db |||||
10 GGGAG 6
RESULT 27
AR092698
LOCUS AR092698 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 10 from patent US 5998193.
ACCESSION AR092698
VERSION AR092698.1 GI:10019450
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese, P., Stapper, M. and Perriman, R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 10 07-DEC-1999;
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db |||||
10 GGGAG 5
RESULT 28
AR092715/c
LOCUS AR092715/c 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 27 from patent US 5998193.
ACCESSION AR092715
VERSION AR092715.1 GI:10019467
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese, P., Stapper, M. and Perriman, R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 27 07-DEC-1999;
Location/Qualifiers
1..10
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/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db |||||
10 GGGAG 5
RESULT 29
AR098894/c
LOCUS AR098894/c 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 30 from patent US 6077685.
ACCESSION AR098894
VERSION AR098894.1 GI:12808660
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofatter, J.A., MacCollin, M.M. and Gusella, J.F.
TITLE Tumor suppressor merlin and antibodies thereof
JOURNAL Patent: US 6077685-A 30 20-JUN-2000;
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db |||||
5 GGGAG 1
RESULT 30
AR099558/c
LOCUS AR099558/c 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 85 from patent US 6077833.
ACCESSION AR099558
VERSION AR099558.1 GI:12809324
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Bennett, C. Frank, and Vickers, T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6077833-A 85 20-JUN-2000;
Location/Qualifiers
1..10
/organism="unknown"
/mol_type="unassigned DNA"
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db |||||
5 GGGAG 1
RESULT 31
AR099558/c
LOCUS AR099558/c 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 85 from patent US 6077833.
ACCESSION AR099558
VERSION AR099558.1 GI:12809324
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Bennett, C. Frank, and Vickers, T.A.
TITLE Oligonucleotide compositions and methods for the modulation of the
expression of B7 protein
JOURNAL Patent: US 6077833-A 85 20-JUN-2000;
Location/Qualifiers
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/mol_type="unassigned DNA"
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db |||||
5 GGGAG 1
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AR106673/C  
LOCUS AR106673 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 1 from patent US 6107078.  
ACCESSION AR106673  
VERSION AR106673.1 GI:12821203  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 6107078-A 1 22-AUG-2000;  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
Db 10 GGGAG 6  
RESULT 32  
LOCUS AR106674 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 2 from patent US 6107078.  
ACCESSION AR106674  
VERSION AR106674.1 GI:12821204  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 6107078-A 2 22-AUG-2000;  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
Db 10 GGGAG 6  
RESULT 33  
LOCUS AR106676 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 4 from patent US 6107078.  
ACCESSION AR106676  
VERSION AR106676.1 GI:12821206  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 6107078-A 4 22-AUG-2000;  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
Db 10 GGGAG 5  
RESULT 34  
LOCUS AR106681 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 9 from patent US 6107078.  
ACCESSION AR106681  
VERSION AR106681.1 GI:12821211  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 6107078-A 9 22-AUG-2000;  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
Db 10 GGGAG 5  
RESULT 35  
LOCUS AR106682 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 10 from patent US 6107078.  
ACCESSION AR106682  
VERSION AR106682.1 GI:12821212  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 6107078-A 10 22-AUG-2000;  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
Db 10 GGGAG 5

JOURNAL Patent: US 6107078-A 4 22-AUG-2000;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
Db 1 GGGAG 5  
RESULT 34  
LOCUS AR106681 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 9 from patent US 6107078.  
ACCESSION AR106681  
VERSION AR106681.1 GI:12821211  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 6107078-A 9 22-AUG-2000;  
source Location/Qualifiers  
1..10  
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/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
Db 1 GGGAG 5  
RESULT 35  
LOCUS AR106682 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 10 from patent US 6107078.  
ACCESSION AR106682  
VERSION AR106682.1 GI:12821212  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese,P., Stapper,M. and Perriman,R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA  
JOURNAL embedded ribozymes and compositions thereof  
FEATURES Patent: US 6107078-A 10 22-AUG-2000;  
source Location/Qualifiers  
1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.3e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGAG 5  
Db 1 GGGAG 5

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Db          1 GGGAG 5

RESULT 36
LOCUS      ARI06699/c
DEFINITION Sequence 27 from patent US 6107078.
ACCESSION  ARI06699
VERSION     ARI06699.1 GI:12821229
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Keese, P., Stapper, M. and Perriman, R.
TITLE        Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
              embedded ribozymes and compositions thereof
JOURNAL      Patent: US 6107078-A 27 22-AUG-2000;
FEATURES     Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      10 GGGAG 6

RESULT 37
LOCUS      ARI48319/c
DEFINITION Sequence 20 from patent US 6225084.
ACCESSION  ARI48319
VERSION     ARI48319.1 GI:15112409
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Falb, D.A. and Gimbrone, M.A. Jr.
TITLE        Compositions and methods for the treatment and diagnosis of
              cardiovascular disease using rchd534 as a target
JOURNAL      Patent: US 6225084-A 20 01-MAY-2001;
FEATURES     Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      10 GGGAG 6

RESULT 38
LOCUS      ARI48329
DEFINITION Sequence 30 from patent US 6225084.
ACCESSION  ARI48329
VERSION     ARI48329.1 GI:15112419
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Keese, P., Stapper, M. and Perriman, R.
TITLE        Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
              embedded ribozymes and compositions thereof
JOURNAL      Patent: US 6107078-A 27 22-AUG-2000;
FEATURES     Location/Qualifiers
              1..10
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              /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      6 GGGAG 2

RESULT 39
LOCUS      ARI75394
DEFINITION Sequence 117 from patent US 6309823.
ACCESSION  ARI75394
VERSION     ARI75394.1 GI:17916693
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Cronin, M.T., Miyada, C.G., Hubbell, E.A., Chee, M., Fodor, S.P.A.,
              Huang, X.C., Lipshutz, R.J., Lobban, P.E., Morris, M.S. and
              Sheldon, E.L.
TITLE        Arrays of nucleic acid probes for analyzing biotransformation genes
              and methods of using the same
JOURNAL      Patent: US 6309823-A 117 30-OCT-2001;
FEATURES     Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      4 GGGAG 8

RESULT 40
LOCUS      ARI78839/c
DEFINITION Sequence 85 from patent US 6319906.
ACCESSION  ARI78839
VERSION     ARI78839.1 GI:20219977
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Bennett, C.Frank. and Vickers, T.A.
TITLE        Oligonucleotide compositions and methods for the modulation of the
              expression of B7 protein
JOURNAL      Patent: US 6319906-A 85 20-NOV-2001;
FEATURES     Location/Qualifiers
              1..10
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              /mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
        |||||
Db      4 GGGAG 8

RESULT 41
LOCUS      ARI78839/c
DEFINITION Sequence 85 from patent US 6319906.
ACCESSION  ARI78839
VERSION     ARI78839.1 GI:20219977
KEYWORDS   .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Bennett, C.Frank. and Vickers, T.A.
TITLE        Oligonucleotide compositions and methods for the modulation of the
              expression of B7 protein
JOURNAL      Patent: US 6319906-A 85 20-NOV-2001;
FEATURES     Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="unassigned DNA"

ORIGIN
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
   |||||
Db 5 GGGAG 1

RESULT 41
LOCUS BD225330 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Methods for the diagnosis and treatment of lung cancer.
ACCESSION BD225330
VERSION BD225330.1 GI:33035080
KEYWORDS JP 2002509706-A/9.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Jen,J., Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE Methods for the diagnosis and treatment of lung cancer
JOURNAL Patent: JP 2002509706-A 9 02-APR-2002;
COMMENT GENZYME CORP. JOHN HOPKINS UNIVERSITY
OS Artificial Sequence
PN JP 2002509706-A/9
PD 02-APR-2002
PF 30-MAR-1999 JP 2000540746
PR 31-MAR-1998 US 60/080044
PI JIN JEN, GARY A. BEAUDRY, STEPHEN L. MADDEN, ARTHUR H. BERTELSEN PC
C12N15/09,A61K45/00,A61K48/00,A61P35/00,C12Q1/68,G01N33/50, PC
G01N33/574,
PC C12N15/00
CC Description of Artificial Sequence: SAGE tags FH Key
LOCUS BD225330
DEFINITION Location/Qualifiers
FT source 1..10
FT /organism='Artificial Sequence'.

FEATURES
source
1..10
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
1
GGGAG 5
|||||
5 GGGAG 9

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
   |||||
Db 5 GGGAG 9

RESULT 42
LOCUS BD225330 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Compositions and methods for the identification of lung tumor
ACCESSION BD225330
VERSION BD225330.1 GI:33035100
KEYWORDS JP 2002509707-A/12.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
TITLE Compositions and methods for the identification of lung tumor cells
JOURNAL Patent: JP 2002509707-A 12 02-APR-2002;
COMMENT GENZYME CORP
OS Artificial Sequence
PN JP 2002509707-A/12
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541180

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PR 31-MAR-1998 US 60/080037
PI GARY A. BEAUDRY, STEPHEN L. MADDEN, ARTHUR H. BERTELSEN PC
C12N15/09,A01K67/027,C07H21/47,C07K16/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
G01N33/566//
PC A61K45/00,A61P9/00,A61P35/00,C12N15/00,C12N5/00 CC
Compositions and methods for the identification of lung tumor CC
cells

FH Key Location/Qualifiers
FT source 1..10
FT /organism='Artificial Sequence'.

FEATURES
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
1
GGGAG 5
|||||
5 GGGAG 9

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.3e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
   |||||
Db 5 GGGAG 9

RESULT 43
LOCUS BD228630/c 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD228630
VERSION BD228630.1 GI:33048400
KEYWORDS JP 2002534056-A/48.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 48 15-OCT-2002;
COMMENT GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/48
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L. ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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PC C12N15/00,C12N5/00,C12N15/00
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FH Key Location/Qualifiers
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238638
VERSION BD238638.1 GI:33048408
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ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 56 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/56
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 GGGAG 4

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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238733
VERSION BD238733.1 GI:33048503
KEYWORDS JP 2002534056-A/151.
SOURCE Homo sapiens (human)
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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103.173 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 3979404

Minimum DB seq length: 10

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Post-processing: Minimum Match 0%

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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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156	5	100.0	10	3	Aaz83318	Aaz83318 Metastati	c 229	5	100.0	10	3	Aaz86444	Aaz86444 Metastati
157	5	100.0	10	3	Aaz83603	Aaz83603 Metastati	230	5	100.0	10	3	AAC74009	Human den
158	5	100.0	10	3	Aaz84320	Aaz84320 Metastati	c 231	5	100.0	10	3	AAC74186	Human mon
159	5	100.0	10	3	Aaz84852	Aaz84852 Metastati	c 232	5	100.0	10	3	AAC74010	Human den
160	5	100.0	10	3	Aaz85025	Aaz85025 Metastati	233	5	100.0	10	3	AAC73959	Human den
c 161	5	100.0	10	3	Aaz85581	Aaz85581 Metastati	c 234	5	100.0	10	3	AAA56548	Human mac
162	5	100.0	10	3	Aaz85849	Aaz85849 Metastati	c 235	5	100.0	10	3	AAA56236	Human mac
163	5	100.0	10	3	Aaz86025	Aaz86025 Metastati	236	5	100.0	10	3	AAA56427	Human mac
c 164	5	100.0	10	3	Aaz80768	Aaz80768 Metastati	237	5	100.0	10	3	AAA56133	Human mon
165	5	100.0	10	3	Aaz82496	Aaz82496 Metastati	c 238	5	100.0	10	3	AAA56327	Human mac
166	5	100.0	10	3	Aaz84027	Aaz84027 Metastati	239	5	100.0	10	3	AAA56547	Human mac
167	5	100.0	10	3	Aaz85543	Aaz85543 Metastati	240	5	100.0	10	3	AAA56520	Human mac

241	5	100.0	10	3	AAA56395	Aaa56395 Human mac	314	5	100.0	10	4	AAH64621	Aah64621 Human col
c 242	5	100.0	10	3	AAA56165	Aaa56165 Human mon	315	5	100.0	10	4	AAH63466	Aah63466 Human ubi
243	5	100.0	10	3	AAA56189	Aaa56189 Human mon	316	5	100.0	10	4	AAH64499	Aah64499 Human ubi
244	5	100.0	10	3	AAA56364	Aaa56364 Human mac	317	5	100.0	10	4	AAH63757	Aah63757 Human ubi
245	5	100.0	10	3	AAA56297	Aaa56297 Human mac	318	5	100.0	10	4	AAH63841	Aah63841 Human ubi
246	5	100.0	10	3	AAA56422	Aaa56422 Human mac	c 319	5	100.0	10	4	AAH64663	Aah64663 Human col
c 247	5	100.0	10	3	AAA06056	Aaa06056 CFTR gene	c 320	5	100.0	10	4	AAH63736	Aah63736 Human ubi
248	5	100.0	10	3	AAA06049	Aaa06049 CFTR gene	c 321	5	100.0	10	4	AAH64015	Aah64015 Human ubi
c 249	5	100.0	10	3	AAZ79748	Aaz79748 Human col	322	5	100.0	10	4	AAH64021	Aah64021 Human ubi
250	5	100.0	10	3	AAZ797834	Aaz797834 Human lun	323	5	100.0	10	4	AAH63171	Aah63171 Human col
251	5	100.0	10	3	AAZ79801	Aaz79801 Human cys	324	5	100.0	10	4	AAH63839	Aah63839 Human ubi
252	5	100.0	10	3	AAZ79784	Aaz79784 Human bil	325	5	100.0	10	4	AAH64479	Aah64479 Human ubi
253	5	100.0	10	3	AAZ79784	Aaz79784 Human bil	326	5	100.0	10	4	AAH63542	Aah63542 Human ubi
c 254	5	100.0	10	3	AAZ89808	Aaz89808 Polynucle	c 327	5	100.0	10	4	AAH63435	Aah63435 Human ubi
255	5	100.0	10	3	AAZ89818	Aaz89818 Different	328	5	100.0	10	4	AAH63702	Aah63702 Human CHR
c 256	5	100.0	10	3	AAZ88020	Aaz88020 Human umb	c 329	5	100.0	10	4	AAH637284	Aah637284 Human CHR
257	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	330	5	100.0	10	4	AAH637307	Aah637307 Human CHR
258	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	331	5	100.0	10	4	AAH637290	Aah637290 Human CHR
c 259	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 332	5	100.0	10	4	AAH637286	Aah637286 Human CHR
260	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	333	5	100.0	10	4	AAH637281	Aah637281 Human CHR
261	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	334	5	100.0	10	4	AAH637292	Aah637292 Human CHR
c 262	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	335	5	100.0	10	4	AAH637291	Aah637291 Human TNF
c 263	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 336	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 264	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 337	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 265	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	338	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 266	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 339	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 267	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	340	5	100.0	10	4	AAH637291	Aah637291 LPS activ
268	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	341	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 269	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	342	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 270	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 343	5	100.0	10	4	AAH637291	Aah637291 LPS activ
271	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 344	5	100.0	10	4	AAH637291	Aah637291 LPS activ
272	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	345	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 273	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	346	5	100.0	10	4	AAH637291	Aah637291 LPS activ
274	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 347	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 275	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 348	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 276	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 349	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 277	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 350	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 278	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	351	5	100.0	10	4	AAH637291	Aah637291 LPS activ
279	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 352	5	100.0	10	4	AAH637291	Aah637291 LPS activ
280	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	353	5	100.0	10	4	AAH637291	Aah637291 LPS activ
281	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 354	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 282	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 355	5	100.0	10	4	AAH637291	Aah637291 LPS activ
283	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 356	5	100.0	10	4	AAH637291	Aah637291 LPS activ
284	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 357	5	100.0	10	4	AAH637291	Aah637291 LPS activ
285	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 358	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 286	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 359	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 287	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	360	5	100.0	10	4	AAH637291	Aah637291 LPS activ
288	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	361	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 289	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	362	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 290	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 363	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 291	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	364	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 292	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	365	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 293	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 366	5	100.0	10	4	AAH637291	Aah637291 LPS activ
294	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 367	5	100.0	10	4	AAH637291	Aah637291 LPS activ
295	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 368	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 296	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	369	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 297	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	370	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 298	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 371	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 299	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 372	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 300	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 373	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 301	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 374	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 302	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 375	5	100.0	10	4	AAH637291	Aah637291 LPS activ
303	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 376	5	100.0	10	4	AAH637291	Aah637291 LPS activ
304	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 377	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 305	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 378	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 306	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 379	5	100.0	10	4	AAH637291	Aah637291 LPS activ
307	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	380	5	100.0	10	4	AAH637291	Aah637291 LPS activ
308	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	381	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 309	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 382	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 310	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	383	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 311	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 384	5	100.0	10	4	AAH637291	Aah637291 LPS activ
312	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 385	5	100.0	10	4	AAH637291	Aah637291 LPS activ
c 313	5	100.0	10	3	AAZ88030	Aaz88030 Human umb	c 386	5	100.0	10	4	AAH637291	Aah637291 LPS activ

C 387	5	100.0	10	5	AAF33285	Aaf33285	Yeast	hig
C 388	5	100.0	10	5	AAF37110	Aaf37110	Yeast	NOR
C 389	5	100.0	10	5	AAF37595	Aaf37595	Yeast	NOR
C 390	5	100.0	10	5	AAF37818	Aaf37818	Yeast	NOR
C 391	5	100.0	10	5	AAF38175	Aaf38175	Yeast	NOR
C 392	5	100.0	10	5	AAF33329	Aaf33329	Yeast	NOR
C 393	5	100.0	10	5	AAF33517	Aaf33517	Yeast	NOR
C 394	5	100.0	10	5	AAF40094	Aaf40094	Yeast	NOR
C 395	5	100.0	10	5	AAF43676	Aaf43676	Yeast	NOR
C 396	5	100.0	10	5	AAF37161	Aaf37161	Yeast	NOR
C 397	5	100.0	10	5	AAF37827	Aaf37827	Yeast	NOR
C 398	5	100.0	10	5	AAF41372	Aaf41372	Yeast	NOR
C 399	5	100.0	10	5	AAF37825	Aaf37825	Yeast	NOR
C 400	5	100.0	10	5	AAF40219	Aaf40219	Yeast	NOR
C 401	5	100.0	10	5	AAF40871	Aaf40871	Yeast	NOR
C 402	5	100.0	10	5	AAF41373	Aaf41373	Yeast	NOR
C 403	5	100.0	10	5	AAF37826	Aaf37826	Yeast	NOR
C 404	5	100.0	10	5	AAF39835	Aaf39835	Yeast	NOR
C 405	5	100.0	10	5	AAF35782	Aaf35782	Yeast	NOR
C 406	5	100.0	10	5	AAF36321	Aaf36321	Yeast	NOR
C 407	5	100.0	10	5	AAF36854	Aaf36854	Yeast	NOR
C 408	5	100.0	10	5	AAF33847	Aaf33847	Yeast	NOR
C 409	5	100.0	10	5	AAF33850	Aaf33850	Yeast	NOR
C 410	5	100.0	10	5	AAF40348	Aaf40348	Yeast	NOR
C 411	5	100.0	10	5	AAF43264	Aaf43264	Yeast	NOR
C 412	5	100.0	10	5	AAF43265	Aaf43265	Yeast	NOR
C 413	5	100.0	10	5	AAF34444	Aaf34444	Yeast	NOR
C 414	5	100.0	10	5	AAF37747	Aaf37747	Yeast	NOR
C 415	5	100.0	10	5	AAF40677	Aaf40677	Yeast	NOR
C 416	5	100.0	10	5	AAF33811	Aaf33811	Yeast	NOR
C 417	5	100.0	10	5	AAF35340	Aaf35340	Yeast	NOR
C 418	5	100.0	10	5	AAF42421	Aaf42421	Yeast	NOR
C 419	5	100.0	10	5	AAF42643	Aaf42643	Yeast	NOR
C 420	5	100.0	10	5	AAF34090	Aaf34090	Yeast	NOR
C 421	5	100.0	10	5	AAF34956	Aaf34956	Yeast	NOR
C 422	5	100.0	10	5	AAF35366	Aaf35366	Yeast	NOR
C 423	5	100.0	10	5	AAF42398	Aaf42398	Yeast	NOR
C 424	5	100.0	10	5	AAF42994	Aaf42994	Yeast	NOR
C 425	5	100.0	10	5	AAF34867	Aaf34867	Yeast	NOR
C 426	5	100.0	10	5	AAF38240	Aaf38240	Yeast	NOR
C 427	5	100.0	10	6	AAS19577	Aas19577	Primer-ex	
C 428	5	100.0	10	6	AAS19589	Aas19589	Primer-ex	
C 429	5	100.0	10	6	ABK90355	Abk90355	Bcl-2-tar	
C 430	5	100.0	10	6	AAS18741	Aas18741	Primer-ex	
C 431	5	100.0	10	6	AD225080	Aed225080	Primer #7	
C 432	5	100.0	10	6	AD225092	Aed225092	Primer #1	
C 433	5	100.0	10	6	AAS98374	Aas98374	Galanin r	
C 434	5	100.0	10	6	AAS98387	Aas98387	Galanin r	
C 435	5	100.0	10	6	AAS98380	Aas98380	Galanin r	
C 436	5	100.0	10	6	AAS98370	Aas98370	Galanin r	
C 437	5	100.0	10	6	AAS98378	Aas98378	Galanin r	
C 438	5	100.0	10	6	AAS98382	Aas98382	Galanin r	
C 439	5	100.0	10	6	AAS98399	Aas98399	Galanin r	
C 440	5	100.0	10	6	AAS98372	Aas98372	Galanin r	
C 441	5	100.0	10	6	AAS98376	Aas98376	Galanin r	
C 442	5	100.0	10	6	AAS98384	Aas98384	Galanin r	
C 443	5	100.0	10	6	AD225297	Aed225297	Human HSD	
C 444	5	100.0	10	6	ABK24243	Abk24243	Retinalde	
C 445	5	100.0	10	6	AAL45322	Aal45322	Human KCN	
C 446	5	100.0	10	6	AAL45320	Aal45320	Human KCN	
C 447	5	100.0	10	6	ABK97526	Abk97526	Human LCA	
C 448	5	100.0	10	6	AAS18304	Aas18304	Primer-ex	
C 449	5	100.0	10	6	AAS18299	Aas18299	Primer-ex	
C 450	5	100.0	10	6	AD225445	Aed225445	Human GNR	
C 451	5	100.0	10	6	AD225432	Aed225432	Human GNR	
C 452	5	100.0	10	6	AAS18502	Aas18502	Vector pH	
C 453	5	100.0	10	6	AD26032	Aad26032	Primer #3	
C 454	5	100.0	10	6	AAS99283	Aas99283	Human F12	
C 455	5	100.0	10	6	ABL88338	Ab188338	Human CHR	
C 456	5	100.0	10	6	ABL88325	Ab188325	Human CHR	
C 457	5	100.0	10	6	ABK55538	Abk55538	Selectin	
C 458	5	100.0	10	6	ABL52211	Ab152211	Human PER	
C 459	5	100.0	10	6	ABL52165	Ab152165	Human PER	

460	5	100.0	10	6	ABL52210	Ab152210	Human PER	
C 461	5	100.0	10	6	ABK81932	Abk81932	Human Cyp	
C 462	5	100.0	10	6	ABK95830	Abk95830	Solute Ca	
C 463	5	100.0	10	6	ABK95857	Abk95857	Solute Ca	
C 464	5	100.0	10	6	ABK95831	Abk95831	Solute Ca	
C 465	5	100.0	10	6	ABK95832	Abk95832	Solute Ca	
C 466	5	100.0	10	6	AAS98896	Aas98896	Colony st	
C 467	5	100.0	10	6	AAS98818	Aas98818	Colony st	
C 468	5	100.0	10	6	AAS98902	Aas98902	Colony st	
C 469	5	100.0	10	6	AAS98828	Aas98828	Colony st	
C 470	5	100.0	10	6	AAS98907	Aas98907	Colony st	
C 471	5	100.0	10	6	AAS98843	Aas98843	Colony st	
C 472	5	100.0	10	6	AAS98829	Aas98829	Colony st	
C 473	5	100.0	10	6	AAS98841	Aas98841	Colony st	
C 474	5	100.0	10	6	ABL01316	Ab101316	Human MMP	
C 475	5	100.0	10	6	ABL01319	Ab101319	Human MMP	
C 476	5	100.0	10	6	AD225885	Aad225885	Primer #7	
C 477	5	100.0	10	6	ABL42696	Ab142696	Human mat	
C 478	5	100.0	10	6	ABL42710	Ab142710	Human mat	
C 479	5	100.0	10	6	ABL42711	Ab142711	Human mat	
C 480	5	100.0	10	6	ABL42738	Ab142738	Human mat	
C 481	5	100.0	10	6	ABL42665	Ab142665	Human mat	
C 482	5	100.0	10	6	ABL42716	Ab142716	Human mat	
C 483	5	100.0	10	6	ABL42734	Ab142734	Human mat	
C 484	5	100.0	10	6	ABL42791	Ab142791	Human mat	
C 485	5	100.0	10	6	ABL42743	Ab142743	Mouse neu	
C 486	5	100.0	10	6	ABL99039	Ab199039	Mouse neu	
C 487	5	100.0	10	6	ABL99037	Ab199037	Mouse neu	
C 488	5	100.0	10	6	ABL60194	Ab160194	Human MUC	
C 489	5	100.0	10	6	ABK89140	Abk89140	RNA seque	
C 490	5	100.0	10	6	ABK51933	Abk51933	Human FMO	
C 491	5	100.0	10	6	AAD45291	Aad45291	Human PON	
C 492	5	100.0	10	6	ABN81468	Abn81468	Human HTA	
C 493	5	100.0	10	6	ABN81469	Abn81469	Human HTA	
C 494	5	100.0	10	6	ABK96056	Abk96056	Human LIP	
C 495	5	100.0	10	6	ABK96057	Abk96057	Human LIP	
C 496	5	100.0	10	6	AAD26171	Aad26171	Human end	
C 497	5	100.0	10	6	AAD26176	Aad26176	Human end	
C 498	5	100.0	10	6	AAD26167	Aad26167	Human end	
C 499	5	100.0	10	6	AAD26169	Aad26169	Human end	
500	5	100.0	10	12	AD113733	Ad113733	Cytoplasm	

ALIGNMENTS

RESULT 1	
AAQ25520	
ID	AAQ25520 standard; DNA; 10 BP.
XX	
AC	AAQ25520;
XX	
DT	25-MAR-2003 (revised)
DT	01-DEC-1992 (first entry)
XX	
XX	Antisense nucleic acid derivative 19.
XX	
KW	HIV; ras; c-myb; AIDS-related complex; ss.
XX	
XX	Synthetic.
XX	
PN	WO9208729-A1.
XX	
PD	29-MAY-1992.
XX	
PF	18-NOV-1991; 91WO-JP001572.
XX	
PR	20-NOV-1990; 90JP-00315007.
XX	
PA	(SANY ) SANKYO CO LTD.
FI	Furukawa H, Momota K, Takiguchi Y, Hotoda H, Kaneko M;
XX	



DR WPI; 1992-200131/24.  
 XX New antiviral and antitumoural antisense nucleic acid derivs. - useful  
 PT for treating AIDS and AIDS-related complex.  
 XX  
 XX Claim 78; Page 200; 235pp; Japanese.  
 PS  
 CC The sequences given in AAQ79358-21 are nucleic acid derivatives which are  
 CC complementary to either a viral or a tumor gene ie. the sequence is  
 CC complementary to the HIV gene at 7947-7975 on the viral genome or to the  
 CC ras or c-myc oncogenes. These derivatives are useful as anticancer and  
 CC antiviral agents, esp. for the treatment of AIDS and AIDS-related  
 CC complex. They may be given orally or parenterally. The derivatives were  
 CC tributed so that they could be monitored easily. (Updated on 25-MAR-2003  
 CC to correct PN field.)  
 XX  
 SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 Db 2 GGGAG 6  
 RESULT 2  
 ID AAQ79358/c  
 XX AAQ79358 standard; DNA; 10 BP.  
 AC AAQ79358;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-JUN-1995 (first entry)  
 XX  
 DE Sequence of AP2 regulatory sequence located at posn. 896 in hEPLH.  
 XX  
 KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9423570-A1.  
 XX  
 PD 27-OCT-1994.  
 XX  
 PF 15-APR-1994; 94WO-US004141.  
 XX  
 PR 15-APR-1993; 93US-00046295.  
 PR 23-JUN-1993; 93US-00082850.  
 XX  
 PA (UUNY) UNIV NEW YORK STATE.  
 XX  
 PI Lee-Huang S;  
 XX  
 DR WPI; 1994-341353/42.  
 XX  
 PT New regulatory regions of human erythropoietin gene - used for studying  
 PT and treating diseases and for prodn. of transgenic animal models (Eng).  
 XX  
 PS Disclosure; Table I, p. 12; 81pp; English.  
 XX  
 CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
 CC hEPLH. This nucleic acid sequence includes EPO coding sequence, a 5'  
 CC flanking region contg. multiple regulatory elements and a 3' flanking  
 CC region contg. multiple regulatory elements. AAQ79354 shows the extended  
 CC 5' flanking region and includes all the 5' regulatory elements. This  
 CC region, consisting of the first 3892 of AAQ79353, was not found in the  
 CC 3.6 kb EPO genomic clone from fetal liver reported by others. The  
 CC flanking region comprises 3892 bp and contains CAAT and TATA boxes and at  
 CC lease 321 potential transcriptional regulatory elements. AAQ79356-Q79362  
 CC show several of these elements and their positions. The nucleotide  
 CC position of these elements is measured from the BamHI site at the 5' end

CC of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 10 BP; 0 A; 8 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 Db 10 GGGAG 6  
 RESULT 3  
 ID AAQ71089/c  
 XX AAQ71089 standard; cDNA; 10 BP.  
 AC AAQ71089;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-APR-1995 (first entry)  
 XX  
 DE Merlin exon 7 splice acceptor site.  
 XX  
 KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
 KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
 KW neurofibromatosis; merlin; moesin-erzin-radinix-like protein; D22S28;  
 KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
 KW merlin-associated tumour; D22S1; posterior capsular lens opacity;  
 KW deafness; balance disorder; paralysis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP613945-A2.  
 XX  
 PD 07-SEP-1994.  
 XX  
 PF 25-FEB-1994; 94EP-00301367.  
 XX  
 PR 25-FEB-1993; 93US-00022034.  
 PR 04-MAR-1993; 93US-00026063.  
 PR 19-AUG-1993; 93US-00108808.  
 PR 22-DEC-1993; 93US-00171718.  
 XX  
 PA (GSHO) GEN HOSPITAL CORP.  
 XX  
 PI Ttofatter JA, Maccollin MM, Gusella JF;  
 XX  
 DR WPI; 1994-272992/34.  
 XX  
 PT The tumour suppressor gene merlin - for treatment and diagnosis of  
 PT tumours and neurofibromatosis (NF2).  
 XX  
 PS Example 6; Page 26; 86pp; English.  
 XX  
 CC The sequences given in AAQ71078-109 represent the splice donor and  
 CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-  
 CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2  
 CC "gene" has been shown by linkage studies to be assigned to chromosome 22.  
 CC The missing or mutated gene in NF2 patients has been shown to be the  
 CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radinix-  
 CC like protein), which possesses tumour suppressor activity, and whose  
 CC tumour suppressor activity is mediated by inter- actions with the  
 CC cytoskeleton. The merlin gene is found on chromosome 22 between the known  
 CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene  
 CC is either lost or mutated. A mutant merlin protein may be encoded by a  
 CC gene in which a mutation of A to T at the first position of the codon  
 CC encoding amino acid 220 causes the substitution of Tyr for Asn. The  
 CC merlin gene may be used in gene therapy for the treatment of a merlin-  
 CC associated tumour or NF2, or for prevention of schwannoma, meningioma,  
 CC posterior capsular lens opacities, deafness or hearing loss, balance  
 CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)  
 XX

```
SQ Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGAG 5
DB 5 GGGAG 1
RESULT 4
AAQ64610/c
ID AAQ64610 standard; cDNA; 10 BP.
XX
AC AAQ64610;
XX
DT 25-MAR-2003 (revised)
DT 15-DEC-1994 (first entry)
XX
DE Alzheimer's/Parkinsons mitochondrial DNA mutation detection.
XX
KW Mitochondrial DNA mutation; associated with Alzheimer's;
KW Parkinson's disease; mismatch primers; PCR; amplification;
KW polymerase chain reaction; ss.
XX
OS Homo sapiens.
XX
PN WO9409162-A1.
XX
PD 28-APR-1994.
XX
PF 20-OCT-1993; 93WO-US010072.
XX
PR 20-OCT-1992; 92US-00963723.
XX
PA (UYEM-) UNIV EMORY SCHOOL MEDICINE.
XX
PI Wallace DC;
XX
WPI; 1994-151346/18.
XX
DR Detection of mitochondrial DNA mutation associated with Alzheimer's
PT disease and/or Parkinson's disease - for diagnosing or predicting a pre-
PT disposition to Alzheimer's disease and/or Parkinson's disease in a
PT patient.
XX
PS Disclosure; Page 36; 83pp; English.
XX
A 12S(956-965) insertion mutation harbours a novel 12S rRNA gene
CC insertion. Direct sequence analysis revealed that the insertion consisted
CC of approximately five cytosines within AAQ64610. This mitochondrial DNA
CC mutation is associated with Alzheimer's and/or Parkinson's diseases. The
CC detection of the mutations is useful for diagnosing or predicting a pre-
CC disposition to either of the diseases. (Updated on 25-MAR-2003 to correct
CC PN field.)
XX
SQ Sequence 10 BP; 0 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGAG 5
DB 9 GGGAG 5
RESULT 5
AA32614
ID AA32614 standard; DNA; 10 BP.
XX
AC AA32614;
XX
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGAG 5
DB 6 GGGAG 10
RESULT 6
AAQ96493
ID AAQ96493 standard; DNA; 10 BP.
XX
AC AAQ96493;
XX
DT 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
DE HIV-1 NL4-3 nef gene nucleotide deletion 88.
XX
KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX
OS Human immunodeficiency virus 1.
XX
PN WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU000063.
XX
XX
23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #14.
XX
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.
XX
PR 28-FEB-1994; 94US-00202927.
XX
PA (MICR-) MICROPROBE CORP.
PA (UYVA ) UNIV YALE.
XX
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX
WPI; 1995-311501/40.
XX
New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT intramolecular duplex with hairpin loop region, having selective
PT cytotoxicity against some tumour cells.
XX
PS Disclosure; Page 50; 107pp; English.
XX
New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC and which have a steroid structure attached to the 3'-end through a
CC linker attached to the A-ring of the steroid skeleton. In particular, the
CC present sequence has a cholesterol moiety attached by its A-ring to to
CC the 3'-phosphate derived through a carbonyl group attached to the ring nitrogen
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC oligonucleotides form stable duplexes at physiological temperature and
CC have selective cytotoxic activity against certain tumour cell lines,
CC including some with multiple drug resistance
XX
SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;
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PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX Claim 13; Page 189; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db |||||
3 GGGAG 7
RESULT 7
AAQ96710/C
ID AAQ96710 standard; DNA; 10 BP.
XX AC AAQ96710;
XX DT 16-OCT-2003 (revised)
XX DT 22-MAR-1996 (first entry)
XX HIV-1 NL4-3 nef gene nucleotide deletion 305.
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX 17-AUG-1995.
XX 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
XX 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.

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PS Claim 13; Page 192; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db |||||
6 GGGAG 2
RESULT 8
AAQ97063
ID AAQ97063 standard; DNA; 10 BP.
XX AC AAQ97063;
XX DT 16-OCT-2003 (revised)
XX DT 27-MAR-1996 (first entry)
XX HIV-1 NL4-3 LTR nucleotide deletion 45.
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX 17-AUG-1995.
XX 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
XX 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX Claim 14; Page 196; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX resulting avirulent HIV strains are still capable of inducing an immune
XX response in humans, and enable the generation of therapeutic, diagnostic
XX and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;

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Qy 1 GGGAG 5
Db 1 GGGAG 5

RESULT 14
AAQ96706/c
ID AAQ96706 standard; DNA; 10 BP.
XX AC AAQ96706;
XX 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX HIV-1 NL4-3 nef gene nucleotide deletion 301.
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX 17-AUG-1995.
XX 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
DT 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
DE HIV-1 NL4-3 nef gene nucleotide deletion 301.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX 17-AUG-1995.
XX 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
LTR region - can be used in a vaccine to inhibit/reduce productive
infection in an individual by a pathogenic strain.
XX Claim 13; Page 192; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
more dezanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
dezanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
resulting avirulent HIV strains are still capable of inducing an immune
response in humans, and enable the generation of therapeutic, diagnostic
and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
standardise OS field)
XX Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PS Claim 13; Page 192; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
more dezanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
dezanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
resulting avirulent HIV strains are still capable of inducing an immune
response in humans, and enable the generation of therapeutic, diagnostic
and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
standardise OS field)
XX Sequence 10 BP; 2 A; 5 C; 0 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db 10 GGGAG 6

RESULT 15
AAQ96491
ID AAQ96491 standard; DNA; 10 BP.
XX AC AAQ96491;
XX 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX HIV-1 NL4-3 nef gene nucleotide deletion 86.

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XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX 17-AUG-1995.
XX 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX (AURE-) AUSTRALIAN RED CROSS SOC.
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
LTR region - can be used in a vaccine to inhibit/reduce productive
infection in an individual by a pathogenic strain.
XX Claim 13; Page 189; 301pp; English.
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
more dezanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
dezanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
resulting avirulent HIV strains are still capable of inducing an immune
response in humans, and enable the generation of therapeutic, diagnostic
and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
standardise OS field)
XX Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db 5 GGGAG 9

RESULT 16
AAQ96711/c
ID AAQ96711 standard; DNA; 10 BP.
XX AC AAQ96711;
XX 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX HIV-1 NL4-3 nef gene nucleotide deletion 306.
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX Human immunodeficiency virus 1.
XX WO9521912-A1.
XX 17-AUG-1995.
XX 14-FEB-1995; 95WO-AU0000063.
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.

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PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 192; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 4 A; 4 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGAG 5
DB 5 GGGAG 1
RESULT 17
AAQ96494
ID AAQ96494 standard; DNA; 10 BP.
XX
XX AAQ96494;
AC
XX
XX 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 89.
DE
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO9521912-A1.
PN
XX
XX 17-AUG-1995.
PD
XX
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX
XX 16-OCT-2003 (revised)
PR 20-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 89.
DE
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO9521912-A1.
PN
XX
XX 17-AUG-1995.
PD
XX
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
PI
XX
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 189; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGAG 5
DB 5 GGGAG 1
RESULT 18
AAQ96490
ID AAQ96490 standard; DNA; 10 BP.
XX
XX AAQ96490;
AC
XX
XX 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 85.
DE
XX
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX
XX Human immunodeficiency virus 1.
OS
XX
XX WO9521912-A1.
PN
XX
XX 17-AUG-1995.
PD
XX
XX 14-FEB-1995; 95WO-AU0000063.
PF
XX
XX 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
XX 23-DEC-1994; 94AU-00000284.
XX
XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
PI
XX
XX WPI; 1995-293115/38.
XX
XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX
XX Claim 13; Page 189; 301pp; English.
XX
XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
XX Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGAG 5
DB 5 GGGAG 1

```





XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 XX WPI; 1995-293115/38.  
 DR  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX  
 PS Claim 13; Page 192; 301pp; English.  
 XX  
 CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 10 BP; 3 A; 5 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 DB |||||  
 8 GGGAG 4

RESULT 22  
 ID AAQ97061 standard; DNA; 10 BP.  
 XX  
 AC AAQ97061;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 27-MAR-1996 (first entry)  
 XX  
 XX HIV-1 NL4-3 LTR nucleotide deletion 43.  
 XX  
 XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 XX Human immunodeficiency virus 1.  
 XX WO9521912-A1.  
 XX  
 PD 17-AUG-1995.  
 XX  
 PF 14-FEB-1995; 95WO-AU0000063.  
 XX  
 PR 14-FEB-1994; 94AU-00003864.  
 PR 21-FEB-1994; 94AU-00004002.  
 PR 23-DEC-1994; 94AU-00000284.  
 XX  
 PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 PA (AURE-) AUSTRALIAN RED CROSS SOC.  
 XX  
 PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 DR WPI; 1995-293115/38.  
 XX  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX  
 PS Claim 14; Page 196; 301pp; English.  
 XX  
 CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The

CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 DB |||||  
 6 GGGAG 10

RESULT 23  
 ID AAQ97064 standard; DNA; 10 BP.  
 XX  
 AC AAQ97064;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 27-MAR-1996 (first entry)  
 XX  
 XX HIV-1 NL4-3 LTR nucleotide deletion 46.  
 DE  
 XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 XX Human immunodeficiency virus 1.  
 XX WO9521912-A1.  
 XX  
 PD 17-AUG-1995.  
 XX  
 PF 14-FEB-1995; 95WO-AU0000063.  
 XX  
 PR 14-FEB-1994; 94AU-00003864.  
 PR 21-FEB-1994; 94AU-00004002.  
 PR 23-DEC-1994; 94AU-00000284.  
 XX  
 PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 PA (AURE-) AUSTRALIAN RED CROSS SOC.  
 XX  
 PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 DR WPI; 1995-293115/38.  
 XX  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX  
 PS Claim 14; Page 196; 301pp; English.  
 XX  
 CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 DB |||||  
 3 GGGAG 7

```

RESULT 24
AAQ88437
ID AAQ88437 standard; DNA; 10 BP.
XX
XX AAQ88437;
XX
XX
XX 19-DEC-1995 (first entry)
XX
XX Human mitochondrial D-loop region DNA probe 16-0.
XX
XX Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
XX D-loop region; biological chip; hybridisation fingerprint;
XX interrogation position; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 10
XX /tag= a
XX /note= "3'-end of probe is covalently attached to chip
XX surface"
XX
XX WO9511995-A1.
XX
XX 04-MAY-1995.
XX
XX 26-OCT-1994; 94WO-US012305.
XX
XX 26-OCT-1993; 93US-00143312.
XX 02-AUG-1994; 94US-00284064.
XX
XX (AFY-) AFFYMAX TECHNOLOGIES NV.
XX
XX Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
XX Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheidon EL;
XX WPI; 1995-178887/23.
XX
XX New arrays of oligo:nucleotide probes - used for comparing known
XX sequences with variants for detection of mutation(s) and sequencing.
XX
XX Disclosure; Page 106; 223pp; English.
XX
XX A DNA chip was prepared for analysing sequences contained in a 1.3kb
XX fragment of human mitochondrial DNA from the D-loop region, the most
XX polymorphic region of human mitochondrial DNA. The chip comprised a set
XX of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
XX varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
XX x 1cm array. Each position in the sequence was represented by at least
XX one probe (usually 2 or more). DNA was amplified from six human donors
XX and then transcribed to give the 1.3kb RNA transcripts which were
XX fragmented and hybridised to the chip. For each individual, a unique
XX hybridisation fingerprint was produced on the chip; all differences could
XX be correlated with differences in the cloned genomic DNA sequence
XX
XX Sequence 10 BP; 2 A; 1 C; 7 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGAG 5
XX |||||
XX 6 GGGAG 10
XX
XX
XX RESULT 25
XX AAQ88493
XX ID AAQ88493 standard; DNA; 10 BP.
XX
XX AAQ88493;
XX
XX
XX 06-MAR-1996 (first entry)
XX
XX Eucalyptus grandis coppicing vigour marker primer V2.
XX
XX Eucalyptus; urophylla; grandis; coppicing vigour marker;
XX RAPD genetic marker; random amplified polymorphic DNA analysis;
XX woody perennial plant; family selection; pedigree; mapping; primer; ss.
XX

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DT 20-DEC-1995 (first entry)
XX
XX Human mitochondrial D-loop region DNA probe 4-4.
XX
XX Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
XX D-loop region; biological chip; hybridisation fingerprint;
XX interrogation position; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX modified_base 10
XX /tag= a
XX /note= "3'-end of probe is covalently attached to chip
XX surface"
XX
XX WO9511995-A1.
XX
XX 04-MAY-1995.
XX
XX 26-OCT-1994; 94WO-US012305.
XX
XX 26-OCT-1993; 93US-00143312.
XX 02-AUG-1994; 94US-00284064.
XX
XX (AFY-) AFFYMAX TECHNOLOGIES NV.
XX
XX Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;
XX Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheidon EL;
XX WPI; 1995-178887/23.
XX
XX New arrays of oligo:nucleotide probes - used for comparing known
XX sequences with variants for detection of mutation(s) and sequencing.
XX
XX Disclosure; Page 107; 223pp; English.
XX
XX A DNA chip was prepared for analysing sequences contained in a 1.3kb
XX fragment of human mitochondrial DNA from the D-loop region, the most
XX polymorphic region of human mitochondrial DNA. The chip comprised a set
XX of 268 overlapping oligonucleotide probes (see AAQ88421-Q88684) of
XX varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
XX x 1cm array. Each position in the sequence was represented by at least
XX one probe (usually 2 or more). DNA was amplified from six human donors
XX and then transcribed to give the 1.3kb RNA transcripts which were
XX fragmented and hybridised to the chip. For each individual, a unique
XX hybridisation fingerprint was produced on the chip; all differences could
XX be correlated with differences in the cloned genomic DNA sequence
XX
XX Sequence 10 BP; 1 A; 1 C; 8 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGAG 5
XX |||||
XX 5 GGGAG 9
XX
XX
XX RESULT 26
XX AAQ99831/C
XX ID AAQ99831 standard; cDNA; 10 BP.
XX
XX AAQ99831;
XX
XX
XX 06-MAR-1996 (first entry)
XX
XX Eucalyptus grandis coppicing vigour marker primer V2.
XX
XX Eucalyptus; urophylla; grandis; coppicing vigour marker;
XX RAPD genetic marker; random amplified polymorphic DNA analysis;
XX woody perennial plant; family selection; pedigree; mapping; primer; ss.
XX

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XX Synthetic.  
 XX WO9519697-A1.  
 PN 27-JUL-1995.  
 XX 19-JAN-1995; 95WO-US000677.  
 PF 21-JAN-1994; 94US-00184567.  
 PR (UYNC-) UNIV NORTH CAROLINA STATE.  
 PA Omalley DM, Sederoff RR, Grattapaglia D;  
 PI WPI; 1995-269212/35.  
 XX Determn. of heritable oligogenic traits in woody plants by genomic  
 PT mapping of multiple markers in a two generation plant family - used to  
 PT select plants with desired characteristics for breeding.  
 PS Example 6; Page 58; 103pp; English.  
 XX RAPD analysis was used to determine whether certain quantitative traits  
 CC were heritable oligogenic traits in Eucalyptus trees. Sets of  
 CC commercially available random 10-mer primers were used to amplify  
 CC fragments from the genomic DNA of E.urophylla, E.grandis and F1 progeny  
 CC obtained by crossing the two species. Subsequent mapping analysis showed  
 CC that the primers in AAQ9829-099833 are all useful for amplifying markers  
 CC of coppicing vigour from E.grandis  
 XX Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGAG 5  
 Db 10 GGGAG 6  
 |||||  
 RESULT 27  
 AAT10087/C  
 ID AAT10087 standard; DNA; 10 BP.  
 XX AAT10087;  
 XX 29-AUG-1996 (first entry)  
 DT Hammerhead ribozyme RNA complementary oligonucleotide.  
 XX Hammerhead; ribozyme; enhanced RNA cleavage; cleavage efficiency;  
 DE viral inactivation; viral RNA transcript; hybridisation; target RNA;  
 KW complementary oligonucleotide; ss.  
 XX Synthetic.  
 XX WO9600232-A1.  
 PN 04-JAN-1996.  
 XX 21-JUN-1995; 95WO-AU000359.  
 PF 24-JUN-1994; 94US-00265484.  
 PR (GENE-) GENE SHEARS PTY LTD.  
 XX Keese P, Stapper M, Perriman R;  
 PI WPI; 1996-068825/07.  
 XX Improved catalytic hammer-head ribozyme(s) and enhanced RNA cleavage -

PT useful in activating target sequences in e.g. infectious viruses.  
 XX Example 3; Page 64; 122pp; English.  
 PS The present oligonucleotide is a complementary oligonucleotide (CO) for  
 CC the ribozyme given in AAT10062 or AAT10072, which are specific examples  
 CC of a claimed, highly generic, hammerhead ribozyme with enhanced RNA  
 CC cleavage. The CO alters the cleavage efficiency of the ribozymes, i.e.  
 CC the cleavage efficiency of the CO in combination with a ribozyme as a  
 CC of a control without the CO is 161. The ribozymes of the invention (opt.  
 CC in conjunction with a CO) have extensive therapeutic and biological  
 CC applications, e.g. disease causing viruses in man, animals and plants may  
 CC be inactivated by administering to an infected subject a ribozyme adapted  
 CC to hybridise to, and cleave RNA transcripts of the virus  
 XX Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGAG 5  
 Db 10 GGGAG 6  
 |||||  
 RESULT 28  
 AAT98839/C  
 ID AAT98839 standard; DNA; 10 BP.  
 XX AAT98839;  
 XX 20-MAR-1998 (first entry)  
 DT Binding site BSN12 identified using the method of the invention.  
 XX Protein-binding site isolation; transcription factor modification;  
 DE DNA-binding protein; inhibitor identification; ss.  
 KW Synthetic.  
 XX WO9727330-A1.  
 PN 31-JUL-1997.  
 PD 24-JAN-1997; 97WO-US001230.  
 PF 24-JAN-1996; 96US-00590571.  
 PR (UYVA ) UNIV YALE.  
 XX Weissman SM, Kulkarni P, Nallur GN;  
 PI WPI; 1997-393714/36.  
 XX Identifying protein-binding sites for DNA-binding proteins - using  
 PT duplexes having 5' and 3' sequences for annealing to amplification  
 PT primers with an internal potential protein-binding site sequence.  
 XX Example 3; Page 19; 52pp; English.  
 PS This sequence represents a binding site identified using the method of  
 CC the invention. This sequence was identified using the 32p-labelled  
 CC oligonucleotide duplex shown in AAT76581 and the primers shown in  
 CC AAT76582-T76583 in the method of the invention. The method is for  
 CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
 CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
 CC having 5' and 3' sequences capable of annealing to primers for  
 CC amplification and an internal sequence having a potential protein-binding  
 CC site, a non-specific inhibitor and a sample containing DNA-binding  
 CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
 CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
 CC amplified duplexes; thereby isolating protein-binding sites for the DNA-

CC binding proteins. The methods can be used to identify protein-binding  
 CC sites which can be used to identify corresponding DNA-binding proteins in  
 CC an expression library. They can also be used to develop products to  
 CC inhibit the function of a given DNA-binding protein or for the  
 CC modification of transcription factors

XX SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGAG 5  
 |||||  
 Db 9 GGGAG 5

## RESULT 29

AAT98848  
 ID AAT98848 standard; DNA; 10 BP.

XX AC AAT98848;

XX DT 20-MAR-1998 (first entry)

XX DE Binding site BSN6 identified using the method of the invention.

XX KW Protein-binding site isolation; transcription factor modification;  
 KW DNA-binding protein; inhibitor identification; ss.

XX OS Synthetic.

XX PN WO9727330-A1.

XX PD 31-JUL-1997.

XX PF 24-JAN-1997; 97WO-US001230.

XX PR 24-JAN-1996; 96US-00590571.

XX PA (UYUA ) UNIV YALE.

XX PI Weissman SM, Kulkarni P, Nallur GN;

XX DR WPI; 1997-393714/36.

XX PT Identifying protein-binding sites for DNA-binding proteins - using  
 PT duplexes having 5' and 3' sequences for annealing to amplification  
 PT primers with an internal potential protein-binding site sequence.

XX PS Example 3; Page 19; 52pp; English.

XX CC This sequence represents a binding site identified using the method of  
 CC the invention. This sequence was identified using the 32p-labelled  
 CC oligonucleotide duplex shown in AAT96581 and the primers shown in  
 CC AAT96582-76583 in the method of the invention. The method is for  
 CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
 CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
 CC having 5' and 3' sequences capable of annealing to primers for  
 CC amplification and an internal sequence having a potential protein-binding  
 CC site, a non-specific inhibitor and a sample containing DNA-binding  
 CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
 CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
 CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
 CC binding proteins. The methods can be used to identify protein-binding  
 CC sites which can be used to identify corresponding DNA-binding proteins in  
 CC an expression library. They can also be used to develop products to  
 CC inhibit the function of a given DNA-binding protein or for the  
 CC modification of transcription factors

XX SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGAG 5  
 |||||  
 Db 3 GGGAG 7

## RESULT 30

AAT98850  
 ID AAT98850 standard; DNA; 10 BP.

XX AC AAT98850;

XX DT 20-MAR-1998 (first entry)

XX DE Binding site BSN13 identified using the method of the invention.

XX KW Protein-binding site isolation; transcription factor modification;  
 KW DNA-binding protein; inhibitor identification; ss.

XX OS Synthetic.

XX PN WO9727330-A1.

XX PD 31-JUL-1997.

XX PF 24-JAN-1997; 97WO-US001230.

XX PR 24-JAN-1996; 96US-00590571.

XX PA (UYUA ) UNIV YALE.

XX PI Weissman SM, Kulkarni P, Nallur GN;

XX DR WPI; 1997-393714/36.

XX PT Identifying protein-binding sites for DNA-binding proteins - using  
 PT duplexes having 5' and 3' sequences for annealing to amplification  
 PT primers with an internal potential protein-binding site sequence.

XX PS Example 3; Page 19; 52pp; English.

XX CC This sequence represents a binding site identified using the method of  
 CC the invention. This sequence was identified using the 32p-labelled  
 CC oligonucleotide duplex shown in AAT96581 and the primers shown in  
 CC AAT96582-76583 in the method of the invention. The method is for  
 CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
 CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
 CC having 5' and 3' sequences capable of annealing to primers for  
 CC amplification and an internal sequence having a potential protein-binding  
 CC site, a non-specific inhibitor and a sample containing DNA-binding  
 CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
 CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
 CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
 CC binding proteins. The methods can be used to identify protein-binding  
 CC sites which can be used to identify corresponding DNA-binding proteins in  
 CC an expression library. They can also be used to develop products to  
 CC inhibit the function of a given DNA-binding protein or for the  
 CC modification of transcription factors

XX SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGAG 5  
 |||||  
 Db 6 GGGAG 10

## RESULT 31

```

AAV48046/C
ID AAV48046 standard; DNA; 10 BP.
XX
XX AC AAV48046;
XX
XX DT 19-OCT-1998 (first entry)
XX
XX DE Human B7-2 targetted oligonucleotide 10991.
XX
XX KW ss; human; B7; T cell; inflammation; autoimmune disease; cell activation;
XX KW cell proliferation.
XX
XX OS Synthetic.
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX modified_base 1..10
XX /*tag= a
XX /note= "Phosphorothioate linkages"
XX
XX WO9829124-A1.
XX
XX PD 09-JUL-1998.
XX
XX PF 16-DEC-1997; 97WO-US023270.
XX
XX PR 31-DEC-1996; 96US-00777266.
XX
XX PA (ISIS-) ISIS PHARM INC.
XX
XX PI Bennett CP, Vickers TA;
XX
XX WPI; 1998-387783/33.
XX
XX New oligo:nucleotide(s) that modulate expression of B7 proteins - used
XX for, e.g. controlling activation and proliferation of T cells,
XX particularly for treatment, diagnosis and prevention of inflammation.
XX
XX Example 1; Page 39; 120pp; English.
XX
XX The oligonucleotides which specifically hybridise to B7 modulate its
XX expression (and thus T cell activation and proliferation). This is
XX particularly useful for treatment and prevention of inflammation and
XX autoimmune diseases, e.g. asthma, (juvenile) diabetes, myasthenia gravis,
XX Grave's disease, rheumatoid arthritis, allograft rejection, psoriasis,
XX (systemic) lupus erythematosus, multiple sclerosis, contact dermatitis,
XX rhinitis, allergy, cancer and metastases. The oligonucleotides may also
XX be used to manipulate T cell activation ex vivo; to determine or detect
XX B7 protein expression; for diagnosis; as assay and purification reagents,
XX and to study physiological roles of B7 proteins
XX
XX Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 1 GGGAG 5
XX |||||
XX Db 3 GGGAG 7
XX
XX RESULT 33
XX AAV34986
XX ID AAV34986 standard; DNA; 10 BP.
XX
XX AC AAV34986;
XX
XX DT 13-OCT-1998 (first entry)
XX
XX DE Synthetic Agaricus bisporus RAPD primer.
XX
XX KW Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.
XX
XX OS Synthetic.
XX
XX PN WO9821975-A1.
XX
XX PD 28-MAY-1998.
XX
XX PF 19-NOV-1996; 96WO-US018686.
XX
XX PR 19-NOV-1996; 96WO-US018686.
XX
XX PA (AMYC-) AMYCEL INC.
XX
XX PI Loftus MG, Lodder SC, Legg EJ;
XX
XX WPI; 1998-312054/27.
XX
XX New strains of Agaricus bisporus with improved cap whiteness - compared
XX with the U1 strain but retaining other desirable features of this strain.
XX
XX Disclosure; Page 10; 26pp; English.
XX
XX The sequence is that of an RAPD (random amplified DNA) primer which was

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XX OS Synthetic.
XX
XX PN JP10262667-A.
XX
XX PD 06-OCT-1998.
XX
XX PF 19-MAR-1997; 97JP-00106563.
XX
XX PR 19-MAR-1997; 97JP-00106563.
XX
XX PA (SAOK ) NIPPON SEISHI KK.
XX
XX WPI; 1998-587287/50.
XX
XX New primer - used for the detection of genetic uniformity of a clone
XX plant body.
XX
XX Example 1; Page 5; 7pp; Japanese.
XX
XX This sequence represents an example of the PCR primer of the invention.
XX The primers of the invention consist of 10 bases and have the formula: 5'
XX -NNNN XY XY XY-3'; where: N, X and Y = optional nucleic acid monomers;
XX and N and X as well as N and Y may be nucleic acids having a same base
XX but X and Y are nucleic acids having different bases. The primers are
XX used to distinguish between plant clone bodies at the DNA level, with
XX high sensitivity
XX
XX Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.9e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 1 GGGAG 5
XX |||||
XX Db 3 GGGAG 7
XX
XX RESULT 33
XX AAV34986
XX ID AAV34986 standard; DNA; 10 BP.
XX
XX AC AAV34986;
XX
XX DT 13-OCT-1998 (first entry)
XX
XX DE Synthetic Agaricus bisporus RAPD primer.
XX
XX KW Random amplified polymorphic DNA; primer; mushroom; RAPD; ss.
XX
XX OS Synthetic.
XX
XX PN WO9821975-A1.
XX
XX PD 28-MAY-1998.
XX
XX PF 19-NOV-1996; 96WO-US018686.
XX
XX PR 19-NOV-1996; 96WO-US018686.
XX
XX PA (AMYC-) AMYCEL INC.
XX
XX PI Loftus MG, Lodder SC, Legg EJ;
XX
XX WPI; 1998-312054/27.
XX
XX New strains of Agaricus bisporus with improved cap whiteness - compared
XX with the U1 strain but retaining other desirable features of this strain.
XX
XX Disclosure; Page 10; 26pp; English.
XX
XX The sequence is that of an RAPD (random amplified DNA) primer which was

```

CC used in the isolation of an Agaricus bisporus mushroom strain which has  
CC whiter caps, less scaling than known strains, particularly for mushrooms  
CC produced in the first break, so it is more valuable (suitable for  
CC marketing fresh rather than canning). It also retains the desirable  
CC characteristics (good cap shape and shelf life, thick stem and veil) of  
CC the U1 strain  
XX  
SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GGGAG 5  
Db 1 GGGAG 5  
  
RESULT 34  
AAV50112/c  
ID AAV50112 standard; DNA; 10 BP.  
XX  
AC AAV50112;  
XX  
DT 21-OCT-1998 (first entry)  
XX  
DE Yeast tag for NORF gene locus NORF2.  
XX  
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;  
KW eukaryotic cell; antifungal; SAGE tag; gene expression;  
KW serial analysis of gene expression; probe; ss.  
XX  
OS Saccharomyces cerevisiae.  
OS Synthetic.  
XX  
FN WO9832847-A2.  
XX  
PD 30-JUL-1998.  
XX  
PF 22-JAN-1998; 98WO-US001216.  
XX  
PR 23-JAN-1997; 97US-0035917P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 1998-427943/36.  
XX  
PT Yeast transcriptome - useful for modulating eukaryotic cell, for  
PT screening antifungal agents, and for identifying genes in cell cycle  
PT progression.  
XX  
PS Claim 1; Page 23; 44pp; English.  
XX  
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene  
CC involved in cell cycle progression selected from the group of  
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)  
CC tags for highly expressed genes and NORF genes are given in AAV50051 to  
CC AAV50345. The present invention describes: (1) a method of using yeast  
CC genes to modulate the cell cycle which comprises administering to a cell  
CC an isolated DNA molecule comprising a yeast gene which is involved in  
CC cell cycle progression selected from differentially expressed genes (SAGE  
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate  
CC antifungal drugs which comprises contacting a test substance with a yeast  
CC cell and monitoring expression of a yeast gene which is involved in cell  
CC cycle progression; (3) a method of identifying human genes which are  
CC involved in cell cycle progression which comprises hybridizing a probe  
CC comprising at least 10 contiguous nucleotides of a yeast gene which is  
CC differentially expressed between at least 2 phases selected from the log  
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining  
CC the phase in the cell cycle, where the probe comprises at least 14  
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to

CC AAV50345), or as an array of probes on a solid support  
XX  
SQ Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 GGGAG 5  
Db 8 GGGAG 4  
  
RESULT 35  
AAV50300/c  
ID AAV50300 standard; DNA; 10 BP.  
XX  
AC AAV50300;  
XX  
DT 21-OCT-1998 (first entry)  
XX  
DE Yeast tag for additional NORF chromosome 11 tag position 93528.  
XX  
KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;  
KW eukaryotic cell; antifungal; SAGE tag; gene expression;  
KW serial analysis of gene expression; probe; ss.  
XX  
OS Saccharomyces cerevisiae.  
OS Synthetic.  
XX  
FN WO9832847-A2.  
XX  
PD 30-JUL-1998.  
XX  
PF 22-JAN-1998; 98WO-US001216.  
XX  
PR 23-JAN-1997; 97US-0035917P.  
XX  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX  
PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX  
DR WPI; 1998-427943/36.  
XX  
PT Yeast transcriptome - useful for modulating eukaryotic cell, for  
PT screening antifungal agents, and for identifying genes in cell cycle  
PT progression.  
XX  
PS Claim 1; Page 27; 44pp; English.  
XX  
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene  
CC involved in cell cycle progression selected from the group of  
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)  
CC tags for highly expressed genes and NORF genes are given in AAV50051 to  
CC AAV50345. The present invention describes: (1) a method of using yeast  
CC genes to modulate the cell cycle which comprises administering to a cell  
CC an isolated DNA molecule comprising a yeast gene which is involved in  
CC cell cycle progression selected from differentially expressed genes (SAGE  
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate  
CC antifungal drugs which comprises contacting a test substance with a yeast  
CC cell and monitoring expression of a yeast gene which is involved in cell  
CC cycle progression; (3) a method of identifying human genes which are  
CC involved in cell cycle progression which comprises hybridizing a probe  
CC comprising at least 10 contiguous nucleotides of a yeast gene which is  
CC differentially expressed between at least 2 phases selected from the log  
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining  
CC the phase in the cell cycle, where the probe comprises at least 14  
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to  
CC AAV50345), or as an array of probes on a solid support  
XX  
SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.9e+06; Mismatches 0; Indels 0; Gaps 0;  
Matches 5; Conservative 0;

Qy 1 GGGAG 5  
|||||  
Db 6 GGGAG 2

RESULT 36  
AAV50068/c  
ID AAV50068 standard; DNA; 10 BP.  
XX AC AAV50068;  
XX DT 21-OCT-1998 (first entry)  
XX DE Yeast tag for highly expressed gene locus NORF2.  
XX KW Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;  
KW eukaryotic cell; antifungal; SAGE tag; gene expression;  
KW serial analysis of gene expression; probe; ss.  
XX OS Saccharomyces cerevisiae.  
XX OS Synthetic.  
XX PN WO9832847-A2.  
XX PD 30-JUL-1998.  
XX PF 22-JAN-1998; 98WO-US001216.  
XX PR 23-JAN-1997; 97US-0035917P.  
XX PA (UJJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
XX PI Velculescu VE, Vogelstein B, Kinzler KW;  
XX WPI; 1998-427943/36.  
XX DR Yeast transcriptome - useful for modulating eukaryotic cell, for  
XX screening antifungal agents, and for identifying genes in cell cycle  
XX progression.  
XX PS Claim 11; Page 21; 44pp; English.  
XX CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene  
XX involved in cell cycle progression selected from the group of  
XX nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)  
XX tags for highly expressed genes and NORF genes are given in AAV50051 to  
XX AAV50345. The present invention describes: (1) a method of using yeast  
XX genes to modulate the cell cycle which comprises administering to a cell  
XX an isolated DNA molecule comprising a yeast gene which is involved in  
XX cell cycle progression selected from differentially expressed genes (SAGE  
XX tags given in AAV50051 to AAV50345); (2) a method for screening candidate  
XX antifungal drugs which comprises contacting a test substance with a yeast  
XX cell and monitoring expression of a yeast gene which is involved in cell  
XX cycle progression; (3) a method of identifying human genes which are  
XX involved in cell cycle progression which comprises hybridizing a probe  
XX comprising at least 10 contiguous nucleotides of a yeast gene which is  
XX differentially expressed between at least 2 phases selected from the log  
XX phase, the S phase and the G2/M phase; and (4) a probe for ascertaining  
XX the phase in the cell cycle, where the probe comprises at least 14  
XX contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to  
XX AAV50345), or as an array of probes on a solid support  
XX Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db

RESULT 38  
AAV35998  
ID AAV35998 standard; DNA; 10 BP.  
XX AC AAV35998;  
XX DT 26-AUG-1998 (first entry)

Db 8 GGGAG 4

RESULT 37  
AAV35939/c  
ID AAV35939 standard; DNA; 10 BP.  
XX AC AAV35939;  
XX DT 26-AUG-1998 (first entry)  
XX DE Primer used in RAPD assay of the invention.  
XX KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;  
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.  
XX OS Synthetic.  
XX OS Sus sp.  
XX PN WO9815837-A1.  
XX PD 16-APR-1998.  
XX PF 07-OCT-1997; 97WO-GB002741.  
XX PR 07-OCT-1996; 96GB-00020904.  
XX PR 18-FEB-1997; 97GB-00003350.  
XX PR 20-MAR-1997; 97GB-00005796.  
XX PR 09-SEP-1997; 97GB-00019002.  
XX PA (MEAT-) MEAT & LIVESTOCK COMMISSION.  
XX PI Maltin CA, Steven J, Warkup CC;  
XX WPI; 1998-240968/21.  
XX DR Assay for alleles or muscle fibre composition characteristic of Duroc  
XX type pigs - comprises determination of genotype or muscle fibre  
XX properties, used to identify animals for breeding programs and to assess  
XX meat quality.  
XX PS Example 3; Page 33; 56pp; English.  
XX CC PCR primers AAV35877-996 were used in a rapid amplification of  
XX polymorphic DNA (RAPD) reaction in the assay of the invention. This assay  
XX is used to determine if an animal has an allele for, or muscle fibre  
XX composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce  
XX meat of superior quality (particularly tenderness) but are normally less  
XX efficient feed converters and fatter than other types. The assay  
XX comprises analysing a tissue sample to determine if the genotype  
XX comprises the allele, and genetic features typical of animals that have  
XX Duroc characteristics for use in breeding programmes (to develop the  
XX animals with Duroc pig characteristics), and to assess meat quality  
XX Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 7 GGGAG 3

RESULT 38  
AAV35998  
ID AAV35998 standard; DNA; 10 BP.  
XX AC AAV35998;  
XX DT 26-AUG-1998 (first entry)

```

XX DE Primer used in to show differences in Large white and Duroc genotypes.
XX XX
XX KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX XX
XX OS Synthetic.
XX OS Sus sp.
XX FN WO9815837-A1.
XX XX
XX PD 16-APR-1998.
XX XX
XX PF 07-OCT-1997; 97WO-GB002741.
XX XX
XX FR 07-OCT-1996; 96GB-00020904.
XX FR 18-FEB-1997; 97GB-00003350.
XX PR 20-MAR-1997; 97GB-00005796.
XX PR 09-SEP-1997; 97GB-00019002.
XX XX
XX PA (MEAT-) MEAT & LIVESTOCK COMMISSION.
XX XX
XX PI Maltin CA, Steven J, Warkup CC;
XX XX
XX DR WPI; 1998-240968/21.
XX XX
XX PT Assay for alleles or muscle fibre composition characteristic of Duroc
XX type pigs - comprises determination of genotype or muscle fibre
XX PT properties, used to identify animals for breeding programs and to assess
XX PT meat quality.
XX XX
XX PS Example 3; Page 35; 56pp; English.
XX XX
XX CC PCR primers AAV35997-6013 were used in a rapid amplification of
XX CC polymorphic DNA (RAPD) assay to show differences in the Large white and
XX CC Duroc genotype using the assay of the invention. This assay is used to
XX CC determine if an animal has an allele for, or muscle fibre composition
XX CC (MFC) characteristic of, the Duroc pig. Duroc pigs produce meat of
XX CC superior quality (particularly tenderness) but are normally less
XX CC efficient feed converters and fatter than other types. The assay
XX CC comprises analysing a tissue sample to determine if the genotype
XX CC comprises the allele, and genetic features typical of animals with Duroc-
XX CC type MFC are present. The method is used to select animals that have
XX CC Duroc characteristics for use in breeding programmes (to develop the
XX CC animals with Duroc pig characteristics), and to assess meat quality
XX XX
XX SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 3 GGGAG 7

RESULT 39
AAV35963/c
ID AAV35963 standard; DNA; 10 BP.
XX XX
XX AC AAV35963;
XX XX
XX DT 26-AUG-1998 (first entry)
XX XX
XX DE Primer used in RAPD assay of the invention.
XX XX
XX KW Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX XX
XX OS Synthetic.
XX OS Sus sp.
XX XX

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PN WO9815837-A1.
XX XX
XX PD 16-APR-1998.
XX XX
XX PF 07-OCT-1997; 97WO-GB002741.
XX XX
XX FR 07-OCT-1996; 96GB-00020904.
XX PR 18-FEB-1997; 97GB-00003350.
XX PR 20-MAR-1997; 97GB-00005796.
XX PR 09-SEP-1997; 97GB-00019002.
XX XX
XX PA (MEAT-) MEAT & LIVESTOCK COMMISSION.
XX XX
XX PI Maltin CA, Steven J, Warkup CC;
XX XX
XX DR WPI; 1998-240968/21.
XX XX
XX PT Assay for alleles or muscle fibre composition characteristic of Duroc
XX type pigs - comprises determination of genotype or muscle fibre
XX PT properties, used to identify animals for breeding programs and to assess
XX PT meat quality.
XX XX
XX PS Example 3; Page 33; 56pp; English.
XX XX
XX CC PCR primers AAV35877-996 were used in a rapid amplification of
XX CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay
XX CC is used to determine if an animal has an allele for, or muscle fibre
XX CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce
XX CC meat of superior quality (particularly tenderness) but are normally less
XX CC efficient feed converters and fatter than other types. The assay
XX CC comprises analysing a tissue sample to determine if the genotype
XX CC comprises the allele, and genetic features typical of animals with Duroc-
XX CC type MFC are present. The method is used to select animals that have
XX CC Duroc characteristics for use in breeding programmes (to develop the
XX CC animals with Duroc pig characteristics), and to assess meat quality
XX XX
XX SQ Sequence 10 BP; 1 A; 7 C; 1 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 10 GGGAG 6

RESULT 40
AAV60193/c
ID AAV60193 standard; DNA; 10 BP.
XX XX
XX AC AAV60193;
XX XX
XX DT 10-AUG-1999 (first entry)
XX XX
XX DE Pyrimidinone derivative of the invention.
XX XX
XX KW Pyrimidinone derivative; labeled binding partner; diagnostic assay;
KW antisense; transfection complex; primer; probe; ss.
XX XX
XX OS Synthetic.
XX XX
XX PN WO9924452-A2.
XX XX
XX PD 20-MAY-1999.
XX XX
XX PF 30-OCT-1998; 98WO-US023119.
XX XX
XX PR 07-NOV-1997; 97US-00966392.
XX PR 10-NOV-1997; 97US-00966875.
XX XX
XX PA (ISIS-) ISIS PHARM INC.
XX XX

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PI Lin K, Matteucci MD;  
 XX WPI, 1999-370671/31.  
 XX Composition comprising pyrimidinone derivatives for diagnostic and  
 PT analytical labels.  
 XX  
 XX Example 4; Page 87; 101pp; English.  
 XX The specification describes pyrimidinone derivatives. These derivatives  
 CC are used as labeled binding partners, particularly as labels for  
 CC diagnostic, analytical and therapeutic applications. The derivatives are  
 CC used as detectable labels for diagnostic assays, to enhance diagnostic  
 CC assays that use oligonucleotides and to improve potency of  
 CC oligonucleotides as antisense reagents that affect gene expression by  
 CC altering intracellular metabolism of complementary RNA sequences encoding  
 CC a target gene. They are also used in transfection complexes to deliver  
 CC oligonucleotides into cell cytoplasm and in PCR e.g. as primers, and  
 CC ligase chain reaction (LCR) e.g. as probes. The derivatives have  
 CC increased affinity and specificity for their complementary sequences and  
 CC facilitate PCR and LCR processes. The present sequence represents a  
 CC pyrimidinone derivative of the invention  
 XX  
 XX Sequence 10 BP; 0 A; 6 C; 0 G; 4 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 Db |||||  
 6 GGGAG 2  
 RESULT 41  
 AAZ07930  
 ID AAZ07930 standard; DNA; 10 BP.  
 XX AC  
 XX AAZ07930;  
 XX  
 XX 20-DEC-1999 (first entry)  
 XX  
 DE Interferon-alpha-inducible gene specific SAGE tag sequence.  
 XX  
 XX Neoplasia; lung cell; proto-oncogene; b-myb; p67; PGP9.5; 8-oxo-dGTPase;  
 KW diagnosis; lung cancer; SAGE; Serial Analysis of Gene Expression; NSCLC;  
 XX ss.  
 KW  
 XX Synthetic.  
 OS  
 XX WO9949774-A2.  
 XX  
 XX 07-OCT-1999.  
 PD  
 XX  
 XX 30-MAR-1999; 99WO-US006947.  
 PF  
 XX 31-MAR-1998; 98US-0080044P.  
 PR  
 XX (GENZ ) GENZYME CORP.  
 PA (UTJO ) UNIV JOHNS HOPKINS.  
 XX  
 XX Jen J, Beaudry GA, Madden SL, Bertelsen AH;  
 PI WPI, 1999-580562/49.  
 XX  
 XX Diagnosing lung cancer by detecting over-expression of specific proto-  
 PT oncogenes, and screening for therapeutic agents that inhibit over-  
 PT expression.  
 XX  
 XX Example; Page 34; 51pp; English.  
 PS  
 XX The invention relates to the diagnosis of neoplasia of lung cells that  
 CC comprises detecting over-expression of one of the proto-oncogenes b-myb,

CC p67, PGP9.5 and 8-oxo-dGTPase. The method is used for diagnosis, and  
 CC monitoring, of lung cancer, or predisposition to this disease,  
 CC particularly non-small cell lung cancer (NSCLC). Therapeutic agents that  
 CC inhibit over-expression of the oncogenes are used to treat lung cancer,  
 CC also to prevent progression of pre-neoplastic or non-malignant states.  
 CC The specified proto-oncogenes have been found to be expressed in many  
 CC primary lung cancers. The method is useful for the early diagnosis and  
 CC monitoring of lung cancer. Sequences AAZ07926-938 represents SAGE tag  
 CC sequences used in SAGE (Serial Analysis of Gene Expression) analysis of  
 CC genes overexpressed NSCLC  
 XX  
 XX Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGAG 5  
 Db |||||  
 5 GGGAG 9  
 RESULT 42  
 AA81860  
 ID AA81860 standard; DNA; 10 BP.  
 XX AC  
 XX AA81860;  
 XX  
 XX 11-MAR-1999 (first entry)  
 DT  
 XX Human rchd528 forward primer OP119.  
 DE  
 XX Human; cardiovascular disease; atherosclerosis; ischaemia; restenosis;  
 KW reperfusion; hypertension; arterial inflammation; diagnosis; rchd528;  
 KW primer; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX Homo sapiens.  
 XX  
 XX US5849578-A.  
 XX  
 XX 15-DEC-1998.  
 PD  
 XX 15-MAR-1996; 96US-00616844.  
 PF  
 XX 10-FEB-1995; 95US-00386844.  
 PR  
 XX 07-JUN-1995; 95US-00458873.  
 PR  
 XX 09-FEB-1996; 96US-00599654.  
 PR  
 XX (MILL-) MILLENNIUM PHARM INC.  
 PA  
 XX Falb DA;  
 XX  
 XX WPI, 1999-069743/06.  
 XX  
 XX DNA encoding rchd528 polypeptide - associated with cardiovascular  
 PT disease.  
 XX  
 XX Example; Col 105; 122pp; English.  
 PS  
 XX The present invention describes rchd528 protein. A method has been  
 CC developed for producing the rchd528 gene product. The present invention  
 CC also describes methods and compositions for the treatment and diagnosis  
 CC of cardiovascular diseases, including: atherosclerosis; ischaemia;  
 CC restenosis; reperfusion; hypertension; and arterial inflammation. The  
 CC present sequence represents a primer used in an example from the present  
 CC invention  
 XX  
 XX Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GGGAG 5
Db      6 GGGAG 10

RESULT 43
AAV81846/C
ID      AAV81846 standard; DNA; 10 BP.
XX
AC      AAV81846;
XX
DT      11-MAR-1999 (first entry)
XX
DE      Human interleukin-1 forward primer OPG20.
XX
KW      Human; cardiovascular disease; atherosclerosis; ischaemia; restenosis;
KW      reperfusion; hypertension; arterial inflammation; diagnosis; rchd528;
KW      primer; ss.
XX
OS      Synthetic.
OS      Homo sapiens.
XX
US      US5849578-A.
XX
PD      15-DEC-1998.
XX
PF      15-MAR-1996; 96US-00616844.
XX
PR      10-FEB-1995; 95US-00386844.
PR      07-JUN-1995; 95US-00458873.
PR      09-FEB-1996; 96US-00599654.
XX
PA      (MILL-) MILLENNIUM PHARM INC.
XX
PI      Falb DA;
XX
WPI; 1999-069743/06.
XX
DNA encoding rchd528 polypeptide - associated with cardiovascular
PT      disease.
XX
XX
PS      Example; Col 99; 122pp; English.
XX
CC      The present invention describes rchd528 protein. A method has been
CC      developed for producing the rchd528 gene product. The present invention
CC      also describes methods and compositions for the treatment and diagnosis
CC      of cardiovascular diseases, including: atherosclerosis; ischaemia;
CC      restenosis; reperfusion; hypertension; and arterial inflammation. The
CC      present sequence represents a primer used in an example from the present
CC      invention
XX
SQ      Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
Db      6 GGGAG 2

RESULT 44
AAV14900
ID      AAV14900 standard; DNA; 10 BP.
XX
AC      AAV14900;
XX
DT      24-MAR-1999 (first entry)
XX
DE      Triple helix forming nucleotides 149-158 of 23S rRNA gene.
XX

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KW      Triple-helix forming region; Triplex formation; DNA detection;
KW      identification; bacteria; oncogene; virus; ds.
XX
OS      Clostridium pasteurianum.
XX
PN      US5861244-A.
XX
XX      19-JAN-1999.
XX
PD      22-DEC-1993; 93US-00173489.
XX
PF      29-OCT-1992; 92US-00968436.
XX
PR      (PROF-) PROFILE DIAGNOSTIC SCI INC.
XX
PA      Hepburn AG, Wang C;
XX
PI      WPI; 1999-130384/11.
XX
PT      Assay of genetic sequences based on triplex formation from double
PT      stranded analyte - and hybrid of anchor and reporter sequences, with
PT      reporter released if triplex formation occurs, used e.g. to identify
PT      bacteria.
XX
PS      Disclosure; Col 23-24; 168pp; English.
XX
CC      The present sequence represents a potential triple-helix forming region.
CC      It can be used to demonstrate the assay of the invention. The assay
CC      comprises adding a sample containing double-stranded DNA test sequences,
CC      e.g. containing the present sequence, to an aqueous medium containing at
CC      least one complex of anchor DNA, attached to a solid support, and
CC      reporter DNA, where either a part of the anchor DNA or reporter DNA is
CC      designed to form a triple-strand structure with part of the test
CC      sequence. Triplex formation results in displacement of the reporter DNA
CC      which is detected as an indication of the presence of the DNA test
CC      sequence. The method is used to detect DNA sequences, particularly for
CC      identification of bacteria (by detecting genes for ribosomal RNA) in
CC      clinical samples, but also detection of oncogenes and Hepatitis B virus
XX
SQ      Sequence 10 BP; 5 A; 0 C; 5 G; 0 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
Db      5 GGGAG 9

RESULT 45
AAV14813/C
ID      AAV14813 standard; DNA; 10 BP.
XX
AC      AAV14813;
XX
DT      24-MAR-1999 (first entry)
XX
DE      Triple helix third strand of Hepatitis B virus nucleotides 427-436.
XX
KW      Triplex formation; DNA detection; triple helix; identification; bacteria;
KW      oncogene; virus; ss.
XX
OS      Synthetic.
OS      Hepatitis B virus.
XX
PN      US5861244-A.
XX
PD      19-JAN-1999.
XX
PF      22-DEC-1993; 93US-00173489.
XX
PR      29-OCT-1992; 92US-00968436.
XX

```

XX (PROP-) PROFILE DIAGNOSTIC SCI INC.  
XX Hepburn AG, Wang C;  
XX WPI; 1999-130384/11.  
XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.  
XX  
PS Disclosure; Col 19-20; 168pp; English.  
XX  
CC The present sequence represents a polynucleotide that is able to form a  
CC triple helix with a double stranded sequence. Cytosine bases in the  
CC present can be replaced with 5-methylcytosine for increased triplex  
CC stability. The present sequence is used in the assay of the invention,  
CC where it can be part of the anchor DNA or reporter DNA sequence. The  
CC assay comprises adding a sample containing double-stranded DNA test  
CC sequences to an aqueous medium containing at least one complex of anchor  
CC DNA, attached to a solid support, and reporter DNA, where either a part  
CC of the anchor DNA or reporter DNA is designed to form a triple-strand  
CC structure with part of the test sequence. Triplex formation results in  
CC displacement of the reporter DNA which is detected as an indication of  
CC the presence of the DNA test sequence. The method is used to detect DNA  
CC sequences, particularly for identification of bacteria (by detecting  
CC genes for ribosomal RNA) in clinical samples, but also detection of  
CC oncogenes and Hepatitis B virus  
XX  
SQ Sequence 10 BP; 0 A; 4 C; 0 G; 6 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 7 GGGAG 3  
|||||  
7 GGGAG 3  
  
RESULT 46  
AA14782  
ID AAX14782 standard; DNA; 10 BP.  
XX AC AAX14782;  
XX  
XX 24-MAR-1999 (first entry)  
XX  
XX Triple helix forming nucleotides 3071-3080 of Hepatitis B virus.  
XX  
XX Triple-helix forming region; Triplex formation; DNA detection;  
KW identification; bacteria; oncogene; virus; ds.  
XX  
XX Hepatitis B virus.  
XX  
XX US5861244-A.  
XX  
XX 19-JAN-1999.  
XX  
XX 22-DEC-1993; 93US-00173489.  
XX  
XX 29-OCT-1992; 92US-00968436.  
XX  
XX (PROP-) PROFILE DIAGNOSTIC SCI INC.  
XX  
XX Hepburn AG, Wang C;  
XX  
XX WPI; 1999-130384/11.  
XX  
XX Assay of genetic sequences based on triplex formation from double  
PT stranded analyte - and hybrid of anchor and reporter sequences, with  
PT reporter released if triplex formation occurs, used e.g. to identify  
PT bacteria.

PT bacteria.  
XX  
PS Disclosure; Col 19-20; 168pp; English.  
XX  
CC The present sequence represents a potential triple-helix forming region.  
CC It can be used to demonstrate the assay of the invention. The assay  
CC comprises adding a sample containing double-stranded DNA test sequences,  
CC e.g. containing the present sequence, to an aqueous medium containing at  
CC least one complex of anchor DNA, attached to a solid support, and  
CC reporter DNA, where either a part of the anchor DNA or reporter DNA is  
CC designed to form a triple-strand structure with part of the test  
CC sequence. Triplex formation results in displacement of the reporter DNA  
CC which is detected as an indication of the presence of the DNA test  
CC sequence. The method is used to detect DNA sequences, particularly for  
CC identification of bacteria (by detecting genes for ribosomal RNA) in  
CC clinical samples, but also detection of oncogenes and Hepatitis B virus  
XX  
SQ Sequence 10 BP; 4 A; 0 C; 6 G; 0 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGAG 5  
Db 3 GGGAG 7  
|||||  
3 GGGAG 7  
  
RESULT 47  
AAX26269  
ID AAX26269 standard; DNA; 10 BP.  
XX AC AAX26269;  
XX  
XX 24-MAY-1999 (first entry)  
XX  
XX Forward primer OPI19.  
XX  
XX Fingerprinting gene; rchd502; transmembrane protein; cardiovascular;  
KW fingerprint/target gene; up-regulated; endothelial cell; shear-stress;  
KW atherosclerosis; ischemia; reperfusion; hypertension; restenosis; human;  
KW PCR primer; ss.  
XX  
XX Synthetic.  
XX Homo sapiens.  
XX  
XX US5882925-A.  
XX  
XX 16-MAR-1999.  
XX  
XX 09-FEB-1996; 96US-00599654.  
XX  
XX 10-FEB-1995; 95US-00386844.  
XX  
XX 07-JUN-1995; 95US-00485573.  
XX  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Falb DA;  
XX  
XX WPI; 1999-214071/18.  
XX  
XX New polynucleotides consisting of residues 1-1929 of the rchd502 gene -  
PT are differentially expressed in cardiovascular disease states, and can  
PT therefore be used to treat and diagnose cardiovascular diseases.  
XX  
XX Disclosure; Col 11; 121pp; English.  
XX  
XX The invention relates to a rchd502 target/fingerprint gene encoding a  
CC transmembrane protein. The invention provides cDNAs contained in plasmids  
CC pFCHD502SF (ATCC 69981) and pFCHD502SJ (ATCC 69982) that encode the  
CC rchd502 polypeptide, and are differentially expressed in cardiovascular  
CC disease states. Cultured genetically engineered host cell containing the  
CC rchd502 polynucleotides in operative association with a nucleotide

CC regulatory element are used for producing a polypeptide rchd502 gene  
 CC product. Identifying that the fingerprint/target gene rchd502 is  
 CC differentially expressed (up-regulated) by endothelial cells subjected to  
 CC shear-stress, provides a tool for the diagnosis and treatment of  
 CC cardiovascular disease e.g. atherosclerosis, ischemia/reperfusion,  
 CC hypertension, restenosis. The fingerprint gene is useful for testing the  
 CC efficacy of candidate drugs in basic research and in clinical trials and  
 CC or imaging of a diseased cardiovascular tissue. The gene may also be used  
 CC in screening for ligands of target gene product receptor domains, as well  
 CC as antagonists of the ligand-receptor interaction  
 XX  
 SQ Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 Db 6 GGGAG 10  
 |||||

RESULT 48  
 AAX26259/c  
 ID AAX26259 standard; DNA; 10 BP.  
 AC AAX26259;  
 XX  
 XX  
 DT 24-MAY-1999 (first entry)  
 DE Forward primer OPG20.  
 DE  
 DE  
 KW Fingerprinting gene; rchd502; transmembrane protein; cardiovascular;  
 KW fingerprint/target gene; up-regulated; endothelial cell; shear-stress;  
 KW atherosclerosis; ischemia; reperfusion; hypertension; restenosis; human;  
 KW PCR primer; ss.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 XX US5882925-A.  
 XX 16-MAR-1999.  
 XX  
 XX 09-FEB-1996; 96US-00599654.  
 XX  
 XX 10-FEB-1995; 95US-00386844.  
 PR 07-JUN-1995; 95US-00485573.  
 XX  
 XX (WILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Falb DA;  
 PI  
 XX  
 XX WPI; 1999-214071/18.  
 XX  
 PT New polynucleotides consisting of residues 1-1299 of the rchd502 gene -  
 PT are differentially expressed in cardiovascular disease states, and can  
 PT therefore be used to treat and diagnose cardiovascular diseases.  
 XX  
 XX Disclosure; Col 10; 121pp; English.  
 XX  
 XX The invention relates to a rchd502 target/fingerprint gene encoding a  
 CC transmembrane protein. The invention provides cDNAs contained in plasmids  
 CC pFCHD502SF (ARCC 69981) and pFCHD502SJ (ARCC 69982) that encode the  
 CC rchd502 polypeptide, and are differentially expressed in cardiovascular  
 CC disease states. Cultured genetically engineered host cell containing the  
 CC rchd502 polynucleotides in operative association with a nucleotide  
 CC regulatory element are used for producing a polypeptide rchd502 gene  
 CC product. Identifying that the fingerprint/target gene rchd502 is  
 CC differentially expressed (up-regulated) by endothelial cells subjected to  
 CC shear-stress, provides a tool for the diagnosis and treatment of  
 CC cardiovascular disease e.g. atherosclerosis, ischemia/reperfusion,  
 CC hypertension, restenosis. The fingerprint gene is useful for testing the

CC efficacy of candidate drugs in basic research and in clinical trials and  
 CC or imaging of a diseased cardiovascular tissue. The gene may also be used  
 CC in screening for ligands of target gene product receptor domains, as well  
 CC as antagonists of the ligand-receptor interaction  
 XX  
 SQ Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 Db 6 GGGAG 2  
 |||||

RESULT 49  
 AAZ28332  
 ID AAZ28332 standard; cDNA; 10 BP.  
 XX  
 AC AAZ28332;  
 XX  
 DT 20-DEC-1999 (first entry)  
 DE Lung cancer indicator polynucleotide #12.  
 DE  
 XX  
 KW Lung cancer; tumour; primary squamous cell; gene expression pattern; ss;  
 KW antibody; detect; diagnosis; transgenic animal; p27 gene.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9950278-A1.  
 XX 07-OCT-1999.  
 XX  
 XX 30-MAR-1999; 99WO-US006938.  
 PR 31-MAR-1998; 98US-0080037P.  
 XX  
 XX (GENZ ) GENZYME CORP.  
 XX  
 XX Beaudry GA, Madden SL, Bertelsen AH;  
 XX WPI; 1999-591271/50.  
 XX  
 PT Polynucleotides which are differentially expressed in lung cancer, used  
 PT for diagnosis and screening for therapeutic agents.  
 XX  
 XX Claim 1; Page 50; 69pp; English.

CC Sequences AAZ28321-228360 are polynucleotides isolated from primary  
 CC squamous cell lung cancers of two patients. These sequences represent a  
 CC profile of gene expression patterns in lung cancer. Sequences AAZ28321-  
 CC 228360 correspond to previously characterised genes, this sequence  
 CC corresponds to the p27 gene. Sequences AAZ28341-228360 do not correspond  
 CC to known genes, although some do correspond to reported Expressed  
 CC Sequence Tags (ESTs). The presence of these polynucleotide sequences in  
 CC lung cells is indicative of lung cancer. The sequences can be used to  
 CC generate antibodies for the detection of tumour cells. Detection of the  
 CC overexpression of the polynucleotides and their gene products can be used  
 CC in the diagnosis of lung cancer or the susceptibility to the disease. The  
 CC sequences can also be used to screen for agents potentially useful for  
 CC treating lung cancer and to generate transgenic animals (for studying  
 CC gene function and for drug screening)

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.9e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 |||||

```

Db          5 GGGAG 9

RESULT 50
AAx86246
ID  AAx86246 standard; DNA; 10 BP.
XX
AC  AAx86246;
XX
DT  22-SEP-1999 (first entry)
XX
DE  SAGE tag used to identify transcripts which are decreased by p53.
XX
KW  p53 transcription tag; p53 status; cancer; cytotoxicity; carcinogenicity;
KW  neoplastic; p53 binding site; PIG-3 promoter; SAGE tag; ss.
XX
OS  Homo sapiens.
XX
PN  W09914356-A2.
XX
PD  25-MAR-1999.
XX
PF  17-SEP-1998; 98WO-US019300.
XX
PR  17-SEP-1997; 97US-0059153P.
PR  30-MAR-1998; 98US-0079817P.
XX
PA  (UYJO ) UNIV JOHNS HOPKINS.
XX
PI  Vogelstein B, Kinzler KW, Polyak K;
DR  WPI; 1999-443793/37.
XX
PT  Use of p53 transcription tags to determine p53 status in, e.g. cancer
PT  diagnosis.
XX
PS  Claim 2; Page 29; 73pp; English.
XX
CC  The specification describes the use of p53 transcription tags for
CC  developing products to determine p53 status, to diagnose cancer and to
CC  evaluate cytotoxicity or carcinogenicity of a test agent. A method for
CC  diagnosing cancer or determining p53 status in a sample suspected for
CC  being neoplastic comprises comparing the level of transcription of an RNA
CC  transcript in a first sample (s1) of a first tissue (t1) to the level of
CC  transcription of the transcript in a second sample (s2) of a second
CC  tissue (s2), where s1 is suspected of being neoplastic and s2 is a normal
CC  human tissue (of the same type) and the transcript is identified by a tag
CC  ; and categorizing s1 as neoplastic or as having a mutant p53 when
CC  transcription is found to be the same or lower in the first, than in s2.
CC  The methods and products can be used to determine p53 status, to diagnose
CC  cancer and to evaluate cytotoxicity or carcinogenicity of a test agent.
CC  AAx86233-64 represent SAGE tags used to identify transcripts which are
CC  decreased by p53
XX
SQ  Sequence 10 BP; 2 A; 0 C; 5 G; 3 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 GGGAG 5
Db  3 GGGAG 7

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Search completed: January 7, 2005, 07:12:01  
 Job time : 259.4 secs

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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 04:56:02 ; Search time 2222.4 Seconds  
(without alignments)  
81.983 Million cell updates/sec

Title: GGCAG

Perfect score: 5

Sequence: 1 gggag 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32022875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 156772

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_ges1:\*

9: gb\_ges2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	5	100.0	10	9	CL436411
C 2	5	100.0	10	9	CL436421
C 3	5	100.0	10	9	CL437642
C 4	5	100.0	10	9	CL439219
C 5	5	100.0	11	1	AJ648107
C 6	5	100.0	11	1	AJ655479
C 7	5	100.0	11	1	AJ657108
C 8	5	100.0	11	5	BQ591023
C 9	5	100.0	11	9	CL437735
C 10	5	100.0	11	9	CL657848
C 11	5	100.0	12	1	AJ679735
C 12	5	100.0	12	9	AJ587934
C 13	5	100.0	12	9	AJ592591
C 14	5	100.0	12	9	AJ594389
C 15	5	100.0	13	4	BG926067
C 16	5	100.0	13	4	BM399550
C 17	5	100.0	13	9	AJ593426
C 18	5	100.0	13	9	CL437499
C 19	5	100.0	13	9	CL690995
C 20	5	100.0	14	1	AJ686563
C 21	5	100.0	14	5	BQ593808
C 22	5	100.0	15	1	AJ582954
C 23	5	100.0	15	1	AJ686764
C 24	5	100.0	15	6	CF304766

25	5	100.0	16	1	AA968729
C 26	5	100.0	16	1	AI075064
C 27	5	100.0	16	1	AI094839
C 28	5	100.0	16	1	AI274782
C 29	5	100.0	16	1	AI560058
C 30	5	100.0	16	1	AI569544
C 31	5	100.0	16	5	BQ588093
C 32	5	100.0	16	8	BZ424445
C 33	5	100.0	16	9	AJ589788
C 34	5	100.0	16	9	AJ595245
C 35	5	100.0	16	9	AJ598372
C 36	5	100.0	17	1	AJ666397
C 37	5	100.0	17	2	AW246940
C 38	5	100.0	17	4	BG926068
C 39	5	100.0	17	9	AJ589066
C 40	5	100.0	17	9	AJ599163
C 41	5	100.0	18	1	AJ648240
C 42	5	100.0	18	2	AW250267
C 43	5	100.0	18	4	BG896958
C 44	5	100.0	18	4	BG925410
C 45	5	100.0	18	4	BG925569
C 46	5	100.0	18	4	BM397051
C 47	5	100.0	18	4	BM397051
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C 60	5	100.0	19	1	AA934650
C 61	5	100.0	19	1	AI033338
C 62	5	100.0	19	1	AI049374
C 63	5	100.0	19	1	AI251781
C 64	5	100.0	19	1	AI360784
C 65	5	100.0	19	1	AI648553
C 66	5	100.0	19	1	AI696833
C 67	5	100.0	19	1	AI719558
C 68	5	100.0	19	1	AI747751
C 69	5	100.0	19	1	AI758301
C 70	5	100.0	19	1	AI811474
C 71	5	100.0	19	1	AJ660242
C 72	5	100.0	19	1	AJ662060
C 73	5	100.0	19	1	AJ666284
C 74	5	100.0	19	1	AJ686305
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C 79	5	100.0	19	6	CF306225
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C 82	5	100.0	19	6	CF307439
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C 85	5	100.0	19	8	AJ309643
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C 87	5	100.0	19	8	AJ313113
C 88	5	100.0	19	8	AJ324165
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C 91	5	100.0	19	8	AJ379786
C 92	5	100.0	19	8	AJ400662
C 93	5	100.0	19	8	AJ412553
C 94	5	100.0	19	8	AJ418201
C 95	5	100.0	19	8	AJ420252
C 96	5	100.0	19	8	AJ422762
C 97	5	100.0	19	8	AJ430028

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AI274782	qv67h03.x
AI560058	tg38h11.x
AI569544	to28d10.x
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BZ424445	100012843
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AJ598372	Arabidops
AJ666397	Arabidops
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AJ599163	Arabidops
AJ648240	AJ648240
AW250267	2821151.5
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BG925410	HNC5-1-B6
BG925569	HNC5-1-E2
BM397051	5009-0-28
BM397051	5009-0-28
BM397954	5009-0-39
BM398017	5009-0-4-
BM399858	5009-0-62
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AJ600946	Arabidops
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CL438990	PST8480-N
AA885444	am14h07.8
AA912825	cl43d11.8
AA918795	cl69c05.8
AA934650	oo71d10.8
AI033338	ox02d04.8
AI049374	ub33a03.f
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AI360784	qx98g07.x
AI648553	tz55e07.x
AI696833	wc74e09.x
AI719558	as41d06.x
AI747751	ul21n05.x
AI758301	ty06a07.x
AI811474	tw43c04.x
AJ660242	AJ660242
AJ662060	AJ662060
AJ666284	AJ666284
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BQ593604	E012766-0
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CF307304	HDAL--06-
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AJ309874	1M0017C14
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c 106 5 100.0 19 8 A2477353 A2477353 1M0296K16  
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c 111 5 100.0 19 8 A2579189 A2579189 1M0363K12  
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c 115 5 100.0 19 8 A2647364 A2647364 1M0513O16  
c 116 5 100.0 19 8 A2654214 A2654214 1M0528H13  
c 117 5 100.0 19 8 A2656937 A2656937 1M0532K13  
c 118 5 100.0 19 8 A2759944 A2759944 1M0553O10  
c 119 5 100.0 19 8 A2760597 A2760597 1M0554N21  
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 10)
            www.Escells.ca
            Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, University of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
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similar to 5730410119Rik, genomic survey sequence.
ACCESSION  CL437642
VERSION     CL437642.1 GI:45573487
KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 10)
            www.Escells.ca
            Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, University of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
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ACCESSION  CL439219
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KEYWORDS   GSS.
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
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            1 (bases 1 to 10)
            www.Escells.ca
            Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, University of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
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Qy 1 GGGAG 5
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Db 6 GGGAG 2

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ONS029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada

Tel: 204 787 2133

Fax: 204 787 2190

Email: hicksg@cc.umanitoba.ca

U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from [http://140.193.242.7/esdb/public\\_search\\_frame.php?PST=PST8879-NL.Se](http://140.193.242.7/esdb/public_search_frame.php?PST=PST8879-NL.Se)

q

Class: Gene Trap.

Location/Qualifiers

```
1. .10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST8879-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICH1"
/notes="Vector: U3NeoSV1"
```

#### ORIGIN

```
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGGAG 5
        |||||
Db      8 GGGAG 4
```

#### RESULT 5

```
AJ648107/c
LOCUS      AJ648107.1 11 bp mRNA linear EST 07-JUL-2004
DEFINITION AJ648107 CSEQRANI19 Sus scrofa cDNA clone C0003263_K08, mRNA
sequence.
```

```
ACCESSION AJ648107
```

```
VERSION AJ648107.1 GI:49324952
```

```
KEYWORDS EST.
```

```
SOURCE Sus scrofa (pig)
```

```
ORGANISM Sus scrofa
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
```

#### REFERENCE

```
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL Unpublished (2004)
```

#### COMMENT

Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross\_match with the -minscore 20  
and -minmatch 12 options. Vector:pBluescriptII(KS) R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pooled ovaries. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, [www.ark-genomics.org](http://www.ark-genomics.org).

#### FEATURES

source

```
1. .11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0003263_K08"
/tissue_type="ovary"
/clone_lib="CSEQRANI19"
/notes="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"
```

#### ORIGIN

```
Query Match      100.0%; Score 5; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGGAG 5
```

```
        |||||
```

```
Db      5 GGGAG 1
```

#### RESULT 6

```
AJ655479/c
```

```
LOCUS      AJ655479 11 bp mRNA linear EST 28-JUN-2004
```

```
DEFINITION AJ655479 KN277 Sus scrofa cDNA clone C0005190_H03, mRNA sequence.
```

```
ACCESSION AJ655479
```

```
VERSION AJ655479.1 GI:49339511
```

```
KEYWORDS EST.
```

```
SOURCE Sus scrofa (pig)
```

```
ORGANISM Sus scrofa
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
```

#### REFERENCE

```
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL Unpublished (2004)
```

#### COMMENT

Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross\_match with the -minscore 20  
and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI  
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
from pooled early embryos, from 8- cell stage to blastocysts.  
Clones available from UK Centre for Functional Genomics in Farm  
Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,  
[www.arkgenomics.org](http://www.arkgenomics.org).

#### FEATURES

source

```
1. .11
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0005190_H03"
/tissue_type="embryo"
/clone_lib="KN277"
/notes="vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled early embryos, from 8-cell stage
to blastocysts."
```

#### ORIGIN

```
Query Match      100.0%; Score 5; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGGAG 5
```

```
        |||||
```

```
Db      11 GGGAG 7
```

#### RESULT 7

```
AJ657108
```

```
LOCUS      AJ657108 11 bp mRNA linear EST 28-JUN-2004
```

```
DEFINITION AJ657108 KN277 Sus scrofa cDNA clone C0005196_K06, mRNA sequence.
```

```
ACCESSION AJ657108
```

```
VERSION AJ657108.1 GI:49341140
```

```
KEYWORDS EST.
```

```
SOURCE Sus scrofa (pig)
```

```
ORGANISM Sus scrofa
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
```



ORIGIN		AUTHORS	Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Query Match	100.0%; Score 5; DB 9; Length 11;	TITLE	Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
Best Local Similarity	100.0%; Pred. No. 1.2e+07;	JOURNAL	Unpublished (2004)
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	COMMENT	Contact: Anderson SI Genomics and Bioinformatics Roslin Institute Roslin, Midlothian, EH25 9PS, UNITED KINGDOM Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross match with the -minscore 20 and -minmatch 12 options. Vector: pBlueScriptII(KS+). R. Site1: EcorI R. Site2: NotI 5' Seq Primer M13P Normalised library constructed from pig uterus. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
Qy	1 GGGAG 5 	FEATURES	Location/Qualifiers 1..12 /organism="Sus scrofa" /mol_type="mRNA" /db_xref="taxon:9823" /clones="C0001780_A09" /tissue_type="uterus" /clone_lib="CSEQPAN04" /note="Vector: pBlueScriptII(KS+); Site 1: EcorI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pig uterus."
Db	9 GGGAG 5 	ORIGIN	Query Match 100.0%; Score 5; DB 1; Length 12; Best Local Similarity 100.0%; Pred. No. 1.2e+07; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GGGAG 5       Db 6 GGGAG 2
RESULT 10		RESULT 12	
CL657848/c		AJ587934	
LOCUS		LOCUS	AJ587934 12 bp DNA linear GSS 15-JAN-2004
DEFINITION	11 bp DNA linear GSS 09-JUL-2004	DEFINITION	Arabidopsis thaliana T-DNA flanking sequence, left border, clone 342D05, genomic survey sequence.
pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.		ACCESSION	AJ587934
CL657848		VERSION	AJ587934.1 GI:37937558
PR1012c H02 - PR1012c.B21 (11) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.		KEYWORDS	GSS; left border; T-DNA flanking sequence.
CL657848		SOURCE	Arabidopsis thaliana (thale cress)
CL657848.1 GI:50139878		ORGANISM	Arabidopsis thaliana
GSS.			Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
Pristionchus pacificus		REFERENCE	1 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepiniec, L., Caboche, M. and Lecharny, A. T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites EMBO Rep. 3 (12), 1152-1157 (2002)
Pristionchus pacificus		AUTHORS	
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;		TITLE	
Neodiplogasteridae; Pristionchus.		JOURNAL	
Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.		MEDLINE	
AppaDB: an AcedB database for the nematode satellite organism		PUBMED	
Pristionchus pacificus		AUTHORS	
Nucleic Acids Res. 32 (1), D421-D422 (2004)		TITLE	
Contact: Sommer RJ		JOURNAL	
Evolutionary Biology		COMMENT	
Max-Planck-Institute for Developmental Biology			
Spemannstr. 37-39, Tuebingen D-72076, Germany			
Tel.: 00497071601371			
Fax: 00497071601498			
Email: raif.sommer@tuebingen.mpg.de			
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.			
Seq primer: T7			
Class: fosmid ends.			
Location/Qualifiers			
1..11			
/organism="Pristionchus pacificus"			
/mol_type="genomic DNA"			
/strain="California"			
/db_xref="taxon:54126"			
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"			
/note="Vector: pEpifos-5 Fosmid vector"			
ORIGIN		ORIGIN	
Query Match	100.0%; Score 5; DB 9; Length 11;	Query Match	100.0%; Score 5; DB 9; Length 11;
Best Local Similarity	100.0%; Pred. No. 1.2e+07;	Best Local Similarity	100.0%; Pred. No. 1.2e+07;
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GGGAG 5 	Qy	1 GGGAG 5 
Db	9 GGGAG 5 	Db	9 GGGAG 5 
RESULT 11		RESULT 11	
AJ679735/c		AJ679735/c	
LOCUS		LOCUS	
DEFINITION	12 bp mRNA linear EST 29-JUN-2004	DEFINITION	Arabidopsis thaliana T-DNA flanking sequence, left border, clone 342D05, genomic survey sequence.
sequence.		ACCESSION	AJ679735
AJ679735		VERSION	AJ679735.1 GI:49412322
EST.		KEYWORDS	
Sus scrofa (pig)		SOURCE	
Sus scrofa		ORGANISM	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.			
1 (bases 1 to 12)		REFERENCE	1 (bases 1 to 12)

```

program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
    source
        1..12
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassillewskija"
            /db_xref="taxon:3702"
            /clone="342D03"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
        1..12
            /note="T-DNA flanking sequence
            left border"
    misc_feature
        1..12
            /note="T-DNA flanking sequence
            left border"
ORIGIN
    Query Match      100.0%; Score 5; DB 9; Length 12;
    Best Local Similarity 100.0%; Pred. No. 1.2e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 1 GGGAG 5
        |||||
    Db 6 GGGAG 10

    RESULT 13
    LOCUS
    DEFINITION
        Arabidopsis thaliana T-DNA flanking sequence, right border, clone
        624D10, genomic survey sequence.
    ACCESSION
        AJ592591
    VERSION
        AJ592591.1 GI:37942215
    KEYWORDS
        GSS; right border; T-DNA flanking sequence.
    SOURCE
        Arabidopsis thaliana
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
    REFERENCE
        1
        Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
        Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
        Lepiniec, L., Caboche, M. and Lecharny, A.
        T-DNA integration into the Arabidopsis genome depends on sequences
        of pre-insertion sites
        EMBO Rep. 3 (12), 1152-1157 (2002)
    JOURNAL
        MEDLINE
        PUBMED
        12446565
    REFERENCE
        2 (bases 1 to 12)
    AUTHORS
        Balzergue, S.
    TITLE
        Direct Submission
    JOURNAL
        Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
        Gaston Cremieux, 91057 Evry cedex, FRANCE
    COMMENT
        PCR was performed on DNA from transformants of Arabidopsis thaliana
        plants from INRA (Versailles). The DNA fragment(s) resulting from
        the PCR were directly sequenced from the left or the right border
        to determine the genomic sequence flanking the insertion. T-DNA
        derived sequences were removed. Information to order the
        corresponding mutant line and a link to a database providing a
        graphical display of the insertion site are available at
        http://dbgap.versailles.inra.fr/publiclines/. This sequence has
        been generated in the framework of the French plant genomics
        program 'Genoplante' (http://www.genoplante.com and
        http://genoplante-info.infobiogen.fr).
        Location/Qualifiers
            1..12
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /cultivar="Wassillewskija"
                /db_xref="taxon:3702"
                /clone="624D10"
                /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            1..12
                /note="T-DNA flanking sequence
                right border"
    misc_feature
        1..12
            /note="T-DNA flanking sequence
            right border"
FEATURES
    source
        1..12
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassillewskija"
            /db_xref="taxon:3702"
            /clone="624D10"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
        1..12
            /note="T-DNA flanking sequence
            right border"
    misc_feature
        1..12
            /note="T-DNA flanking sequence
            right border"

```

---

```

program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
    source
        1..12
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassillewskija"
            /db_xref="taxon:3702"
            /clone="342D03"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
        1..12
            /note="T-DNA flanking sequence
            left border"
    misc_feature
        1..12
            /note="T-DNA flanking sequence
            left border"
ORIGIN
    Query Match      100.0%; Score 5; DB 9; Length 12;
    Best Local Similarity 100.0%; Pred. No. 1.2e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 1 GGGAG 5
        |||||
    Db 6 GGGAG 10

    RESULT 14
    LOCUS
    DEFINITION
        Arabidopsis thaliana T-DNA flanking sequence, left border, clone
        397G07, genomic survey sequence.
    ACCESSION
        AJ594389
    VERSION
        AJ594389.1 GI:37944013
    KEYWORDS
        GSS; left border; T-DNA flanking sequence.
    SOURCE
        Arabidopsis thaliana
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
        rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
    REFERENCE
        1
        Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
        Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
        Lepiniec, L., Caboche, M. and Lecharny, A.
        T-DNA integration into the Arabidopsis genome depends on sequences
        of pre-insertion sites
        EMBO Rep. 3 (12), 1152-1157 (2002)
    JOURNAL
        MEDLINE
        PUBMED
        12446565
    REFERENCE
        2 (bases 1 to 12)
    AUTHORS
        Balzergue, S.
    TITLE
        Direct Submission
    JOURNAL
        Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
        Gaston Cremieux, 91057 Evry cedex, FRANCE
    COMMENT
        PCR was performed on DNA from transformants of Arabidopsis thaliana
        plants from INRA (Versailles). The DNA fragment(s) resulting from
        the PCR were directly sequenced from the left or the right border
        to determine the genomic sequence flanking the insertion. T-DNA
        derived sequences were removed. Information to order the
        corresponding mutant line and a link to a database providing a
        graphical display of the insertion site are available at
        http://dbgap.versailles.inra.fr/publiclines/. This sequence has
        been generated in the framework of the French plant genomics
        program 'Genoplante' (http://www.genoplante.com and
        http://genoplante-info.infobiogen.fr).
        Location/Qualifiers
            1..12
                /organism="Arabidopsis thaliana"
                /mol_type="genomic DNA"
                /cultivar="Wassillewskija"
                /db_xref="taxon:3702"
                /clone="397G07"
                /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
            1..12
                /note="T-DNA flanking sequence
                left border"
    misc_feature
        1..12
            /note="T-DNA flanking sequence
            left border"
ORIGIN
    Query Match      100.0%; Score 5; DB 9; Length 12;
    Best Local Similarity 100.0%; Pred. No. 1.2e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

    QY 1 GGGAG 5
        |||||
    Db 4 GGGAG 8

    RESULT 15
    BG26067/c

```

```

LOCUS      BG926067              13 bp      mRNA      linear      EST 06-NOV-2001
DEFINITION HNC23-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION  BG926067
VERSION     BG926067.1   GI:14320590
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 13)
AUTHORS     Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
            Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
JOURNAL     Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE     21482651
PUBMED      11597177
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay.kumar-1@gsk.com
Seq primer: 47.

FEATURES             Location/Qualifiers
     source           1..13
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="cartilage"
                     /lab_host="E.coli DH10 B"
                     /clone_lib="HNC (Human Normal Cartilage)"
                     /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                     Directional"

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
    |||||
Db 5 GGGAG 1

RESULT 16
LOCUS      BM399550/c            13 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM399550
VERSION     BM399550.1   GI:18199603
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
            Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE   1  (bases 1 to 13)
AUTHORS     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
            EST from Tetrahymena thermophila, strain CU428.1, growing cells
            Unpublished (2002)
JOURNAL     Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu

FEATURES             Location/Qualifiers
     source           1..13
                     /organism="Tetrahymena thermophila"
                     /mol_type="mRNA"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
    |||||
Db 6 GGGAG 2

RESULT 17
LOCUS      AU593426              13 bp      DNA      linear      GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
380B04, genomic survey sequence.
ACCESSION  AU593426
VERSION     AU593426.1   GI:37943050
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; euroside II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
AUTHORS     Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
            T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE     22363535
PUBMED      12446565
REFERENCE   2  (bases 1 to 13)
AUTHORS     Balzergue,S.
            Direct Submission
JOURNAL     Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
            PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment (s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).

FEATURES             Location/Qualifiers
     source           1..13
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="380B04"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

misc_feature       1..13
                    /note="T-DNA flanking sequence
                    left border"

ORIGIN

```



```

Query Match      100.0%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
    |||||
Db 7 GGGAG 11

RESULT 18
CL437499
LOCUS      13 bp DNA linear GSS 18-MAR-2004
DEFINITION PST5642-NL.Seq M1CB1 Mus musculus genomic clone PST5642-NL.Seq
similar to Fau, genomic survey sequence.
ACCESSION  CL437499
VERSION    CL437499.1 GI:45573241
KEYWORDS  GSS.
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 13)
www.EScells.ca
Hicks,G.G.
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicks@gcc.umanitoba.ca
U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST5642-NL.Se
q
Class: Gene Trap:
Location/Qualifiers
1..13
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST5642-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="M1CB1"
/note="Vector: U3NeosV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
    |||||
Db 7 GGGAG 11

RESULT 19
CL690995/c
LOCUS      13 bp DNA linear GSS 10-JUL-2004
DEFINITION PRI0155b_B11.2 - PRI0155b.BR (13) Mixed stage fosmid library of P..
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION  CL690995
VERSION    CL690995.1 GI:50212903
KEYWORDS  GSS.
SOURCE    Pristionchus pacificus
ORGANISM  Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
1 (bases 1 to 13)
Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: raif.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
Location/Qualifiers
1..13
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus
var. California"
/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
    |||||
Db 8 GGGAG 4

RESULT 20
AJ686563/c
LOCUS      14 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ686563 CSEQRAN04 Sus scrofa CDNA clone C0001812_D07, mRNA
sequence.
ACCESSION  AJ686563
VERSION    AJ686563.1 GI:49419153
KEYWORDS  EST.
SOURCE    Sus scrofa (pig)
ORGANISM  Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 14)
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
Location/Qualifiers
1..14
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0001812_D07"
/tissue_type="uterus"

FEATURES
source

```



COMMENT Contact: Anderson SI  
Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred  
v0.020425.c. Vector identified by cross match with the -minscore 20  
and -minmatch 12 options. Vector: pBluescriptII(+) R. Site1: EcoRI  
R. Site2: NotI 5'. Seq Primer M13F Normalised library constructed  
from pig uterus. Clones available from UK Centre for Functional  
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,  
EH25 9PS, www.arkgenomics.org.

FEATURES  
source  
1..15  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0001812.M09"  
/tissue\_type="uterus"  
/clone\_lib="CSQRAN04"  
/note="Vector: pBluescriptII(+); Site 1: EcoRI; Site 2:  
NotI; Single pass sequencing. Normalised library  
constructed from pig uterus."

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||

Db 10 GGGAG 6

RESULT 24  
LOCUS CF304766  
DEFINITION ABFI--05-006.g1 ABF3-overexpressing transgenic rice lambda phage  
clone ABFI--05-006, ORYZA sativa (japonica cultivar-group) cDNA  
CF304766  
ACCESSION CF304766.1 GI:33676527  
VERSION EST.  
KEYWORDS  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1 (bases 1 to 15)  
AUTHORS Kim,J.S., Jun,K.W., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,  
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.  
TITLE Large-scale Sequencing Analysis of Rice ESTs  
JOURNAL Unpublished (2003)  
COMMENT Contact: Nahm B.H.  
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

FEATURES  
source  
1..15  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:39947"  
/clone="ABFI--05-006"  
/tissue\_type="leaf"  
/dev\_stage="14 days after germination"  
/lab\_host="E.coli SOLR"  
/clone\_lib="ABF3-overexpressing transgenic rice lambda  
phage cDNA library (ABFI)"  
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:  
XhoI; Leaf was dried for 2hrs. cDNA was inserted into

lamda Uni-ZAP XR vector at 5' end with EcoRI and 3' end  
with XhoI site. mRNA was prepared from ABA-responsive  
element binding transcription factor 3 overexpression  
line."

ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 15;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||

Db 6 GGGAG 10

RESULT 25  
LOCUS AA968729  
DEFINITION or9h11.91 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE1601157.3  
similar to SW:FRPE\_HUMAN P02811 BASIC PROLINE-RICH PEPTIDE P-E  
;contains element M8R1 repetitive element ;, mRNA sequence.  
AA968729  
ACCESSION AA968729.1 GI:3143909  
VERSION EST.  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 16)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bto.llnl.gov/bbrp/image/image.html

FEATURES  
source  
1..16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE1601157"  
/tissue\_type="pooled germ cell tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP GC3"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled  
germ cell tumors, and was then primed with a Not I -  
oligo(dT) primer. Double-stranded cDNA was ligated to Eco  
RI adaptors (Pharmacia), digested with Not I and cloned  
into the Not I and Eco RI sites of the modified p773  
vector. Library is not normalized. Library was  
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN  
Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||

```

Db          5 GGGAG 9

RESULT 26
LOCUS      AI075064/c
DEFINITION ou61g11.x1 NCI CGAP_Br2 Homo sapiens cDNA clone IMAGE:1632356 3',
            similar to TR:Q24348 Q24348 FIBRILLARIN ;, mRNA sequence.
ACCESSION  AI075064
VERSION     AI075064.1 GI:3399844
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
            NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGP), Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CCAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 712 Std Error: 0.00
            Seq primer: -40ml3 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES   source
            1..16
            /location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1632356"
            /sex="female, pooled"
            /tissue_type="breast"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Br2"
            /note="Vector: pTT73D-Pac (Pharmacia) with a modified
            polylinker; 1st strand cDNA was prepared from pooled bulk
            breast tumor tissue, and was then primed with a Not I -
            oligo(dT) primer. Double-stranded cDNA was ligated to Eco
            RI adaptors (Pharmacia), digested with Not I and cloned
            into the Not I and Eco RI sites of the modified pTT73
            vector. This library is the normalized version of
            NCI CGAP_Br1.1. Library was constructed by Bento Soares
            and M. Fatima Bonaldo."
ORIGIN
            Query Match          100.0%; Score 5; DB 1; Length 16;
            Best Local Similarity 100.0%; Pred. No. 1.2e+07;
            Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGAG 5
            |||||
Db          16 GGGAG 12

RESULT 27
LOCUS      AI094839/c
DEFINITION ga22c08.x1 NCI CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1687502 3',
            similar to TR:O00599 O00599 CON1.; contains element MSRI repetitive
            element ;, mRNA sequence.
ACCESSION  AI094839
VERSION     AI094839.1 GI:3433815
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
            NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov

```

```

ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
            NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTGP), Tumor Gene Index
JOURNAL   Unpublished (1998)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
            Ph.D.
            CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            CDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CCAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Trace considered overall poor quality
            Seq primer: -40ml3 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES   source
            1..16
            /location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:1687502"
            /tissue_type="glioblastoma (pooled)"
            /lab_host="DH10B"
            /clone_lib="NCI CGAP Brn23"
            /note="Organ: brain; Vector: pTT73D-Pac (Pharmacia) with a
            modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
            strand cDNA was primed with a Not I - oligo(dT) primer [5'-
            TGTTACCAATCTGAAGTGGGAGCGCGCATATCTTTTTTTTTTTTTTTTTT
            T 3']; double-stranded cDNA was ligated to Eco RI
            adaptors (Pharmacia), digested with Not I and cloned into
            the Not I and Eco RI sites of the modified pTT73 vector.
            Library is normalized, and was constructed by Bento
            Soares and M. Fatima Bonaldo."
ORIGIN
            Query Match          100.0%; Score 5; DB 1; Length 16;
            Best Local Similarity 100.0%; Pred. No. 1.2e+07;
            Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGAG 5
            |||||
Db          10 GGGAG 6

RESULT 28
LOCUS      AI274782/c
DEFINITION qv67h03.x1 NCI CGAP_Ut1 Homo sapiens cDNA clone IMAGE:1986677 3',
            similar to WP:F59E12.9 C11534 ;contains element MSRI repetitive
            element ;, mRNA sequence.
ACCESSION  AI274782
VERSION     AI274782.1 GI:3897056
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
            NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
AUTHORS   National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov

```

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Cloned through the NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Insert Length: 1556 Std Error: 0.00  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

## FEATURES

source

1. .16  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1986677"  
 /tissue\_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut1"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 Kb. Life Technologies catalog #: 11538-014"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 |||||  
 Db 10 GGGAG 6

## RESULT 29

A1560058

LOCUS

DEFINITION  
 tq38h11.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2211141 3'  
 similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RP15  
 PRECURSOR. ;contains MSRI.t2 MSRI repetitive element ;, mRNA  
 sequence.

ACCESSION

A1560058

VERSION

A1560058.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 16)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Cloned through the NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 2104 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

## FEATURES

source

1. .16  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2211141"  
 /tissue\_type="well-differentiated endometrial adenocarcinoma, 7 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut1"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5

|||||

Db 8 GGGAG 12

## RESULT 30

A1569544/c

LOCUS

DEFINITION

to28d10.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2180371 3'

similar to TR:Q18447 Q18444 COSMID C34D4. ;contains MSRI.b2 MSRI

repetitive element ;, mRNA sequence.

ACCESSION

A1569544

VERSION

A1569544.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 16)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Sequencing by: Washington University Genome Sequencing Center  
 Cloned through the NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 1683 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1

POLYA=No.

Location/Qualifiers

1. .16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2180371"

/tissue\_type="serous papillary carcinoma, high grade, 2

pooled tumors"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Ut4"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;

Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.48 kb. Life Technologies catalog #: 11542-016"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
 |||||  
 Db 8 GGGAG 4

## RESULT 31

BQ588093  
 LOCUS BQ588093 16 bp mRNA linear EST 06-DEC-2002  
 DEFINITION E012336-024-009-A19-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
 024-009-A19 5-PRIME, mRNA sequence.

ACCESSION BQ588093  
 VERSION BQ588093.1 GI:26117675  
 KEYWORDS EST.

## SOURCE

ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Title Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 16 Std Error: 0.00

Plate: 9 row: A column: 19

Seq primer: SP6; CATACGATTAGTGACACTATAG.

## FEATURES

source

1..16  
 Location/Qualifiers  
 /organism="Beta vulgaris"  
 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding line)"  
 /db\_xref="GABI:184766"  
 /db\_xref="taxon:161934"  
 /clone="024-009-A19"  
 /tissue\_type="leaf"  
 /lab\_host="EMD10B"  
 /clone\_lib="MP1Z-ADIS-024-leaf"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinzelleneher Saatzzucht AG Binbeck, Germany, contact:  
 b.schul@kws.de; cloning sites SalI-NotI, primer sites and  
 orientation:  
 SP6-SalI-CCACGGCGTCG-5prime-cDNA-polyA-CC-NotI-r7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database:http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
 |||||  
 Db 7 GGGAG 11

## RESULT 32

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Qy

## Db

## RESULT 33

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

## FEATURES

## source

## Qy

## Db

## Query Match

## Best Local Similarity

## Matches

## Conservative

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

## 1.2e+07

## Mismatches

## Indels

## Gaps

## Score

## DB

## Length

## Pred. No.

```

MEDLINE      22363535
PUBMED       12446565
REFERENCE    2 (bases 1 to 16)
AUTHORS      Balzerque,S.
TITLE        Direct Submission
JOURNAL      Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at
              http://dbgap.versailles.inra.fr/publiclines/. This sequence has
              been generated in the framework of the French plant genomics
              program 'Genoplante' (http://www.genoplante.com and
              http://genoplante-info.infobiogen.fr).

FEATURES     source
              1..16
              /organism="Arabidopsis thaliana"
              /mol_type="genomic DNA"
              /cultivar="Wassillewskija"
              /db_xref="taxon:3702"
              /clone="558A09"
              /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
              misc_feature 1..16
              /note="T-DNA flanking sequence
              right border"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. NO. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
        |||||
Db      6 GGGAG 2

RESULT 34
AJ595245/c
LOCUS     Arabidopsis thaliana T-DNA flanking sequence, right border, clone
DEFINITION 413H04, genomic survey sequence.
ACCESSION AJ595245
VERSION    AJ595245.1 GI:37944869
KEYWORDS   GSS; right border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE   1
AUTHORS     Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE       T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE     22363535
PUBMED      12446565
REFERENCE   2 (bases 1 to 16)
AUTHORS     Balzerque,S.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at
              http://dbgap.versailles.inra.fr/publiclines/. This sequence has
              been generated in the framework of the French plant genomics
              program 'Genoplante' (http://www.genoplante.com and
              http://genoplante-info.infobiogen.fr).

FEATURES     source
              1..16
              /organism="Arabidopsis thaliana"
              /mol_type="genomic DNA"
              /cultivar="Wassillewskija"
              /db_xref="taxon:3702"
              /clone="558A09"
              /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
              misc_feature 1..16
              /note="T-DNA flanking sequence
              right border"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. NO. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
        |||||
Db      6 GGGAG 2

RESULT 34
AJ595245/c
LOCUS     Arabidopsis thaliana T-DNA flanking sequence, right border, clone
DEFINITION 413H04, genomic survey sequence.
ACCESSION AJ595245
VERSION    AJ595245.1 GI:37944869
KEYWORDS   GSS; right border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE   1
AUTHORS     Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE       T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE     22363535
PUBMED      12446565
REFERENCE   2 (bases 1 to 16)
AUTHORS     Balzerque,S.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a

```

```

graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES     source
              1..16
              /organism="Arabidopsis thaliana"
              /mol_type="genomic DNA"
              /cultivar="Wassillewskija"
              /db_xref="taxon:3702"
              /clone="413H04"
              /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
              misc_feature 1..16
              /note="T-DNA flanking sequence
              right border"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. NO. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
        |||||
Db      6 GGGAG 2

RESULT 35
AJ598372/c
LOCUS     Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 467B08, genomic survey sequence.
ACCESSION AJ598372
VERSION    AJ598372.1 GI:37948000
KEYWORDS   GSS; left border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE   1
AUTHORS     Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE       T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
JOURNAL     EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE     22363535
PUBMED      12446565
REFERENCE   2 (bases 1 to 16)
AUTHORS     Balzerque,S.
TITLE       Direct Submission
JOURNAL     Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
COMMENT      PCR was performed on DNA from transformants of Arabidopsis thaliana
              plants from INRA (Versailles). The DNA fragment(s) resulting from
              the PCR were directly sequenced from the left or the right border
              to determine the genomic sequence flanking the insertion. T-DNA
              derived sequences were removed. Information to order the
              corresponding mutant line and a link to a database providing a
              graphical display of the insertion site are available at
              http://dbgap.versailles.inra.fr/publiclines/. This sequence has
              been generated in the framework of the French plant genomics
              program 'Genoplante' (http://www.genoplante.com and
              http://genoplante-info.infobiogen.fr).

FEATURES     source
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              /organism="Arabidopsis thaliana"
              /mol_type="genomic DNA"
              /cultivar="Wassillewskija"
              /db_xref="taxon:3702"
              /clone="467B08"
              /clone_lib="Arabidopsis thaliana T-DNA insertion lines"

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misc_feature 1..16
/Note="T-DNA flanking sequence
left border"

ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
    |||||
Db 6 GGGAG 2

RESULT 36
AJ666397/c 17 bp mRNA linear EST 28-JUN-2004
LOCUS AJ666397 CSEQRAN09 Sus scrofa cDNA clone C0000033_K10, mRNA
DEFINITION sequence.
ACCESSION AJ666397
VERSION AJ666397.1 GI:49350848
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
JOURNAL embryo development in pigs and cattle
COMMENT Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -minmatch 12 options. Vector: pBlueScriptII (KS+). R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES
Location/Qualifiers
1..17
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C0000033_K10"
/tissue_type="placenta"
/clone_lib="CSEQRAN09"
/note="Vector: pBlueScriptII (KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

ORIGIN
Query Match 100.0%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
    |||||
Db 12 GGGAG 8

RESULT 37
AW246940
LOCUS AW246940 17 bp mRNA linear EST 07-JAN-2000
DEFINITION mRNA sequence.
ACCESSION AW246940
VERSION AW246940.1 GI:65899933
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORIGIN
Query Match 100.0%; Score 5; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
    |||||
Db 9 GGGAG 13

RESULT 38
BG926068/c 17 bp mRNA linear EST 06-NOV-2001
LOCUS BG926068 HNC23-1-E10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION BG926068
VERSION BG926068.1 GI:14320591
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sache, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries

ORIGIN
Query Match 100.0%; Score 5; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
    |||||
Db 9 GGGAG 13

RESULT 38
BG926068/c 17 bp mRNA linear EST 06-NOV-2001
LOCUS BG926068 HNC23-1-E10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION sequence.
ACCESSION BG926068
VERSION BG926068.1 GI:14320591
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sache, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, M.W.
TITLE Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteochondritic cartilage cDNA libraries

```







```

Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-l@gek.com
Seq primer: T7.

FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="cartilage"
                /lab_host="E.coli DH10 B"
                /clone_lib="HOA (Human Osteoarthritic Cartilage)"
                /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
                Directional"

ORIGIN
    Query Match      100.0%; Score 5; DB 4; Length 18;
    Best Local Similarity 100.0%; Pred. No. 1.2e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
    |||||
Db 11 GGGAG 7

RESULT 44
BG925410/c
LOCUS      BG925410
DEFINITION HNC5-1-B6.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION  BG925410
VERSION    BG925410.1 GI:14319933
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE   1 (bases 1 to 18)
AUTHORS    Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
            Sathe G., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M. and
            Lark M.W.
TITLE      Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
JOURNAL    Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE    21482651
PUBMED     11597177
COMMENT    Contact: Sanjay Kumar
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-l@gek.com
            Seq primer: T7.

FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="cartilage"
                /lab_host="E.coli DH10 B"
                /clone_lib="HNC (Human Normal Cartilage)"
                /note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
                Directional"

ORIGIN
    Query Match      100.0%; Score 5; DB 4; Length 18;
    Best Local Similarity 100.0%; Pred. No. 1.2e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
    |||||
Db 11 GGGAG 7

RESULT 45
BG925569/c
LOCUS      BG925569
DEFINITION HNC5-1-B2.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION  BG925569
VERSION    BG925569.1 GI:14320092
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE   1 (bases 1 to 18)
AUTHORS    Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
            Sathe G., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M. and
            Lark M.W.
TITLE      Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
JOURNAL    Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE    21482651
PUBMED     11597177
COMMENT    Contact: Sanjay Kumar
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-l@gek.com
            Seq primer: T7.

FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /tissue_type="cartilage"
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Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM397051
VERSION    BM397051.1 GI:18197104
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila

REFERENCE   1 (bases 1 to 18)
AUTHORS    Turkewitz A.P., Karrer K.M., Jahn C., Ozias E., Kirk K.E.,
            Frankel J. and Klobutcher L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
            Unpublished (2002)
JOURNAL    Contact: Turkewitz AP
            Molecular Genetics and Cell Biology

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Db 10 GGGAG 6

RESULT 45
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LOCUS      BG925569
DEFINITION HNC5-1-B2.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION  BG925569
VERSION    BG925569.1 GI:14320092
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE   1 (bases 1 to 18)
AUTHORS    Kumar S., Connor J.R., Dodds R.A., Halsey W., Van Horn M., Mao J.,
            Sathe G., Mui P., Agarwal P., Badger A.M., Lee J.C., Gowen M. and
            Lark M.W.
TITLE      Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
JOURNAL    Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE    21482651
PUBMED     11597177
COMMENT    Contact: Sanjay Kumar
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-l@gek.com
            Seq primer: T7.

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RESULT 46
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DEFINITION 5009-0-28-D09.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM397051
VERSION    BM397051.1 GI:18197104
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila

REFERENCE   1 (bases 1 to 18)
AUTHORS    Turkewitz A.P., Karrer K.M., Jahn C., Ozias E., Kirk K.E.,
            Frankel J. and Klobutcher L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
            Unpublished (2002)
JOURNAL    Contact: Turkewitz AP
            Molecular Genetics and Cell Biology

```

```

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Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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RESULT 47
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5009-0-28-D09.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM397051
VERSION
BM397051.1 GI:18197104
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 18)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

REFERENCE
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

JOURNAL
COMMENT
Contact: Turkewitz AP
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920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
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RESULT 47
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Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
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VERSION
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KEYWORDS
EST.
SOURCE
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ORGANISM
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
1 (bases 1 to 18)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

REFERENCE
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

JOURNAL
COMMENT
Contact: Turkewitz AP
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920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

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Db 2 GGGAG 6

RESULT 47
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LOCUS
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5009-0-28-D09.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
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VERSION
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KEYWORDS
EST.
SOURCE
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ORGANISM
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
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Db 2 GGGAG 6

RESULT 47
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5009-0-28-D09.t.2 Chilcoat/Turkewitz cDNA (large fraction)
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ACCESSION
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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
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5009-0-28-D09.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Db 2 GGGAG 6

RESULT 47
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5009-0-28-D09.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM397051
VERSION
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 606
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/organism="Tetrahymena thermophila"
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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ACCESSION  BM399858
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AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Oxiak,E., Kirk,K.E.,
           Frankel,J. and Klobutcher,L.

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TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
           Molecular Genetics and Cell Biology
           University of Chicago
           920 E. 58th Street, Chicago, IL 60637, USA
           Tel: 773 702 4374
           Fax: 773 702 3172
           Email: apturkew@midway.uchicago.edu
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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DB 10 GGGAG 6

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 05:37:38 ; Search time 58 Seconds

(without alignments)

61.275 Million cell updates/sec

Title: GGGAG

Perfect score: 5

Sequence: 1 gggag 5

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 896372

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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82	5	100.0	10	3	US-08-906-691-21
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c 96	5	100.0	10	3	US-09-581-326-15
c 97	5	100.0	10	3	US-08-778-794A-117
c 98	5	100.0	10	3	US-09-326-186B-85
c 99	5	100.0	10	4	US-09-154-750A-49
c 100	5	100.0	10	4	US-09-394-457C-9

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c 161	5	100.0	11	4	US-09-249-155A-138	Sequence 138, App	c 234	5	100.0	12	2	US-08-173-489C-339	Sequence 339, App
c 162	5	100.0	11	4	US-09-249-155A-192	Sequence 192, App	c 235	5	100.0	12	2	US-08-173-489C-353	Sequence 353, App
c 163	5	100.0	11	4	US-09-249-155A-231	Sequence 231, App	c 236	5	100.0	12	2	US-08-471-973A-23	Sequence 23, Appl
c 164	5	100.0	11	4	US-09-249-155A-235	Sequence 235, App	c 237	5	100.0	12	2	US-07-923-871C-32	Sequence 32, Appl
c 165	5	100.0	11	4	US-09-249-155A-255	Sequence 251, App	c 238	5	100.0	12	2	US-08-403-888A-104	Sequence 104, App
c 166	5	100.0	11	4	US-09-249-155A-255	Sequence 255, App	c 239	5	100.0	12	2	US-08-265-484B-28	Sequence 28, Appl
c 167	5	100.0	11	4	US-09-249-155A-299	Sequence 299, App	c 240	5	100.0	12	3	US-09-035-357-23	Sequence 23, Appl
c 168	5	100.0	11	4	US-09-813-031-9	Sequence 9, Appl	c 241	5	100.0	12	3	US-09-090-947-7	Sequence 7, Appl
c 169	5	100.0	11	4	US-09-813-031-17	Sequence 17, Appl	c 242	5	100.0	12	3	US-07-794-396-5	Sequence 5, Appl
c 170	5	100.0	11	4	US-09-813-990A-9	Sequence 9, Appl	c 243	5	100.0	12	3	US-08-480-173A-24	Sequence 24, Appl
c 171	5	100.0	11	4	US-09-813-990A-17	Sequence 17, Appl	c 244	5	100.0	12	3	US-08-777-266A-87	Sequence 87, Appl
c 172	5	100.0	11	5	PCT-US95-04477-46	Sequence 46, Appl	c 245	5	100.0	12	3	US-08-676-140-1	Sequence 1, Appl
c 173	5	100.0	11	6	5175384-8	Patent No. 5175384	c 246	5	100.0	12	3	US-08-765-257A-28	Sequence 28, Appl



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C 248	5	100.0	12	3	US-09-094-714A-53	Sequence 63, Appl	C 321	5	100.0	13	1	US-08-250-740-31	Sequence 31, Appl
C 249	5	100.0	12	3	US-09-094-714A-54	Sequence 64, Appl	C 322	5	100.0	13	1	US-08-413-118-53	Sequence 53, Appl
C 250	5	100.0	12	3	US-08-929-856-73	Sequence 73, Appl	C 323	5	100.0	13	1	US-08-434-501-12	Sequence 12, Appl
C 251	5	100.0	12	3	US-08-211-882-6	Sequence 6, Appl	C 324	5	100.0	13	1	US-08-434-501-13	Sequence 13, Appl
C 252	5	100.0	12	3	US-09-115-061-12	Sequence 12, Appl	C 325	5	100.0	13	1	US-08-435-684A-4	Sequence 4, Appl
C 253	5	100.0	12	3	US-09-115-061-16	Sequence 16, Appl	C 326	5	100.0	13	1	US-08-435-684A-4	Sequence 4, Appl
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C 255	5	100.0	12	3	US-08-973-124-299	Sequence 299, App	C 328	5	100.0	13	1	US-08-259-148A-60	Sequence 60, Appl
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C 257	5	100.0	12	3	US-09-261-079-16	Sequence 16, Appl	C 330	5	100.0	13	1	US-08-373-127B-4	Sequence 4, Appl
C 258	5	100.0	12	3	US-09-281-418-50	Sequence 50, Appl	C 331	5	100.0	13	1	US-08-458-101-30	Sequence 30, Appl
C 259	5	100.0	12	3	US-09-281-418-122	Sequence 122, App	C 332	5	100.0	13	1	US-08-434-547-12	Sequence 12, Appl
C 260	5	100.0	12	3	US-09-281-418-125	Sequence 125, App	C 333	5	100.0	13	2	US-08-434-547-13	Sequence 13, Appl
C 261	5	100.0	12	3	US-09-281-418-157	Sequence 157, App	C 334	5	100.0	13	2	US-08-184-009-30	Sequence 30, Appl
C 262	5	100.0	12	3	US-09-281-418-193	Sequence 193, App	C 335	5	100.0	13	2	US-08-525-506-4	Sequence 4, Appl
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C 266	5	100.0	12	3	US-09-284-832-10	Sequence 10, Appl	C 339	5	100.0	13	2	US-08-173-489C-243	Sequence 243, App
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C 271	5	100.0	12	3	US-08-945-140-10	Sequence 10, Appl	C 344	5	100.0	13	2	US-08-053-451B-134	Sequence 134, App
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C 275	5	100.0	12	3	US-09-043-149-24	Sequence 24, Appl	C 348	5	100.0	13	3	US-08-777-266A-88	Sequence 88, Appl
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C 279	5	100.0	12	3	US-09-043-149-49	Sequence 49, Appl	C 352	5	100.0	13	3	US-08-871-678C-4	Sequence 4, Appl
C 280	5	100.0	12	3	US-09-308-759A-2	Sequence 2, Appl	C 353	5	100.0	13	3	US-09-085-028-4	Sequence 4, Appl
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C 306	5	100.0	12	5	PCT-US95-03602-1	Sequence 1, Appl	C 379	5	100.0	13	6	US-09-500-700-27	Sequence 27, Appl
C 307	5	100.0	12	5	PCT-US95-03602-2	Sequence 2, Appl	C 380	5	100.0	14	1	US-09-500-700-27	Sequence 27, Appl
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C 312	5	100.0	13	1	US-08-105-483-30	Sequence 30, Appl	C 385	5	100.0	14	1	US-08-151-574-50	Sequence 50, Appl
C 313	5	100.0	13	1	US-08-220-151-53	Sequence 53, Appl	C 386	5	100.0	14	1	US-07-832-855-7	Sequence 7, Appl
C 314	5	100.0	13	1	US-08-050-073-269	Sequence 269, App	C 387	5	100.0	14	1	US-08-050-073-232	Sequence 232, App
C 315	5	100.0	13	1	US-08-123-449A-17	Sequence 17, Appl	C 388	5	100.0	14	1	US-08-050-073-233	Sequence 233, App
C 316	5	100.0	13	1	US-08-310-356-30	Sequence 30, Appl	C 389	5	100.0	14	2	US-08-173-489C-97	Sequence 97, Appl
C 317	5	100.0	13	1	US-07-965-411A-12	Sequence 12, Appl	C 390	5	100.0	14	2	US-08-173-489C-98	Sequence 98, Appl
C 318	5	100.0	13	1	US-07-965-411A-13	Sequence 13, Appl	C 391	5	100.0	14	2	US-08-173-489C-276	Sequence 276, App
C 319	5	100.0	13	1	US-08-458-050-17	Sequence 17, Appl	C 392	5	100.0	14	2	US-08-173-489C-317	Sequence 317, App
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INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-963-723A-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 9 GGGAG 5

RESULT 2  
US-08-202-927-14  
; Sequence 14, Application US/08202927  
; Patent No. 5646126  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Yung-chi  
; APPLICANT: Lukhtanov, Eugeny A.  
; APPLICANT: Meyer Jr., Rich B.  
; APPLICANT: Pai, Balakrishna S.  
; APPLICANT: Reed, Michael W.  
; APPLICANT: Zhou, James H.  
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
; TITLE OF INVENTION: Anticancer Activity  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klein & Szekeres  
; STREET: 4199 Campus Drive, Suite 700  
; CITY: Irvine  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92715

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675  
REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
OTHER INFORMATION: a cholesterol moiety which has its A ring linked to  
OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
OTHER INFORMATION: formula 3)."  
US-08-202-927-14

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 10

RESULT 3  
US-08-074-879-3  
; Sequence 3, Application US/08074879  
; Patent No. 5656423  
; GENERAL INFORMATION:  
; APPLICANT: Orth, Gerard  
; APPLICANT: Volpers, Christoph  
; APPLICANT: Streek, Rolf  
; TITLE OF INVENTION: DNA Sequences Derived from the Genome of  
; TITLE OF INVENTION: the Papillomavirus HPV39, Their Use in In Vitro Diagnosis  
; TITLE OF INVENTION: and for the Production of an Immunogenic Composition  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; STREET: 1300 I Street, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005-3315

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/074,879  
FILING DATE: 16-JUN-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 92/1136  
FILING DATE: 09-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Potter, Jane E.R.  
REGISTRATION NUMBER: 33,332  
REFERENCE/DOCKET NUMBER: 02356.0066-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-074-879-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 4 GGGAG 8

RESULT 4  
US-08-468-057A-3  
; Sequence 3, Application US/08468057A  
; Patent No. 5665535  
; GENERAL INFORMATION:  
; APPLICANT: Orth, Gerard  
; APPLICANT: Volpers, Christoph

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; APPLICANT: Streek, Rolf
; TITLE OF INVENTION: DNA Sequences Derived from the Genome of
; the Papillomavirus HPV39, Their Use in In Vitro Diagnosis
; TITLE OF INVENTION: and for the Production of an Immunogenic Composition
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,057A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/074,879
; FILING DATE: 16-JUN-1993
; APPLICATION NUMBER: WO 92/1136
; FILING DATE: 09-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E.R.
; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 02356.0066-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-468-057A-3

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 4 GGGAG 8
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RESULT 5
US-08-171-718-30/c
; Sequence 30, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Irofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-171-718-30

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 5 GGGAG 1
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RESULT 6
US-08-480-994-20/c
; Sequence 20, Application US/08480994
; Patent No. 5834248
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,994
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
```

REFERENCE/DOCKET NUMBER: 7853-033  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 20:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-08-480-994-20

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
DB 6 GGGAG 2

## RESULT 7

US-08-480-994-30  
Sequence 30, Application US/08480994  
Patent No. 5834248  
GENERAL INFORMATION:  
APPLICANT: PALB, DEAN A.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 38  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,994  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/485,573  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/386,844  
FILING DATE: 10-FEB-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-033  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-08-480-994-30

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
DB 6 GGGAG 10

## RESULT 8

US-08-441-887A-40  
Sequence 40, Application US/08441887A  
Patent No. 5837832  
GENERAL INFORMATION:  
APPLICANT: Chee, Mark  
APPLICANT: Cronin, Maureen T.  
APPLICANT: Fodor, Stephen P.A.  
APPLICANT: Huang, Xiaohua X.  
APPLICANT: Hubbell, Earl A.  
APPLICANT: Lipshutz, Robert J.  
APPLICANT: Lobban, Peter E.  
APPLICANT: Morris, Macdonald S.  
APPLICANT: Sheldon, Edward L.  
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
NUMBER OF SEQUENCES: 360  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441,887A  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,312  
FILING DATE: 26-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/082,937  
FILING DATE: 25-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joseph O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 018547-00416005  
TELEPHONE: 650-326-2400  
TELEFAX: 650-326-2422  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (probe)  
US-08-441-887A-40

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||||  
DB 6 GGGAG 10

RESULT 9  
US-08-441-887A-96  
; Sequence 96, Application US/08441887A  
; Patent No. 5837832  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua X.  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; APPLICANT: Sheldon, Edward L.  
; APPLICANT: Townsend and Crew LLP  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
; TITLE OF INVENTION: Biological Chips  
; NUMBER OF SEQUENCES: 360  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,887A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/082,937  
; FILING DATE: 25-JUN-1993  
; NAME: Liebeschuetz, Joseph O.  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004160US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-326-2400  
; TELEFAX: 650-326-2422  
; INFORMATION FOR SEQ ID NO: 96:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
US-08-441-887A-96

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 5 GGGAG 9

RESULT 10  
US-08-441-887A-348/c  
; Sequence 348, Application US/08441887A  
; Patent No. 5837832  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.

; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua X.  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; APPLICANT: Sheldon, Edward L.  
; APPLICANT: Townsend and Crew LLP  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
; TITLE OF INVENTION: Biological Chips  
; NUMBER OF SEQUENCES: 360  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,887A  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/082,937  
; FILING DATE: 25-JUN-1993  
; NAME: Liebeschuetz, Joseph O.  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004160US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-326-2400  
; TELEFAX: 650-326-2422  
; INFORMATION FOR SEQ ID NO: 348:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
US-08-441-887A-348

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 7 GGGAG 3

RESULT 11  
US-08-441-887A-349/c  
; Sequence 349, Application US/08441887A  
; Patent No. 5837832  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua X.  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; APPLICANT: Sheldon, Edward L.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on

;; TITLE OF INVENTION: Biological Chips  
;; NUMBER OF SEQUENCES: 360  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, 8th Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/441,887A  
;; FILING DATE: 16-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/143,312  
;; FILING DATE: 26-OCT-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/441,887A  
;; FILING DATE: 16-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/082,937  
;; FILING DATE: 25-JUN-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Liebeschuetz, Joseph O.  
;; REGISTRATION NUMBER: 37,505  
;; REFERENCE/DOCKET NUMBER: 018547-004160US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650-326-2400  
;; TELEFAX: 650-326-2422  
;; INFORMATION FOR SEQ ID NO: 349:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (probe)  
US-08-441-887A-349

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 8 GGGAG 4

RESULT 12  
US-08-441-887A-350/c  
; Sequence 350, Application US/08441887A  
; Patent No. 5837832  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua X.  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; APPLICANT: Sheldon, Edward L.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
; NUMBER OF SEQUENCES: 360  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA

;; ZIP: 94111  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/441,887A  
;; FILING DATE: 16-MAY-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/143,312  
;; FILING DATE: 26-OCT-1993  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/082,937  
;; FILING DATE: 25-JUN-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Liebeschuetz, Joseph O.  
;; REGISTRATION NUMBER: 37,505  
;; REFERENCE/DOCKET NUMBER: 018547-004160US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 650-326-2400  
;; TELEFAX: 650-326-2422  
;; INFORMATION FOR SEQ ID NO: 350:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (probe)  
US-08-441-887A-350

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 9 GGGAG 5

RESULT 13  
US-08-441-887A-351/c  
; Sequence 351, Application US/08441887A  
; Patent No. 5837832  
; GENERAL INFORMATION:  
; APPLICANT: Chee, Mark  
; APPLICANT: Cronin, Maureen T.  
; APPLICANT: Fodor, Stephen P.A.  
; APPLICANT: Huang, Xiaohua X.  
; APPLICANT: Hubbell, Earl A.  
; APPLICANT: Lipshutz, Robert J.  
; APPLICANT: Lobban, Peter E.  
; APPLICANT: Morris, Macdonald S.  
; APPLICANT: Sheldon, Edward L.  
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
; NUMBER OF SEQUENCES: 360  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, 8th Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/441,887A

;  
; FILING DATE: 16-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/143,312  
; FILING DATE: 26-OCT-1993  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/082,937  
; FILING DATE: 25-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Liebeschuetz, Joseph O.  
; REGISTRATION NUMBER: 37,505  
; REFERENCE/DOCKET NUMBER: 018547-004160US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-326-2400  
; TELEFAX: 650-326-2422  
; INFORMATION FOR SEQ ID NO: 351:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (probe)  
US-08-441-887A-351

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.1e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 1 GGGAG 5  
Db 10 GGGAG 6

## RESULT 14

US-08-616-844-20/c  
; Sequence 20, Application US/08616844  
; Patent No. 5849578  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/616,844  
; FILING DATE: 15-MAR-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/599,654  
; FILING DATE: 09-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CORUZZI, LAURA A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic oligonucleotide"

;  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic oligonucleotide"  
; HYPOTHETICAL: NO  
US-08-616-844-20

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.1e+05; Indels 0; Gaps 0;  
Matches 5; Conservative 0; Mismatches 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 2

## RESULT 15

US-08-616-844-30  
; Sequence 30, Application US/08616844  
; Patent No. 5849578  
; GENERAL INFORMATION:  
; APPLICANT: FALB, DEAN A.  
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE  
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
; NUMBER OF SEQUENCES: 54  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PENNIE & EDMONDS  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/616,844  
; FILING DATE: 15-MAR-1996  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/599,654  
; FILING DATE: 09-FEB-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,573  
; FILING DATE: 07-JUN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/386,844  
; FILING DATE: 10-FEB-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CORUZZI, LAURA A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7853-053  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "synthetic oligonucleotide"



US-08-616-844-30  
HYPOTHETICAL: NO

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 6 GGGAG 10

## RESULT 16

US-08-173-489C-169  
; Sequence 169, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HEPBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10021.

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 169:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: genomic DNA  
DESCRIPTION: hepatitis B virus ayw isolate,  
DESCRIPTION: nucleotides 3071 to 3080  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Hepatitis B virus  
INDIVIDUAL ISOLATE: ayw  
PUBLICATION INFORMATION:  
AUTHORS: Galibert, F, Mandart, E, Fitoussi, F,  
AUTHORS: Tiollais, P, Charnay, P.  
TITLE: Nucleotide sequence of the  
TITLE: Hepatitis B virus genome (subtype ayw) cloned  
TITLE: in E coli  
JOURNAL: Nature  
VOLUME: 281  
PAGES: 646-650  
DATE: 1979  
RELEVANT RESIDUES IN SEQ ID NO: 169 :FROM 1 TO 10

US-08-173-489C-169

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 3 GGGAG 7

## RESULT 17

US-08-173-489C-200/c  
; Sequence 200, Application US/08173489C  
; Patent No. 5861244  
; GENERAL INFORMATION:  
; APPLICANT: WANG, C. -G.  
; APPLICANT: HEPBURN, A. G.  
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
; NUMBER OF SEQUENCES: 365  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
; STREET: 510 EAST 73RD STREET,  
; CITY: NEW YORK  
; STATE: NEW YORK  
; COUNTRY: USA  
; ZIP: 10021.

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 200:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 bases  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: third strand derived from Hepatitis B  
DESCRIPTION: isolate adr sequence region in Seq ID No. 5861244199  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
PUBLICATION INFORMATION:  
RELEVANT RESIDUES IN SEQ ID NO: 200 :FROM 1 TO 10

US-08-173-489C-200

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 7 GGGAG 3

## RESULT 18

US-08-173-489C-287

```
; Sequence 287, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelmann, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 287:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 16S rRNA gene from Clostridium
; DESCRIPTION: pasteurianum (Accession # M23930) nucleotides
; DESCRIPTION: 149 to 158
; HYPOTHEICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Clostridium pasteurianum
; PUBLICATION INFORMATION:
; AUTHORS: Weisburg, W G, Tully, J G, Rose, D L,
; AUTHORS: Petzel, J P, Oyaizu, H, Yang, D, Mandelco,
; AUTHORS: L, Sechrest, J, Lawrence, T G, Van Etten, J,
; AUTHORS: Maniloff, J, Woese, C R.
; TITLE: A phylogenetic analysis of
; TITLE: the mycoplasmas: Basis for their classification
; JOURNAL: Journal of Bacteriology
; VOLUME: 171
; PAGES: 6455-6467
; DATE: 1989
; RELEVANT RESIDUES IN SEQ ID NO: 287 :FROM 1 TO 10
US-08-173-489C-287

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 5 GGGAG 9

RESULT 19
US-08-590-571-19/c
; Sequence 19, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-19

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
Db 9 GGGAG 5

RESULT 20
US-08-590-571-29
; Sequence 29, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
```

REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 29:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-590-571-29

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 3 GGGAG 7

## RESULT 21

US-08-590-571-31/c  
Sequence 31, Application US/08590571  
Patent No. 5861246  
GENERAL INFORMATION:  
APPLICANT: Sherman Weissman and Girish N. Nallur  
TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611

COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,571  
FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-590-571-31

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 9 GGGAG 5

## RESULT 22

US-08-590-571-32  
Sequence 32, Application US/08590571  
Patent No. 5861246  
GENERAL INFORMATION:  
APPLICANT: Sherman Weissman and Girish N. Nallur  
TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,571  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-590-571-32

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 6 GGGAG 10

## RESULT 23

US-08-599-654-20/c  
Sequence 20, Application US/08599654  
Patent No. 5882925  
GENERAL INFORMATION:  
APPLICANT: FALB, DEAN A  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE  
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE  
NUMBER OF SEQUENCES: 54  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PENNIE & EDMONDS  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/599,654  
FILING DATE: 09-FEB-1996  
CLASSIFICATION: 800

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-041
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNTE
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; US-08-599-654-20

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 6 GGGAG 2

RESULT 24
US-08-599-654-30
; Sequence 30, Application US/08599654
; Patent No. 5882925
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/599,654
; FILING DATE: 09-FEB-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-041
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
```

```
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; US-08-599-654-30

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 6 GGGAG 10

RESULT 25
US-08-545-253A-15/c
; Sequence 15, Application US/08545253A
; Patent No. 5908978
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; APPLICANT: Henry V. Ameron
; APPLICANT: Phillip Wilcox
; APPLICANT: E. George Kuhlman
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
; TITLE OF INVENTION: SELECTION IN
; TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5908978th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,253A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; US-08-545-253A-15

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
```



TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
US-08-485-573-30

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 6 GGGAG 10  
|||||

RESULT 29  
US-08-265-484B-1/c  
Sequence 1, Application US/08265484B  
Patent No. 5998193  
GENERAL INFORMATION:  
APPLICANT: Keese, Paul  
APPLICANT: Stapper, Marianne  
APPLICANT: Perriman, Rhonda  
TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
TITLE OF INVENTION: Ribozymes and Compositions Thereof  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,484B  
FILING DATE: 24-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45284  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other Nucleic Acid  
US-08-265-484B-1

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 10 GGGAG 6  
|||||

RESULT 30  
US-08-265-484B-2  
Sequence 2, Application US/08265484B  
Patent No. 5998193  
GENERAL INFORMATION:  
APPLICANT: Keese, Paul  
APPLICANT: Stapper, Marianne  
APPLICANT: Perriman, Rhonda  
TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
TITLE OF INVENTION: Ribozymes and Compositions Thereof  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,484B  
FILING DATE: 24-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other Nucleic Acid  
US-08-265-484B-2

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
DB 1 GGGAG 5  
|||||

RESULT 31  
US-08-265-484B-4  
Sequence 4, Application US/08265484B  
Patent No. 5998193  
GENERAL INFORMATION:  
APPLICANT: Keese, Paul  
APPLICANT: Stapper, Marianne  
APPLICANT: Perriman, Rhonda  
TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
TITLE OF INVENTION: Ribozymes and Compositions Thereof  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
; US-08-265-484B-4

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
DB 1 GGGAG 5

RESULT 32
US-08-265-484B-9
; Sequence 9, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perrinan, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
```

```
;
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
; US-08-265-484B-9

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
DB 1 GGGAG 5

RESULT 33
US-08-265-484B-10
; Sequence 10, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perrinan, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
; US-08-265-484B-10

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5
DB 1 GGGAG 5

RESULT 34
US-08-265-484B-27/c
; Sequence 27, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
```

APPLICANT: Stapper, Marianne  
APPLICANT: Perleman, Rhonda  
TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
TITLE OF INVENTION: Ribozymes and Compositions Thereof  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/265,484B  
FILING DATE: 24-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 45284  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Other Nucleic Acid  
US-08-265-484B-27

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 10 GGGAG 6

RESULT 35  
US-08-388-353-86  
Sequence 86, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353

FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 86:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-86

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 10

RESULT 36  
US-08-388-353-87  
Sequence 87, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: DiGiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 87:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-87



Query Match 100.0%; Score 5; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 |||||  
 Db 5 GGGAG 9

## RESULT 37

US-08-388-353-88  
 ; Sequence 88, Application US/08388353  
 ; Patent No. 6010895  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deacon, Nicholas J.  
 ; APPLICANT: Learmont, Jennifer C.  
 ; APPLICANT: McPhee, Dale A.  
 ; APPLICANT: Crowe, Suzanne  
 ; APPLICANT: Cooper, David  
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 800  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Scully, Scott, Murphy & Presser  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City  
 ; STATE: New York  
 ; COUNTRY: United States  
 ; ZIP: 11530  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/388,353  
 ; FILING DATE: 14-FEB-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Digiglio, Frank S.  
 ; REGISTRATION NUMBER: 31,346  
 ; REFERENCE/DOCKET NUMBER: 9606  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 742-4366  
 ; TELEFAX: (516) 742-4366  
 ; TELEX: 230 901 SANS UR  
 ; INFORMATION FOR SEQ ID NO: 88:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-388-353-88

Query Match 100.0%; Score 5; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 |||||  
 Db 4 GGGAG 8

## RESULT 38

US-08-388-353-89  
 ; Sequence 89, Application US/08388353  
 ; Patent No. 6010895  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deacon, Nicholas J.  
 ; APPLICANT: Learmont, Jennifer C.  
 ; APPLICANT: McPhee, Dale A.  
 ; APPLICANT: Crowe, Suzanne  
 ; APPLICANT: Cooper, David

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 800  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Scully, Scott, Murphy & Presser  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City  
 ; STATE: New York  
 ; COUNTRY: United States  
 ; ZIP: 11530  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/388,353  
 ; FILING DATE: 14-FEB-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Digiglio, Frank S.  
 ; REGISTRATION NUMBER: 31,346  
 ; REFERENCE/DOCKET NUMBER: 9606  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 742-4366  
 ; TELEFAX: (516) 742-4366  
 ; TELEX: 230 901 SANS UR  
 ; INFORMATION FOR SEQ ID NO: 89:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA (genomic)  
 ; US-08-388-353-89

Query Match 100.0%; Score 5; DB 3; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 |||||  
 Db 3 GGGAG 7

## RESULT 39

US-08-388-353-90  
 ; Sequence 90, Application US/08388353  
 ; Patent No. 6010895  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Deacon, Nicholas J.  
 ; APPLICANT: Learmont, Jennifer C.  
 ; APPLICANT: McPhee, Dale A.  
 ; APPLICANT: Crowe, Suzanne  
 ; APPLICANT: Cooper, David  
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
 ; NUMBER OF SEQUENCES: 800  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Scully, Scott, Murphy & Presser  
 ; STREET: 400 Garden City Plaza  
 ; CITY: Garden City  
 ; STATE: New York  
 ; COUNTRY: United States  
 ; ZIP: 11530  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/388,353  
 ; FILING DATE: 14-FEB-1995  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 90:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-90

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
DB 2 GGGAG 6

RESULT 40  
US-08-388-353-91  
; Sequence 91, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Cooper, David  
; APPLICANT: Crowe, Suzanne  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 91:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-91

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
DB 1 GGGAG 5

RESULT 41  
US-08-388-353-302/c  
; Sequence 302, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 302:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-302

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|||  
DB 10 GGGAG 6

RESULT 42  
US-08-388-353-303/c  
; Sequence 303, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 303:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-303

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 9 GGGAG 5

RESULT 43  
US-08-388-353-304/C  
Sequence 304, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 304:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-304

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 8 GGGAG 4

RESULT 44  
US-08-388-353-305/C  
Sequence 305, Application US/08388353  
Patent No. 6010895  
GENERAL INFORMATION:  
APPLICANT: Deacon, Nicholas J.  
APPLICANT: Learmont, Jennifer C.  
APPLICANT: McPhee, Dale A.  
APPLICANT: Crowe, Suzanne  
APPLICANT: Cooper, David  
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
NUMBER OF SEQUENCES: 800  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Scully, Scott, Murphy & Presser  
STREET: 400 Garden City Plaza  
CITY: Garden City  
STATE: New York  
COUNTRY: United States  
ZIP: 11530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/388,353  
FILING DATE: 14-FEB-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 305:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-305

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||

```
Db          7 GGGAG 3

RESULT 45
US-08-388-353-306/c
; Sequence 306, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 306:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-306

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Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGAG 5
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Db          5 GGGAG 1

RESULT 47
US-08-388-353-694
; Sequence 694, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 307:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-307

Query Match          100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGAG 5
           |||||
Db          5 GGGAG 1

RESULT 46
US-08-388-353-307/c
; Sequence 307, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City

Query Match          100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGAG 5
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Db          6 GGGAG 2

RESULT 46
US-08-388-353-307/c
; Sequence 307, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
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TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 694:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-694

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 6 GGGAG 10

RESULT 48  
US-08-388-353-695  
; Sequence 695, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 14-FEB-1995  
APPLICATION NUMBER: US/08/388,353  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 695:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-695

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Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 5 GGGAG 9

RESULT 49  
US-08-388-353-696  
; Sequence 696, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 14-FEB-1995  
APPLICATION NUMBER: US/08/388,353  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Digiglio, Frank S.  
REGISTRATION NUMBER: 31,346  
REFERENCE/DOCKET NUMBER: 9606  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 742-4343  
TELEFAX: (516) 742-4366  
TELEX: 230 901 SANS UR  
INFORMATION FOR SEQ ID NO: 696:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-388-353-696

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 3.1e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
Db 4 GGGAG 8

RESULT 50  
US-08-388-353-697  
; Sequence 697, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglo, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 697:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-697

Query Match      100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No. 3.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
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Db       3 GGGAG 7

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Search completed: January 7, 2005, 11:05:38  
Job time : 61 secs

GenCore version 5.1.6  
Copyright (C) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 06:51:47 ; Search time 270.2 Seconds  
(without alignments)  
106.177 Million cell updates/sec

Title: GGGAG

Perfect score: 5

Sequence: 1 gggag 5

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Maximum Match 100%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	5	100.0	10	9	US-09-989-789-569
5	5	100.0	10	9	US-09-989-789-570
6	5	100.0	10	9	US-09-989-789-601
7	5	100.0	10	9	US-09-989-789-604
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9	5	100.0	10	9	US-09-989-789-609
10	5	100.0	10	9	US-09-989-789-610
11	5	100.0	10	9	US-09-989-789-645
12	5	100.0	10	9	US-09-989-789-1271

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14	5	100.0	10	9	US-09-989-789-1283	Sequence 1283, Ap
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21	5	100.0	10	9	US-09-989-789-1630	Sequence 1630, Ap
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82	5	100.0	10	10	US-09-990-186-1704	Sequence 1704, Ap
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111	5	100.0	10	10	US-09-989-994-1696	Sequence 1696, App	c 184	5	100.0	10	15	US-10-329-465-163	Sequence 163, App
112	5	100.0	10	10	US-09-989-994-1697	Sequence 1697, App	c 185	5	100.0	10	15	US-10-329-465-183	Sequence 183, App
113	5	100.0	10	10	US-09-989-994-1698	Sequence 1698, App	c 186	5	100.0	10	15	US-10-329-465-202	Sequence 202, App
114	5	100.0	10	10	US-09-989-994-1699	Sequence 1699, App	c 187	5	100.0	10	15	US-10-329-465-243	Sequence 243, App
115	5	100.0	10	10	US-09-989-994-1700	Sequence 1700, App	c 188	5	100.0	10	15	US-10-223-765-199	Sequence 199, App
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117	5	100.0	10	10	US-09-989-994-1702	Sequence 1702, App	c 190	5	100.0	10	15	US-10-223-765-211	Sequence 211, App
118	5	100.0	10	10	US-09-989-994-1703	Sequence 1703, App	c 191	5	100.0	10	15	US-10-223-765-219	Sequence 219, App
119	5	100.0	10	10	US-09-989-994-1704	Sequence 1704, App	c 192	5	100.0	10	15	US-10-223-765-226	Sequence 226, App
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122	5	100.0	10	10	US-09-798-260-117	Sequence 117, App	c 195	5	100.0	10	15	US-10-223-765-254	Sequence 254, App
123	5	100.0	10	10	US-09-945-505-27	Sequence 27, Appli	c 196	5	100.0	10	15	US-10-223-765-259	Sequence 259, App
c 124	5	100.0	10	10	US-09-945-505-35	Sequence 35, Appli	c 197	5	100.0	10	15	US-10-223-765-265	Sequence 265, App
c 125	5	100.0	10	10	US-09-851-871-85	Sequence 85, Appli	c 198	5	100.0	10	15	US-10-223-765-271	Sequence 271, App
126	5	100.0	10	13	US-10-033-145-48	Sequence 48, Appli	c 199	5	100.0	10	15	US-10-223-765-274	Sequence 274, App
c 127	5	100.0	10	13	US-09-834-095-16	Sequence 16, Appli	c 200	5	100.0	10	15	US-10-355-820-1	Sequence 1, Appli
128	5	100.0	10	13	US-10-033-145-56	Sequence 56, Appli	c 201	5	100.0	10	15	US-10-355-820-2	Sequence 2, Appli
c 129	5	100.0	10	13	US-10-033-145-135	Sequence 135, App	c 202	5	100.0	10	15	US-10-390-045-14	Sequence 14, Appli
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c 131	5	100.0	10	13	US-10-033-145-172	Sequence 172, App	c 204	5	100.0	10	15	US-10-390-045-43	Sequence 43, Appli
c 132	5	100.0	10	13	US-10-033-145-269	Sequence 269, App	c 205	5	100.0	10	15	US-10-044-674-62	Sequence 62, Appli
133	5	100.0	10	13	US-10-033-145-321	Sequence 321, App	c 206	5	100.0	10	15	US-10-044-674-68	Sequence 68, Appli
134	5	100.0	10	13	US-10-033-145-449	Sequence 449, App	c 207	5	100.0	10	15	US-10-330-627-11	Sequence 11, Appli
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142	5	100.0	10	13	US-10-033-145-637	Sequence 637, App	c 215	5	100.0	10	15	US-10-330-627-419	Sequence 419, App
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c 146	5	100.0	10	13	US-10-033-145-1165	Sequence 1165, App	c 219	5	100.0	10	15	US-10-330-627-641	Sequence 641, App
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149	5	100.0	10	13	US-10-033-145-1218	Sequence 1218, App	c 222	5	100.0	10	15	US-10-330-627-680	Sequence 680, App
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151	5	100.0	10	13	US-10-033-145-1300	Sequence 1300, App	c 224	5	100.0	10	15	US-10-330-627-779	Sequence 779, App
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c 154	5	100.0	10	13	US-10-033-145-1427	Sequence 1427, App	c 227	5	100.0	10	15	US-10-330-627-791	Sequence 791, App
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158	5	100.0	10	13	US-10-033-145-1526	Sequence 1526, App	c 231	5	100.0	10	15	US-10-330-627-836	Sequence 836, App



c 232	5	100.0	10	15	US-10-330-627-855	Sequence 855, App	c 305	5	100.0	11	9	US-09-813-031-9	Sequence 9, Appli
c 233	5	100.0	10	15	US-10-330-627-861	Sequence 861, App	c 306	5	100.0	11	9	US-09-813-031-17	Sequence 17, Appl
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c 235	5	100.0	10	15	US-10-330-627-948	Sequence 948, App	c 308	5	100.0	11	9	US-09-813-990A-17	Sequence 17, Appl
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c 237	5	100.0	10	15	US-10-330-627-961	Sequence 961, App	c 310	5	100.0	11	9	US-09-263-959-684	Sequence 684, App
c 238	5	100.0	10	15	US-10-330-627-993	Sequence 993, App	c 311	5	100.0	11	9	US-09-263-959-707	Sequence 707, App
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c 244	5	100.0	10	15	US-10-330-627-1266	Sequence 1266, App	c 317	5	100.0	11	10	US-09-943-115A-58	Sequence 58, Appl
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c 247	5	100.0	10	15	US-10-330-627-1341	Sequence 1341, App	c 321	5	100.0	11	10	US-09-249-155-53	Sequence 53, Appl
c 248	5	100.0	10	15	US-10-330-627-1397	Sequence 1397, App	c 322	5	100.0	11	10	US-09-249-155-138	Sequence 138, App
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c 251	5	100.0	10	15	US-10-330-627-1400	Sequence 1400, App	c 324	5	100.0	11	10	US-09-249-155-235	Sequence 235, App
c 252	5	100.0	10	15	US-10-330-627-1461	Sequence 1461, App	c 325	5	100.0	11	10	US-09-249-155-251	Sequence 251, App
c 253	5	100.0	10	15	US-10-330-627-1503	Sequence 1503, App	c 326	5	100.0	11	10	US-09-996-484-61	Sequence 61, Appl
c 254	5	100.0	10	15	US-10-330-627-1548	Sequence 1548, App	c 327	5	100.0	11	10	US-09-851-871-86	Sequence 86, Appl
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c 256	5	100.0	10	15	US-10-186-950-30	Sequence 30, Appl	c 329	5	100.0	11	13	US-10-027-632-176254	Sequence 176254, A
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c 258	5	100.0	10	15	US-10-091-281-166	Sequence 166, App	c 331	5	100.0	11	15	US-10-266-138B-18	Sequence 18, Appl
c 259	5	100.0	10	15	US-10-099-816B-5	Sequence 5, Appl	c 332	5	100.0	11	15	US-10-266-138B-32	Sequence 32, Appl
c 260	5	100.0	10	15	US-10-027-632-52785	Sequence 52785, A	c 333	5	100.0	11	15	US-10-104-025-14	Sequence 14, Appl
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c 262	5	100.0	10	15	US-10-197-019-90	Sequence 90, Appl	c 335	5	100.0	11	15	US-10-265-509B-18	Sequence 18, Appl
c 263	5	100.0	10	15	US-10-356-732-33	Sequence 33, Appl	c 336	5	100.0	11	15	US-10-265-509B-32	Sequence 32, Appl
c 264	5	100.0	10	15	US-10-257-021-89	Sequence 89, Appl	c 337	5	100.0	11	15	US-10-027-859-9	Sequence 9, Appli
c 265	5	100.0	10	15	US-10-257-021-91	Sequence 91, Appl	c 338	5	100.0	11	15	US-10-084-839-3614	Sequence 3614, Ap
c 266	5	100.0	10	15	US-10-257-021-111	Sequence 111, App	c 339	5	100.0	11	15	US-10-192-078-30	Sequence 30, Appl
c 267	5	100.0	10	15	US-10-386-099-14	Sequence 14, Appl	c 340	5	100.0	11	15	US-10-091-281-178	Sequence 178, App
c 268	5	100.0	10	15	US-10-386-099-15	Sequence 15, Appl	c 341	5	100.0	11	15	US-10-091-281-369	Sequence 369, App
c 269	5	100.0	10	15	US-10-401-194-80	Sequence 80, Appl	c 342	5	100.0	11	15	US-10-027-632-58970	Sequence 58970, A
c 270	5	100.0	10	15	US-10-401-194-84	Sequence 84, Appl	c 343	5	100.0	11	15	US-10-027-632-176254	Sequence 176254, A
c 271	5	100.0	10	15	US-10-401-194-83	Sequence 83, Appl	c 344	5	100.0	11	15	US-10-396-122-102	Sequence 102, App
c 272	5	100.0	10	16	US-10-193-507-83	Sequence 83, Appl	c 345	5	100.0	11	15	US-10-314-322-53	Sequence 53, Appl
c 273	5	100.0	10	16	US-10-444-206-85	Sequence 85, Appl	c 346	5	100.0	11	15	US-10-314-322-138	Sequence 138, App
c 274	5	100.0	10	16	US-10-293-222-58	Sequence 58, Appl	c 347	5	100.0	11	15	US-10-314-322-192	Sequence 192, App
c 275	5	100.0	10	16	US-10-293-222-65	Sequence 65, Appl	c 348	5	100.0	11	15	US-10-314-322-231	Sequence 231, App
c 276	5	100.0	10	16	US-10-293-222-90	Sequence 90, Appl	c 349	5	100.0	11	15	US-10-314-322-235	Sequence 235, App
c 277	5	100.0	10	16	US-10-293-222-153	Sequence 153, App	c 350	5	100.0	11	15	US-10-314-322-251	Sequence 251, App
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c 283	5	100.0	10	16	US-10-407-846-2	Sequence 2, Appli	c 356	5	100.0	11	17	US-10-450-797-39	Sequence 39, Appl
c 284	5	100.0	10	16	US-10-276-608-74	Sequence 74, Appl	c 357	5	100.0	11	17	US-10-450-797-49	Sequence 49, Appl
c 285	5	100.0	10	16	US-10-398-877-33	Sequence 33, Appl	c 358	5	100.0	11	17	US-10-450-797-66	Sequence 66, Appl
c 286	5	100.0	10	16	US-10-434-479-14	Sequence 14, Appl	c 359	5	100.0	11	17	US-10-450-797-81	Sequence 81, Appl
c 287	5	100.0	10	16	US-10-434-479-37	Sequence 37, Appl	c 360	5	100.0	11	17	US-10-450-797-110	Sequence 110, App
c 288	5	100.0	10	16	US-10-434-479-43	Sequence 43, Appl	c 361	5	100.0	11	17	US-10-450-797-131	Sequence 131, App
c 289	5	100.0	10	16	US-10-816-079-12	Sequence 12, Appl	c 362	5	100.0	11	17	US-10-450-797-159	Sequence 159, App
c 290	5	100.0	10	17	US-10-723-940-93	Sequence 93, Appl	c 363	5	100.0	11	17	US-10-450-797-166	Sequence 166, App
c 291	5	100.0	10	17	US-10-670-011-398	Sequence 7, Appli	c 364	5	100.0	11	17	US-10-450-797-203	Sequence 203, App
c 292	5	100.0	10	18	US-10-827-995-15	Sequence 15, Appl	c 365	5	100.0	11	17	US-10-450-797-228	Sequence 228, App
c 293	5	100.0	10	18	US-10-641-962-85	Sequence 85, Appl	c 366	5	100.0	11	17	US-10-450-797-279	Sequence 279, App
c 294	5	100.0	10	18	US-10-487-934-115	Sequence 115, App	c 367	5	100.0	11	17	US-10-450-797-295	Sequence 295, App
c 295	5	100.0	10	18	US-10-487-934-116	Sequence 116, App	c 368	5	100.0	11	17	US-10-450-797-441	Sequence 441, App
c 296	5	100.0	10	18	US-10-487-934-134	Sequence 134, App	c 369	5	100.0	11	17	US-10-450-797-444	Sequence 444, App
c 297	5	100.0	10	18	US-10-487-934-152	Sequence 152, App	c 370	5	100.0	11	17	US-10-450-797-551	Sequence 551, App
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c 300	5	100.0	10	18	US-10-487-934-204	Sequence 204, App	c 373	5	100.0	11	17	US-10-450-797-607	Sequence 607, App
c 301	5	100.0	10	18	US-10-602-494-372	Sequence 372, App	c 374	5	100.0	11	17	US-10-450-797-620	Sequence 620, App
c 302	5	100.0	10	18			c 375	5	100.0	11	17		
c 303	5	100.0	10	18			c 376	5	100.0	11	17		
c 304	5	100.0	10	18			c 377	5	100.0	11	17		



; PRIOR APPLICATION NUMBER: 09/157,206  
 ; PRIOR FILING DATE: 1998-09-18  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 14  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Sequence  
 US-09-907-074A-14

Query Match 100.0%; Score 5; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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 Db 3 GGGAG 7

## RESULT 2

US-09-907-074A-15/c  
 ; Sequence 15, Application US/09907074A  
 ; Publication No. US20010055773A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Jayasena, Sumedha  
 ; APPLICANT: Gold, Larty  
 ; TITLE OF INVENTION: Homogeneous Detection of a Target Through Nucleic Acid  
 ; TITLE OF INVENTION: Ligand-Ligand Beacon Interaction  
 ; FILE REFERENCE: NEX64/PCT-USC  
 ; CURRENT APPLICATION NUMBER: US/09/907,074A  
 ; CURRENT FILING DATE: 2001-07-17  
 ; PRIOR APPLICATION NUMBER: 09/581,326  
 ; PRIOR FILING DATE: 2000-08-11  
 ; PRIOR APPLICATION NUMBER: PCT/US98/26599  
 ; PRIOR FILING DATE: 1998-12-15  
 ; PRIOR APPLICATION NUMBER: 60/068,135  
 ; PRIOR FILING DATE: 1997-12-15  
 ; PRIOR APPLICATION NUMBER: 09/157,206  
 ; PRIOR FILING DATE: 1998-09-18  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 15  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 ; OTHER INFORMATION: Sequence  
 US-09-907-074A-15

Query Match 100.0%; Score 5; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
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 Db 8 GGGAG 4

## RESULT 3

US-09-154-750A-49  
 ; Sequence 49, Application US/09154750A  
 ; Publication No. US20020050597A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Vogelstein, Bert  
 ; APPLICANT: Kinzler, Kenneth  
 ; APPLICANT: Polyak, Kornelia  
 ; TITLE OF INVENTION: p53-Induced Apoptosis  
 ; FILE REFERENCE: 1107.75357  
 ; CURRENT APPLICATION NUMBER: US/09/154,750A

; CURRENT FILING DATE: 1998-09-17  
 ; PRIOR APPLICATION NUMBER: 60/059,153  
 ; PRIOR FILING DATE: 1997-09-17  
 ; PRIOR APPLICATION NUMBER: 60/079817  
 ; PRIOR FILING DATE: 1998-03-30  
 ; NUMBER OF SEQ ID NOS: 93  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 49  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-154-750A-49

Query Match 100.0%; Score 5; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 |||||  
 Db 3 GGGAG 7

## RESULT 4

US-09-989-789-569  
 ; Sequence 569, Application US/09989789  
 ; Patent No. US20020063379A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LIU, Qiang  
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
 ; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
 ; FILE REFERENCE: 8325-0011.20 / S11-US2  
 ; CURRENT APPLICATION NUMBER: US/09/989,789  
 ; CURRENT FILING DATE: 2002-03-25  
 ; NUMBER OF SEQ ID NOS: 4085  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 569  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: example target  
 ; OTHER INFORMATION: DNA  
 US-09-989-789-569

Query Match 100.0%; Score 5; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
 |||||  
 Db 3 GGGAG 7

## RESULT 5

US-09-989-789-570  
 ; Sequence 570, Application US/09989789  
 ; Patent No. US20020063379A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LIU, Qiang  
 ; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
 ; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
 ; FILE REFERENCE: 8325-0011.20 / S11-US2  
 ; CURRENT APPLICATION NUMBER: US/09/989,789  
 ; CURRENT FILING DATE: 2002-03-25  
 ; NUMBER OF SEQ ID NOS: 4085  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 570  
 ; LENGTH: 10  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: example target  
 ; OTHER INFORMATION: DNA

## US-09-989-789-570

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 3 GGGAG 7

## RESULT 6

US-09-989-789-601  
; Sequence 601, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 601  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-601

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 2 GGGAG 6

## RESULT 7

US-09-989-789-604  
; Sequence 604, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 604  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-604

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 3 GGGAG 7

## RESULT 8

US-09-989-789-605  
; Sequence 605, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 605  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-605

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 2 GGGAG 6

## RESULT 9

US-09-989-789-609  
; Sequence 609, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 609  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-609

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5  
|||||  
Db 2 GGGAG 6

## RESULT 10

US-09-989-789-610  
; Sequence 610, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25

```

; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 610
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-610

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 2 GGGAG 6

RESULT 11
US-09-989-789-645
; Sequence 645, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-645

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 2 GGGAG 6

RESULT 12
US-09-989-789-1271
; Sequence 1271, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1271
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1271
```

```

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 3 GGGAG 7

RESULT 13
US-09-989-789-1272
; Sequence 1272, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1272
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1272

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 3 GGGAG 7

RESULT 14
US-09-989-789-1283
; Sequence 1283, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1283
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1283

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 2 GGGAG 6

RESULT 15
US-09-989-789-1288
```

```
; Sequence 1288, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1288
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1288

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
Db      2 GGGAG 6

RESULT 16
US-09-989-789-1303
; Sequence 1303, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1303
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1303

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
Db      3 GGGAG 7

RESULT 17
US-09-989-789-1304
; Sequence 1304, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
```

```
; SEQ ID NO 1304
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1304

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
Db      3 GGGAG 7

RESULT 18
US-09-989-789-1317
; Sequence 1317, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1317
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1317

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAG 5
Db      3 GGGAG 7

RESULT 19
US-09-989-789-1345
; Sequence 1345, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1345
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1345

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
Db 3 GGGAG 7

## RESULT 20

US-09-989-789-1620  
; Sequence 1620, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1620  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1620

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
Db 3 GGGAG 7

## RESULT 21

US-09-989-789-1630  
; Sequence 1630, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1630  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1630

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
Db 3 GGGAG 7

## RESULT 22

US-09-989-789-1631  
; Sequence 1631, Application US/09989789  
; Patent No. US20020063379A1

; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1631  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1631

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
Db 3 GGGAG 7

## RESULT 23

US-09-989-789-1655  
; Sequence 1655, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1655  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-789-1655

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAG 5  
|  
|  
|  
|  
Db 3 GGGAG 7

## RESULT 24

US-09-989-789-1656  
; Sequence 1656, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1656  
; LENGTH: 10

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1656

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 3 GGGAG 7

RESULT 25
US-09-989-789-1657
; Sequence 1657, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1657
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1657

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 3 GGGAG 7

RESULT 26
US-09-989-789-1666
; Sequence 1666, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1666
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1666

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GGGAG 5
Db 5 GGGAG 9

RESULT 27
US-09-989-789-1668
; Sequence 1668, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1668

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 5 GGGAG 9

RESULT 28
US-09-989-789-1674
; Sequence 1674, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1674
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1674

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 5 GGGAG 9

RESULT 29
US-09-989-789-1685
; Sequence 1685, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
```



```
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1685
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1685

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
Db      3 GGGAG 7

RESULT 30
US-09-989-789-1696
; Sequence 1696, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1696
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1696

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
Db      3 GGGAG 7

RESULT 31
US-09-989-789-1697
; Sequence 1697, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1697
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1697

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
Db      3 GGGAG 7

RESULT 32
US-09-989-789-1698
; Sequence 1698, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1698
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1698

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
Db      2 GGGAG 6

RESULT 33
US-09-989-789-1699
; Sequence 1699, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1699
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1699

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGAG 5
Db      1 GGGAG 5
```

```
Db          3 GGGAG 7

RESULT 34
US-09-989-789-1700
; Sequence 1700, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1700
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1700

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGAG 5
           |||||
Db          3 GGGAG 7

RESULT 35
US-09-989-789-1701
; Sequence 1701, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1701
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1701

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGAG 5
           |||||
Db          3 GGGAG 7

RESULT 36
US-09-989-789-1702
; Sequence 1702, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
```

```
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1702
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1702

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGAG 5
           |||||
Db          2 GGGAG 6

RESULT 37
US-09-989-789-1703
; Sequence 1703, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1703
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1703

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGAG 5
           |||||
Db          3 GGGAG 7

RESULT 38
US-09-989-789-1704
; Sequence 1704, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1704
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
```



```
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-371-900-30
Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db 6 GGGAG 10
|||||
;
RESULT 42
US-09-970-820-20/c
; Sequence 20, Application US/09970820
; Patent No. US20020170077A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/970,820
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-970-820-20
Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db 6 GGGAG 10
|||||
;
RESULT 43
US-09-970-820-30
; Sequence 30, Application US/09970820
; Patent No. US20020170077A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/970,820
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-970-820-30
Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
Db 6 GGGAG 10
|||||
;
RESULT 44
US-09-986-718-20/c
; Sequence 20, Application US/09986718
; Patent No. US20020178458A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/970,820
; FILING DATE: 05-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-970-820-20
Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGAG 5
```

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; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,718
; FILING DATE: 09-NO. US20020178458A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,573
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-986-718-20

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 6 GGGAG 2

RESULT 45
US-09-986-718-30
; Sequence 30, Application US/09986718
; Patent No. US20020178458A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,718
; FILING DATE: 09-NO. US20020178458A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,573
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
```

```
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-986-718-30

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 6 GGGAG 10

RESULT 46
US-09-846-033B-142
; Sequence 142, Application US/09846033B
; Publication No. US20030044404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 142
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-142

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAG 5
Db 2 GGGAG 6

RESULT 47
US-09-846-033B-146
; Sequence 146, Application US/09846033B
; Publication No. US20030044404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
```

```
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo BioSciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-146
```

```
Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GGGAG 5
    |||||
```

```
Db 5 GGGAG 9
```

## RESULT 48

```
US-09-990-186-569
; Sequence 569, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 569
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-569
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Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGAG 5
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Db 3 GGGAG 7
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## RESULT 49

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US-09-990-186-570
; Sequence 570, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
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; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 570
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-570
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Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGAG 5
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Db 3 GGGAG 7
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## RESULT 50

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US-09-990-186-601
; Sequence 601, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 601
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-601
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Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGAG 5
    |||||
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Db 2 GGGAG 6
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Search completed: January 7, 2005, 11:31:24
Job time : 273.2 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GGGGG  
Perfect score: 5  
Sequence: 1 gggggg 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : GenEmbl.\*

- 1: gb\_ba.\*
- 2: gb\_hg.\*
- 3: gb\_in.\*
- 4: gb\_om.\*
- 5: gb\_ov.\*
- 6: gb\_pat.\*
- 7: gb\_ph.\*
- 8: gb\_pl.\*
- 9: gb\_pr.\*
- 10: gb\_ro.\*
- 11: gb\_sts.\*
- 12: gb\_sw.\*
- 13: gb\_un.\*
- 14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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c 2	5	100.0	10	6	A19427 oligonucleo
3	5	100.0	10	6	A72419 Sequence 6
c 4	5	100.0	10	6	A72420 Sequence 7
5	5	100.0	10	6	A76186 Sequence 14
6	5	100.0	10	6	A76256 Sequence 27
7	5	100.0	10	6	A76259 Sequence 30
c 8	5	100.0	10	6	A80129 Sequence 6
9	5	100.0	10	6	A80130 Sequence 7
c 10	5	100.0	10	6	A82122 Sequence 1
11	5	100.0	10	6	A82123 Sequence 2
c 12	5	100.0	10	6	AR016487 Sequence
13	5	100.0	10	6	AR030034 Sequence
c 14	5	100.0	10	6	AR030035 Sequence
15	5	100.0	10	6	AR030217 Sequence
16	5	100.0	10	6	AR030222 Sequence
17	5	100.0	10	6	AR030233 Sequence
18	5	100.0	10	6	AR030236 Sequence
19	5	100.0	10	6	AR030238 Sequence

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21	5	100.0	10	6	AR032143 Sequence
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23	5	100.0	10	6	AR043654 Sequence
c 24	5	100.0	10	6	AR049732 Sequence
25	5	100.0	10	6	AR058463 Sequence
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28	5	100.0	10	6	AR074337 Sequence
c 29	5	100.0	10	6	AR074448 Sequence
30	5	100.0	10	6	AR074449 Sequence
c 31	5	100.0	10	6	AR074661 Sequence
32	5	100.0	10	6	AR078332 Sequence
c 33	5	100.0	10	6	AR081128 Sequence
34	5	100.0	10	6	AR081129 Sequence
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c 37	5	100.0	10	6	AR088073 Sequence
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84	5	100.0	10	6	BD238838 Preparati
c 85	5	100.0	10	6	BD238903 Preparati
86	5	100.0	10	6	BD238978 Preparati
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88	5	100.0	10	6	BD239038 Preparati
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c 94	BD239303	10	6	BD239303	Preparati	c 167	5	100.0	10	6	AR336862	Sequence
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c 121	El17309	10	6	El17309	PCR primer	c 194	5	100.0	10	6	AX152116	Sequence
c 122	E39492	10	6	E39492	Genes with	c 195	5	100.0	10	6	AX152232	Sequence
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c 124	E39544	10	6	E39544	Genes with	c 197	5	100.0	10	6	AX152325	Sequence
c 125	E39586	10	6	E39586	Genes with	c 198	5	100.0	10	6	AX152337	Sequence
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c 130	E39706	10	6	E39706	Genes with	c 203	5	100.0	10	6	AX152614	Sequence
c 131	E39746	10	6	E39746	Genes with	c 204	5	100.0	10	6	AX152647	Sequence
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c 138	I21133	10	6	I21133	Sequence 18	c 211	5	100.0	10	6	AX152905	Sequence
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c 140	I22192	10	6	I22192	Sequence 6	c 213	5	100.0	10	6	AX152927	Sequence
c 141	I36118	10	6	I36118	Sequence 18	c 214	5	100.0	10	6	AX152991	Sequence
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c 146	I59753	10	6	I59753	Sequence 17	c 219	5	100.0	10	6	AX153157	Sequence
c 147	I59754	10	6	I59754	Sequence 18	c 220	5	100.0	10	6	AX153160	Sequence
c 148	I79745	10	6	I79745	Sequence 41	c 221	5	100.0	10	6	AX153270	Sequence
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c 241	5	100.0	10	6	AX302567	Sequence	AX302567	Sequence	c 314	5	100.0	10	6	BD166766	Human liv
c 242	5	100.0	10	6	AX302604	Sequence	AX302604	Sequence	c 315	5	100.0	10	6	BD166812	Human liv
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c 244	5	100.0	10	6	AX302619	Sequence	AX302619	Sequence	c 317	5	100.0	10	6	BD167007	Human liv
c 245	5	100.0	10	6	AX339649	Sequence	AX339649	Sequence	c 318	5	100.0	10	6	BD167030	Human liv
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c 248	5	100.0	10	6	AX339652	Sequence	AX339652	Sequence	c 321	5	100.0	11	6	A76177	Sequence 5
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c 277	5	100.0	10	6	AX814773	Sequence	AX814773	Sequence	c 350	5	100.0	11	6	BD244871	Oligonucl
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c 279	5	100.0	10	6	AX816209	Sequence	AX816209	Sequence	c 352	5	100.0	11	6	BD272413	A method
c 280	5	100.0	10	6	AX825541	Sequence	AX825541	Sequence	c 353	5	100.0	11	6	C0766430	Sequence
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DEFINITION Oligonucleotide.
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VERSION A19426.1 GI:578952
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ACCESSION A19427  
VERSION A19427.1 GI:578953  
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SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 10)  
AUTHORS van Gorcom,R.F.M., van Hartingsveldt,W., van Paridon,P.A.,  
Veenstra,A.E., Luitzen,R.G.M. and Selden,G.C.M.  
TITLE Cloning and expression of microbial phytase  
JOURNAL Patent: EP 0420358-A 16 03-APR-1991;  
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ACCESSION A72419  
VERSION A72419.1 GI:6063742  
KEYWORDS  
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ORGANISM unidentified  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Leader,D.J. and Waugh,R.  
TITLE PLANT U14 NUCLEIC ACID SEQUENCES AND DERIVATIVES THEREOF  
JOURNAL Patent: WO 9530747-A 6 16-NOV-1995;  
GENE SHEARS PTY LTD (AU); LEADER DAVID JOHN (GB)

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KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Leader,D.J. and Waugh,R.  
TITLE PLANT U14 NUCLEIC ACID SEQUENCES AND DERIVATIVES THEREOF  
JOURNAL Patent: WO 9530747-A 7 16-NOV-1995;  
GENE SHEARS PTY LTD (AU); LEADER DAVID JOHN (GB)

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VERSION A76186.1 GI:6088296  
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ORGANISM unidentified  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Taylor,P.N.  
TITLE IMPROVEMENTS IN OR RELATING TO DNA CLONING TECHNIQUES AND PRODUCTS  
FOR USE THEREWITH  
JOURNAL Patent: WO 9319186-A 14 30-SEP-1993;  
UNIV HULL (GB)

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ORGANISM synthetic construct  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Sandal,N. and Marcker,K.  
TITLE BIOLOGICAL MATERIAL

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KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Sandal,N. and Marcker,K.
TITLE BIOLOGICAL MATERIAL
JOURNAL Patent: WO 9319181-A 30 30-SEP-1993;
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DEFINITION Sequence 6 from Patent WO9530748.
ACCESSION A80129
VERSION A80129.1 GI:6092861
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REFERENCE 1 (bases 1 to 10)
AUTHORS Leader,D.J. and Waugh,R.
TITLE PLANT U14 NUCLEIC ACID SEQUENCES AND DERIVATIVES THEREOF
JOURNAL Patent: WO 9530748-A 6 16-NOV-1995;
GENE SHEARS PTY LTD (AU); LEADER DAVID JOHN (GB)
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REFERENCE 1 (bases 1 to 10)
AUTHORS Leader,D.J. and Waugh,R.
TITLE PLANT U14 NUCLEIC ACID SEQUENCES AND DERIVATIVES THEREOF
JOURNAL Patent: WO 9530748-A 7 16-NOV-1995;
GENE SHEARS PTY LTD (AU); LEADER DAVID JOHN (GB)
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ACCESSION A82122
VERSION A82122.1 GI:6731987
KEYWORDS
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ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Leader,D.J. and Brown,J.W.
TITLE Process for producing stabilised RNA molecules within cells, RNA molecules thus produced and nucleic acid precursors of such molecules
JOURNAL Patent: EP 0887405-A 1 30-DEC-1998;
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REFERENCE 1 (bases 1 to 10)  
AUTHORS Leader,D.J. and Brown,J.W.  
TITLE Process for producing stabilised RNA molecules within cells, RNA molecules thus produced and nucleic acid precursors of such molecules  
JOURNAL Patent: EP 0887405-A 2 30-DEC-1998;  
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VERSION AR016487.1 GI:3972764  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Glazer,P.M., Lin,L.Michael. and George,J.  
TITLE Methods and compositions for effecting homologous recombination  
JOURNAL Patent: US 5776744-A 2 07-JUL-1998;  
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VERSION AR030034.1 GI:5943248  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation

JOURNAL Patent: US 5861244-A 223 19-JAN-1999;  
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KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Wang,C.-G. and Hepburn,A.G.  
TITLE Genetic sequence assay using DNA triple strand formation  
JOURNAL Patent: US 5861244-A 224 19-JAN-1999;  
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SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Weissman,S.M., Nallur,G.N. and Kulkarni,P.  
TITLE Multiple selection process for binding sites of DNA-binding proteins  
JOURNAL Patent: US 5861246-A 28 19-JAN-1999;  
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REFERENCE 1 (bases 1 to 10)
AUTHORS Weisman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding
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JOURNAL Patent: US 5861246-A 33 19-JAN-1999;
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Weisman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding
proteins
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REFERENCE 1 (bases 1 to 10)
AUTHORS Weisman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding
proteins
JOURNAL Patent: US 5861246-A 47 19-JAN-1999;
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGG 5
Db 4 GGGGG 8
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RESULT 19
AR030238
LOCUS AR030238 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 49 from patent US 5861246.
ACCESSION AR030238
VERSION AR030238.1 GI:5943452
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Weisman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding
proteins
JOURNAL Patent: US 5861246-A 49 19-JAN-1999;
FEATURES
source Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGG 5
Db 3 GGGGG 7
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RESULT 20
AR032142/c
LOCUS AR032142 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 3 from patent US 5866700.
ACCESSION AR032142
VERSION AR032142.1 GI:5946431
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Pfeiderer,W., Schnell,R. and Matysiak,S.
TITLE Solid-phase synthesis of oligoribonucleotides
JOURNAL Patent: US 5866700-A 3 02-FEB-1999;
FEATURES
source Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGG 5
Db 3 GGGGG 7
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SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 10) Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y., Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and Inbach,J.Louis.
TITLE	Oligonucleotides having a conserved G4 core sequence
JOURNAL	Patent: US 5952490-A 145 14-SEP-1999;
FEATURES	Location/Qualifiers source 1..10 /organism="unknown" /mol_type="unassigned DNA"
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Best Local Similarity	100.0%; Pred.No. 3.1e+07;
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Qy	1 GGGGG 5 
Db	1 GGGGG 5
RESULT 29	
LOCUS	AR074448 10 bp DNA linear PAT 28-AUG-2000
DEFINITION	Sequence 19 from patent US 5955075.
ACCESSION	AR074448
VERSION	AR074448.1 GI:10001203
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 10) Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE	Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL	Patent: US 5955075-A 19 21-SEP-1999;
FEATURES	Location/Qualifiers source 1..10 /organism="unknown" /mol_type="unassigned DNA"
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Best Local Similarity	100.0%; Pred.No. 3.1e+07;
Matches	5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GGGGG 5 
Db	6 GGGGG 2
RESULT 30	
LOCUS	AR074449 10 bp DNA linear PAT 28-AUG-2000
DEFINITION	Sequence 20 from patent US 5955075.
ACCESSION	AR074449
VERSION	AR074449.1 GI:10001204
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 10) Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE	Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL	Patent: US 5955075-A 20 21-SEP-1999;
FEATURES	Location/Qualifiers source 1..10 /organism="unknown" /mol_type="unassigned DNA"
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
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Db 8 GGGGG 4

RESULT 31
AR074661/c
LOCUS      AR074661
DEFINITION Sequence 45 from patent US 5955274.
ACCESSION  AR074661
VERSION     AR074661.1 GI:10001414
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Ligon,J.M. and Beck,J.J.
TITLE     Detection of fungal pathogens using the polymerase chain reaction
JOURNAL   Patent: US 5955274-A 45 21-SEP-1999;
FEATURES   Location/Qualifiers
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
    |||||
Db 6 GGGGG 2

RESULT 32
AR078332
LOCUS      AR078332
DEFINITION Sequence 1 from patent US 5962426.
ACCESSION  AR078332
VERSION     AR078332.1 GI:10005078
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Glazer,P.M.
TITLE     Triple-helix forming oligonucleotides for targeted mutagenesis
JOURNAL   Patent: US 5962426-A 1 05-OCT-1999;
FEATURES   Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
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Db 6 GGGGG 10

RESULT 33
AR081128/c
LOCUS      AR081128
DEFINITION Sequence 19 from patent US 5972353.
ACCESSION  AR081128
VERSION     AR081128.1 GI:10007856
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KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL   Patent: US 5972353-A 19 26-OCT-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
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QY 1 GGGGG 5
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Db 6 GGGGG 2

RESULT 34
AR081129/c
LOCUS      AR081129
DEFINITION Sequence 20 from patent US 5972353.
ACCESSION  AR081129
VERSION     AR081129.1 GI:10007857
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL   Patent: US 5972353-A 20 26-OCT-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
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Db 8 GGGGG 4

RESULT 35
AR085325/c
LOCUS      AR085325
DEFINITION Sequence 19 from patent US 5981711.
ACCESSION  AR085325
VERSION     AR085325.1 GI:10012094
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE     MN-specific antibodies and hybridomas
JOURNAL   Patent: US 5981711-A 19 09-NOV-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 6 GGGGG 2

RESULT 36
AR085326/c
LOCUS AR085326 10 bp DNA PAT 01-SEP-2000
DEFINITION Sequence 20 from patent US 5981711.
ACCESSION AR085326
VERSION AR085326.1 GI:10012095
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 20 09-NOV-1999;
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Qy 1 GGGGG 5
Db 8 GGGGG 4

RESULT 37
AR088073/c
LOCUS AR088073 10 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 19 from patent US 5989838.
ACCESSION AR088073
VERSION AR088073.1 GI:10014836
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 19 23-NOV-1999;
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Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 6 GGGGG 2

RESULT 38
AR088074/c
LOCUS AR088074 10 bp DNA PAT 07-SEP-2000
DEFINITION Sequence 20 from patent US 5989838.
ACCESSION AR088074
VERSION AR088074.1 GI:10014837
KEYWORDS
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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 20 23-NOV-1999;
FEATURES
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Location/Qualifiers
1..10
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/mol_type="unassigned DNA"

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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 8 GGGGG 4

RESULT 39
AR092699/c
LOCUS AR092699 10 bp DNA PAT 08-SEP-2000
DEFINITION Sequence 11 from patent US 5998193.
ACCESSION AR092699
VERSION AR092699.1 GI:10019451
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL Patent: US 5998193-A 11 07-DEC-1999;
FEATURES
source
Location/Qualifiers
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 7 GGGGG 3

RESULT 40
AR092700
LOCUS AR092700 10 bp DNA PAT 08-SEP-2000
DEFINITION Sequence 12 from patent US 5998193.
ACCESSION AR092700
VERSION AR092700.1 GI:10019452
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL Patent: US 5998193-A 12 07-DEC-1999;
FEATURES
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
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Db       4 GGGGG 8

RESULT 41
LOCUS      AR092702
DEFINITION Sequence 14 from patent US 5998193.
ACCESSION  AR092702
VERSION     AR092702.1 GI:10019454
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Keese,P., Stapper,M. and Perriman,R.
TITLE     Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
          embedded ribozymes and compositions thereof
JOURNAL    Patent: US 5998193-A 14 07-DEC-1999;
FEATURES   Location/Qualifiers
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QY      1 GGGGG 5
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Db       3 GGGGG 7

RESULT 42
LOCUS      AR092706
DEFINITION Sequence 18 from patent US 5998193.
ACCESSION  AR092706
VERSION     AR092706.1 GI:10019458
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Keese,P., Stapper,M. and Perriman,R.
TITLE     Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
          embedded ribozymes and compositions thereof
JOURNAL    Patent: US 5998193-A 18 07-DEC-1999;
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
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Db       4 GGGGG 8

RESULT 43
LOCUS      AR092708
DEFINITION Sequence 20 from patent US 5998193.
          linear          DNA          10 bp          PAT 08-SEP-2000
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ACCESSION  AR092708
VERSION     AR092708.1 GI:10019460
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Keese,P., Stapper,M. and Perriman,R.
TITLE     Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
          embedded ribozymes and compositions thereof
JOURNAL    Patent: US 5998193-A 20 07-DEC-1999;
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QY      1 GGGGG 5
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Db       4 GGGGG 8

RESULT 44
LOCUS      AR092709
DEFINITION Sequence 21 from patent US 5998193.
ACCESSION  AR092709
VERSION     AR092709.1 GI:10019461
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Keese,P., Stapper,M. and Perriman,R.
TITLE     Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
          embedded ribozymes and compositions thereof
JOURNAL    Patent: US 5998193-A 21 07-DEC-1999;
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QY      1 GGGGG 5
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Db       3 GGGGG 7

RESULT 45
LOCUS      AR092710
DEFINITION Sequence 22 from patent US 5998193.
ACCESSION  AR092710
VERSION     AR092710.1 GI:10019462
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Keese,P., Stapper,M. and Perriman,R.
TITLE     Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
          embedded ribozymes and compositions thereof
JOURNAL    Patent: US 5998193-A 22 07-DEC-1999;
FEATURES   Location/Qualifiers
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Qy 1 GGGGG 5
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Db 6 GGGGG 10

RESULT 46
LOCUS      AR092711      10 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 23 from patent US 5998193.
ACCESSION  AR092711
VERSION     AR092711.1 GI:10019463
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Keese,P., Stapper,M. and Perriman,R.
TITLE     Ribozymes with optimized hybridizing arms, stems, and loops, trna
          embedded ribozymes and compositions thereof
JOURNAL    Patent: US 5998193-A 23 07-DEC-1999;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
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Db 4 GGGGG 8

RESULT 47
LOCUS      AR092712/c    10 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 24 from patent US 5998193.
ACCESSION  AR092712
VERSION     AR092712.1 GI:10019464
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Keese,P., Stapper,M. and Perriman,R.
TITLE     Ribozymes with optimized hybridizing arms, stems, and loops, trna
          embedded ribozymes and compositions thereof
JOURNAL    Patent: US 5998193-A 24 07-DEC-1999;
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 7 GGGGG 3

/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 7 GGGGG 3

RESULT 48
LOCUS      AR094553      10 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 1 from patent US 6001657.
ACCESSION  AR094553
VERSION     AR094553.1 GI:10021585
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Hardin,C.C., Brown,B.A. II, Roberts,J.F. and Pelaez,S.C.
TITLE     Antibodies that selectively bind quadruplex nucleic acids
JOURNAL    Patent: US 6001657-A 1 14-DEC-1999;
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
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Db 4 GGGGG 8

RESULT 49
LOCUS      AR096853      10 bp      DNA      linear      PAT 08-SEP-2000
DEFINITION Sequence 4 from patent US 6008400.
ACCESSION  AR096853
VERSION     AR096853.1 GI:10026024
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Scaringe,S. and Caruthers,M.H.
TITLE     Orthoester reagents for use as protecting groups in oligonucleotide
          synthesis
JOURNAL    Patent: US 6008400-A 4 28-DEC-1999;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 9 GGGGG 5

RESULT 50
LOCUS      AR098905      10 bp      DNA      linear      PAT 14-FEB-2001
DEFINITION Sequence 41 from patent US 6077685.
ACCESSION  AR098905
VERSION     AR098905.1 GI:12808671
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS   Trofatter,J.A., MacCollin,M.M. and Gusella,J.P.
TITLE     Tumor suppressor merlin and antibodies thereof
JOURNAL    Patent: US 6077685-A 41 20-JUN-2000;
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FEATURES      Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred.No.3.1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
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Db       5 GGGGG 9

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Job time : 520 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:35:05 ; Search time 254.4 Seconds  
(without alignments)  
103.173 Million cell updates/sec

Title: GGGGG

Perfect score: 5

Sequence: 1 99999 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3979404

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

N\_Geneseq\_23Sep04:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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3	5	100.0	10 2	AaQ79368
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5	5	100.0	10 2	AaQ79359
6	5	100.0	10 2	AaQ79358
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8	5	100.0	10 2	AaQ64610
9	5	100.0	10 2	AaQ08734
10	5	100.0	10 2	AaX32616
11	5	100.0	10 2	AaX08758
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13	5	100.0	10 2	AaQ96685
14	5	100.0	10 2	AaQ96686
15	5	100.0	10 2	AaQ96683
16	5	100.0	10 2	AaQ96687
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19	5	100.0	10 2	AaQ93130
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AaQ88493	Human mit
AaT14138	Cytokine
AaT05376	Setorix n
AaT04915	Mammalian
AaQ81070	supf gene
AaT27213	HIV-1 det
AaT35000	HIV inhib
AaT35713	Primer DB
AaT10084	Hammerhea
AaT98862	Core-bind
AaT98847	Binding s
AaT98859	Core-bind
AaT98864	Core-bind
AaT98851	Binding s
AaT70006	Triplex-f
AaT70007	Oligonucl
AaT80370	Oligo HCV
AaT47062	Oligonucl
AaV62570	Septoria
AaV45390	Mouse CD3
AaV67001	CD3-epsil
AaZ86960	PCR prime
AaV32461	Oligonucl
AaV56865	Regulator
AaV50112	Yeast tag
AaV50068	Yeast tag
AaV35941	Primer us
AaX04582	Inverted
AaX04583	Inverted
AaX54730	Tumour ne
AaX54777	Inducible
AaX14836	Triple he
AaX14837	Triple he
AaX99946	Human par
AaX22183	Random am
AaX38077	Human FKH
AaA07996	DNA seque
AaA07995	DNA seque
AaA34177	Human ade
AaA34224	Human ade
AaZ78372	Human den
AaZ77991	Human den
AaZ78289	Human den
AaZ78293	Human den
AaZ78417	Human den
AaZ78615	Human den
AaZ79320	Human den
AaZ79555	Human den
AaZ79676	Human den
AaZ78097	Human den
AaZ79592	Human den
AaZ77585	Human den
AaZ77792	Human den
AaZ77968	Human den
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AaZ77601	Human den
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AaZ78631	Human den
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AaZ79230	Human den
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AaZ77789	Human den
AaZ78185	Human den
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C 240	5	100.0		

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Aaz83070	Metastati
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Aaz84975	Metastati
Aaz30900	Control s
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Aaa93854	Oligonucle
Aaa93857	Oligonucle
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Aac73962	Human den
Aac73990	Human den
Aac74131	Human den
Aac73938	Human den
Aac74032	Human den
Aac74152	Human den
Aac74138	Human den
Aac74102	Human den
Aac74196	Human den
Aac74047	Human den
Aaa13751	Stem cell
Aaa56447	Human mac
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C 242	5	100.0	10	3	AA556269	Human mac
C 243	5	100.0	10	3	AA556482	Human mac
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C 255	5	100.0	10	3	AA506058	CfTR gene
C 256	5	100.0	10	3	AA579800	Human cys
C 257	5	100.0	10	3	AA579727	Human col
C 258	5	100.0	10	3	AA579780	Human bre
C 259	5	100.0	10	3	AA579801	Human cys
C 260	5	100.0	10	3	AA516550	Initiator
C 261	5	100.0	10	3	AA520299	Human tum
C 262	5	100.0	10	3	AA520346	Human ind
C 263	5	100.0	10	3	AA560401	Example t
C 264	5	100.0	10	3	AA552469	Human MN
C 265	5	100.0	10	3	AA561030	Protein b
C 266	5	100.0	10	3	AA561012	Protein b
C 267	5	100.0	10	3	AA561028	Protein b
C 268	5	100.0	10	3	AA561025	Protein b
C 269	5	100.0	10	3	AA561016	Protein b
C 270	5	100.0	10	3	AA570754	PCR prime
C 271	5	100.0	10	3	AA564304	Stem nucl
C 272	5	100.0	10	4	AA592220	Human IGE
C 273	5	100.0	10	4	AA5167381	Human PKB
C 274	5	100.0	10	4	AA520558	Consensus
C 275	5	100.0	10	4	AA525058	Consensus
C 276	5	100.0	10	4	AA525055	5' termin
C 277	5	100.0	10	4	AA519564	Translati
C 278	5	100.0	10	4	AA565225	DNA bindi
C 279	5	100.0	10	4	AA590455	Egr -1 bin
C 280	5	100.0	10	4	AA504428	Human DAX
C 281	5	100.0	10	4	AA504427	Human DAX
C 282	5	100.0	10	4	AA504439	Human DAX
C 283	5	100.0	10	4	AA563741	Human ubi
C 284	5	100.0	10	4	AA563985	Human ubi
C 285	5	100.0	10	4	AA564002	Human ubi
C 286	5	100.0	10	4	AA563400	Human can
C 287	5	100.0	10	4	AA563782	Human ubi
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C 301	5	100.0	10	4	AA563518	Human ubi
C 302	5	100.0	10	4	AA563860	Human ubi
C 303	5	100.0	10	4	AA563859	Human ubi
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C 306	5	100.0	10	4	AA563665	Human ubi
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C 308	5	100.0	10	4	AA564345	Human ubi
C 309	5	100.0	10	4	AA563191	Human col
C 310	5	100.0	10	4	AA564189	Human ubi
C 311	5	100.0	10	4	AA564232	Human ubi
C 312	5	100.0	10	4	AA564510	Human ubi
C 313	5	100.0	10	4	AA563171	Human col

C 314	5	100.0	10	4	AAH63722	Human ubi
C 315	5	100.0	10	4	AAH64668	Human coli
C 316	5	100.0	10	4	AAH63307	Human coli
C 317	5	100.0	10	4	AAH63528	Human ubi
C 318	5	100.0	10	4	AAH64180	Human ubi
C 319	5	100.0	10	4	AAH57286	Human CHR1
C 320	5	100.0	10	4	AAH57291	Human CHR1
C 321	5	100.0	10	4	AAH57291	C. cibari
C 322	5	100.0	10	4	AAH20553	Human MTR1
C 323	5	100.0	10	4	AAH20553	Human MTR1
C 324	5	100.0	10	4	AAH06402	Translati
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C 326	5	100.0	10	4	AAH04110	Human SCF
C 327	5	100.0	10	4	AAH10957	E. coli a
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C 329	5	100.0	10	4	AAH91834	C. cibari
C 330	5	100.0	10	4	AAH32831	LPS activ
C 331	5	100.0	10	4	AAH32884	LPS activ
C 332	5	100.0	10	4	AAH32822	LPS activ
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C 334	5	100.0	10	4	AAH32911	LPS activ
C 335	5	100.0	10	4	AAH32850	LPS activ
C 336	5	100.0	10	4	AAH32908	LPS activ
C 337	5	100.0	10	4	AAH32790	LPS activ
C 338	5	100.0	10	4	AAH32710	LPS activ
C 339	5	100.0	10	4	AAH32764	LPS activ
C 340	5	100.0	10	4	AAH32644	LPS activ
C 341	5	100.0	10	4	AAH32853	LPS activ
C 342	5	100.0	10	4	ABA81670	Human pho
C 343	5	100.0	10	4	ABA81659	Human pho
C 344	5	100.0	10	5	AAH23888	Human SCF
C 345	5	100.0	10	5	AAH41714	Anti-PEP
C 346	5	100.0	10	5	AAH41708	Anti-PEP
C 347	5	100.0	10	5	AAH41704	Anti-PEP
C 348	5	100.0	10	5	AAH41694	Anti-PEP
C 349	5	100.0	10	5	AAH06186	Human nor
C 350	5	100.0	10	5	AAH04211	Human SCF
C 351	5	100.0	10	5	AAH70437	Human DRD
C 352	5	100.0	10	5	AAH69621	Human IL4
C 353	5	100.0	10	5	AAH69646	Human IL4
C 354	5	100.0	10	5	AAH74015	Human SLIC
C 355	5	100.0	10	5	AAH02803	Human pre
C 356	5	100.0	10	5	AAH02802	Human pre
C 357	5	100.0	10	5	AAH10446	Human ste
C 358	5	100.0	10	5	ABA83125	Lutheran
C 359	5	100.0	10	5	ABA83162	Lutheran
C 360	5	100.0	10	5	ABA83177	Galactin-
C 361	5	100.0	10	5	ABA83167	Mesotheli
C 362	5	100.0	10	5	AAH40195	Yeast NOR
C 363	5	100.0	10	5	AAH35160	Yeast NOR
C 364	5	100.0	10	5	AAH37508	Yeast NOR
C 365	5	100.0	10	5	AAH42809	Yeast NOR
C 366	5	100.0	10	5	AAH33285	Yeast hig
C 367	5	100.0	10	5	AAH33329	Yeast NOR
C 368	5	100.0	10	5	AAH39136	Yeast NOR
C 369	5	100.0	10	5	AAH40930	Yeast NOR
C 370	5	100.0	10	5	AAH42413	Yeast NOR
C 371	5	100.0	10	5	AAH42422	Yeast NOR
C 372	5	100.0	10	5	AAH33811	Yeast NOR
C 373	5	100.0	10	5	AAH35900	Yeast NOR
C 374	5	100.0	10	5	AAH39189	Yeast NOR
C 375	5	100.0	10	5	AAH40640	Yeast NOR
C 376	5	100.0	10	5	AAH40931	Yeast NOR
C 377	5	100.0	10	5	AAH42421	Yeast NOR
C 378	5	100.0	10	5	AAH34090	Yeast NOR
C 379	5	100.0	10	5	AAH35288	Yeast NOR
C 380	5	100.0	10	5	AAH41909	Yeast NOR
C 381	5	100.0	10	5	AAH42398	Yeast NOR
C 382	5	100.0	10	5	AAH42810	Yeast NOR
C 383	5	100.0	10	5	AAH44018	Yeast NOR
C 384	5	100.0	10	5	AAH39759	Yeast NOR
C 385	5	100.0	10	6	AAH16881	Translati
C 386	5	100.0	10	6	ABK52524	RNA3', ter

C 387	5	100.0	10	6	AAS988394	Aas988394 Galanin r	460	5	100.0	10	6	ABQ71676 Zinc fing
C 388	5	100.0	10	6	AAS988395	Aas988395 Galanin r	C 461	5	100.0	10	6	ABQ88701 Human CFL
C 389	5	100.0	10	6	AAD25297	Aad25297 Human HSD	462	5	100.0	10	6	ABT05365 Human NAG
C 390	5	100.0	10	6	AAL45335	Aal45335 Human KCN	463	5	100.0	10	6	ABT05351 Human NAG
C 391	5	100.0	10	6	AAS18304	Aas18304 Primer-ex	464	5	100.0	10	6	AAD25202 Human hom
C 392	5	100.0	10	6	AAS18284	Aas18284 Primer-ex	C 465	5	100.0	10	6	ABA99340 Human ALD
C 393	5	100.0	10	6	AAS99276	Aas99276 Human F12	466	5	100.0	10	6	ABK46452 Immunost
C 394	5	100.0	10	6	AAD26088	Aad26088 Human apo	C 467	5	100.0	10	6	AAD35463 Rat SCF 5
C 395	5	100.0	10	6	AAD26079	Aad26079 Human apo	468	5	100.0	10	6	ABN80617 Human P45
C 396	5	100.0	10	6	ABL88350	Ab188350 Human CHR	C 469	5	100.0	10	6	ABN80617 Human P45
C 397	5	100.0	10	6	ABL88325	Ab188325 Human CHR	C 470	5	100.0	10	6	ABN80641 Human P45
C 398	5	100.0	10	6	AAD32208	Aad32208 Human NFK	C 471	5	100.0	10	6	ABN87956 Human GSR
C 399	5	100.0	10	6	ABL52191	Ab152191 Human PER	C 472	5	100.0	10	6	ABV78397 Human Th1
C 400	5	100.0	10	6	ABK85686	Abk85686 Human SCY	473	5	100.0	10	6	ABV78565 Human FUS
C 401	5	100.0	10	6	ABK95839	Abk95839 Solute Ca	C 474	5	100.0	10	6	ABV78362 Human TNF
C 402	5	100.0	10	6	ABK95841	Abk95841 Solute Ca	C 475	5	100.0	10	6	ABV78447 Human GIT
C 403	5	100.0	10	6	AAS98818	Aas98818 Colony st	476	5	100.0	10	6	ABV78405 Human Th1
C 404	5	100.0	10	6	AAS98843	Aas98843 Colony st	C 477	5	100.0	10	6	ABV78480 Human Th1
C 405	5	100.0	10	6	AAS98893	Aas98893 Colony st	C 478	5	100.0	10	6	ABV78310 Human TNF
C 406	5	100.0	10	6	ABL011316	Ab1011316 Human MMP	479	5	100.0	10	6	ABV84781 Human Chr
C 407	5	100.0	10	6	AAD25882	Aad25882 Primer #4	C 480	5	100.0	10	6	ABV84352 Human Na+
C 408	5	100.0	10	6	ABL42314	Ab142314 Human mat	C 481	5	100.0	10	6	ABV84501 Human IGF
C 409	5	100.0	10	6	ABL42664	Ab142664 Human mat	C 482	5	100.0	10	6	ABV84639 Human Na+
C 410	5	100.0	10	6	ABL42918	Ab142918 Human mat	C 483	5	100.0	10	6	ABV84547 Human gal
C 411	5	100.0	10	6	ABL42800	Ab142800 Human mat	484	5	100.0	10	6	ABV84249 Human mul
C 412	5	100.0	10	6	ABL42849	Ab142849 Human mat	C 485	5	100.0	10	6	ABV84742 Human imm
C 413	5	100.0	10	6	ABL42858	Ab142858 Human mat	C 486	5	100.0	10	6	ABV84765 Human imm
C 414	5	100.0	10	6	ABL42315	Ab142315 Human mat	C 487	5	100.0	10	6	ABV73847 SCF unive
C 415	5	100.0	10	6	ABL42640	Ab142640 Human mat	488	5	100.0	10	6	AAS95618 Apolipop
C 416	5	100.0	10	6	ABL57663	Ab157663 Human SCY	489	5	100.0	10	6	AAS95620 Apolipop
C 417	5	100.0	10	6	ABL57675	Ab157675 Human SCY	490	5	100.0	10	6	ABK09440 Human NPR
C 418	5	100.0	10	6	ABL57672	Ab157672 Human SCY	C 491	5	100.0	10	6	ABK09444 Human NPR
C 419	5	100.0	10	6	ABL60194	Ab160194 Human MUC	492	5	100.0	10	6	ABK23714 Transcrip
C 420	5	100.0	10	6	ABA94621	Ab94621 Nucleotid	C 493	5	100.0	10	6	ABK23472 Transcrip
C 421	5	100.0	10	6	ABA94626	Ab94626 Nucleotid	494	5	100.0	10	6	ABK23541 Transcrip
C 422	5	100.0	10	6	ABA94625	Ab94625 Nucleotid	C 495	5	100.0	10	6	ABK23664 Transcrip
C 423	5	100.0	10	6	ABA94619	Ab94619 Nucleotid	C 496	5	100.0	10	6	ABK23684 Transcrip
C 424	5	100.0	10	6	ABA94622	Ab94622 Nucleotid	497	5	100.0	10	6	ABK23510 Transcrip
C 425	5	100.0	10	6	ABA94620	Ab94620 Nucleotid	C 498	5	100.0	10	6	ABK23559 Transcrip
C 426	5	100.0	10	6	ABK37021	Abk37021 Human ALA	C 499	5	100.0	10	6	ABK23811 Transcrip
C 427	5	100.0	10	6	ABK12726	Abk12726 Oligonucl	500	5	100.0	10	12	AD113733 Cytocoplasm
C 428	5	100.0	10	6	ABK12724	Abk12724 Oligonucl						
C 429	5	100.0	10	6	ABN81497	Abn81497 Human HTA						
C 430	5	100.0	10	6	ABK81402	Abk81402 SCYA21 ge						
C 431	5	100.0	10	6	ABK96071	Abk96071 Human LIP						
C 432	5	100.0	10	6	ABK96055	Abk96055 Human LIP						
C 433	5	100.0	10	6	ABK96056	Abk96056 Human LIP						
C 434	5	100.0	10	6	ABK10419	Abk10419 Synthetic						
C 435	5	100.0	10	6	ABK96073	Abk96073 Human LIP						
C 436	5	100.0	10	6	AAS96201	Aas96201 Human Ace						
C 437	5	100.0	10	6	ABA97042	Ab97042 ZFP36 ext						
C 438	5	100.0	10	6	ABA97044	Ab97044 ZFP36 ext						
C 439	5	100.0	10	6	ABA97030	Ab97030 ZFP36 ext						
C 440	5	100.0	10	6	ABA97036	Ab97036 ZFP36 ext						
C 441	5	100.0	10	6	AAD26165	Aad26165 Human end						
C 442	5	100.0	10	6	AAL48057	Aal48057 Human CSF						
C 443	5	100.0	10	6	AAS16393	Aas16393 Primer-ex						
C 444	5	100.0	10	6	AAS95402	Aas95402 Human ICA						
C 445	5	100.0	10	6	AAD26425	Aad26425 Human GRM						
C 446	5	100.0	10	6	AAD26862	Aad26862 Human GPR						
C 447	5	100.0	10	6	ABL39511	Ab139511 Human ETF						
C 448	5	100.0	10	6	ABL52259	Ab152259 Human PHK						
C 449	5	100.0	10	6	ABQ71845	Abq71845 Zinc fing						
C 450	5	100.0	10	6	ABQ71583	Abq71583 Zinc fing						
C 451	5	100.0	10	6	ABQ71668	Abq71668 Zinc fing						
C 452	5	100.0	10	6	ABQ71515	Abq71515 Zinc fing						
C 453	5	100.0	10	6	ABQ71485	Abq71485 Zinc fing						
C 454	5	100.0	10	6	ABQ71537	Abq71537 Zinc fing						
C 455	5	100.0	10	6	ABQ71296	Abq71296 Zinc fing						
C 456	5	100.0	10	6	ABQ71538	Abq71538 Zinc fing						
C 457	5	100.0	10	6	ABQ71516	Abq71516 Zinc fing						
C 458	5	100.0	10	6	ABQ71611	Abq71611 Zinc fing						
C 459	5	100.0	10	6	ABQ71295	Abq71295 Zinc fing						

## ALIGNMENTS

## RESULT 1

AAQ49543	ID	AAQ49543	standard; DNA; 10 BP.
XX	AC	AAQ49543;	
XX	DT	25-MAR-2003 (revised)	
DT	DT	20-APR-1994 (first entry)	
XX	XX	Primer to amplify BCNR locus marker B9.2.	
DE	XX	Phytopathogenic nematode; beet cyst nematode resistance; BCNR locus;	
XX	KW	sugar beet; ss.	
XX	OS	Synthetic.	
XX	PN	WO9319181-A1.	
XX	PD	30-SEP-1993.	
XX	PF	23-MAR-1993; 93WO-EP000702.	
XX	PR	25-MAR-1992; 92DK-0000396.	
XX	PA	(SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.	
PA	PA	(SANO ) SANDOZ PATENT GMBH.	
PA	PA	(SANO ) SANDOZ LTD.	

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XX Sandal N, Marcker K, Stiekema W, Lange W, Klein-Lankhorst R;
PI Steen P;
XX WPI; 1993-320747/40.
XX Recombinant DNA comprising Beet Cyst Nematode Resistance Locus - confers
PT nematode resistance to beet species.
XX Claim 2; Page 61; 82pp; English.
XX This primer is used to amplify a BCNR locus marker of ca. 700bp from wild
CC beet species belonging to section Procumbentes. (Updated on 25-MAR-2003
CC to correct PN field.)
XX
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      2 GGGGG 6

RESULT 2
AAQ49546
ID AAQ49546 standard; DNA; 10 BP.
XX
AC AAQ49546;
XX
DT 25-MAR-2003 (revised)
DT 20-APR-1994 (first entry)
XX
DE Primer to amplify BCNR locus marker B9.1.
XX
XX Phytopathogenic nematode; beet cyst nematode resistance; BCNR locus;
KW sugar beet; ss.
XX
OS Synthetic.
XX
PN WO9319181-A1.
XX
PD 30-SEP-1993.
XX
PF 23-MAR-1993; 93WO-EP000702.
XX
PR 25-MAR-1992; 92DK-00000396.
XX
XX (SANO ) SANDOZ-ERFINDUNGEN VERW GRS MBH.
PA (SANO ) SANDOZ PATENT GMBH.
PA (SANO ) SANDOZ LTD.
XX
PI Sandal N, Marcker K, Stiekema W, Lange W, Klein-Lankhorst R;
PI Steen P;
XX
XX WPI; 1993-320747/40.
XX
PT Recombinant DNA comprising Beet Cyst Nematode Resistance Locus - confers
PT nematode resistance to beet species.
XX
PS Claim 2; Page 61; 82pp; English.
XX
XX This primer is used to amplify a BCNR locus marker of ca. 1100bp from
CC wild beet species belonging to section Procumbentes. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      2 GGGGG 6

RESULT 3
AAQ79368
ID AAQ79368 standard; DNA; 10 BP.
XX
AC AAQ79368;
XX
DT 25-MAR-2003 (revised)
DT 05-JUN-1995 (first entry)
XX
DE Regulatory element AP2/Rev located at posn. 708 of the extended 3'
DE flanking region of human erythropoietin.
XX
KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.
XX
OS Synthetic.
XX
PN WO9423570-A1.
XX
PD 27-OCT-1994.
XX
PF 15-APR-1994; 94WO-US004141.
XX
PR 15-APR-1993; 93US-00046295.
PR 23-JUN-1993; 93US-00082850.
XX
XX (UUNY ) UNIV NEW YORK STATE.
PA
XX
XX Lee-Huang S;
PI
XX WPI; 1994-341353/42.
XX
XX New regulatory regions of human erythropoietin gene - used for studying
XX and treating diseases and for prodn. of transgenic animal models (Eng).
XX
XX Disclosure; Table II, page 14; 81pp; English.
XX
XX AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone
XX hPSLH. This nucleic acid sequence includes a coding sequence, a 5'
XX flanking region contg. multiple regulatory elements and a 3' flanking
XX region contg. multiple regulatory elements. AAQ79355 consists of the last
XX 1777 bases of AAQ79753. It corresp. to the non-coding 3' flanking region
XX of AAQ79753 and includes all the regulatory elements contained therein.
XX It extends from the 5'-most PstI site 3' of the end of the coding
XX sequence to a BamHI site. It comprises 1777 bp exhibiting many stem-loop
XX structures. It also contains TATA boxes in forward and reverse
XX orientation, and at least about 184 potential transcriptional regulatory
XX elements. AAQ79365-Q79369 list several of these elements and their
XX positions. The nucleotide posns. are measured from first nucleotide at
XX the extended 3' end of hPSLH as shown in AAQ79355. (Updated on 25-MAR-
XX 2003 to correct PN field.)
XX
SQ Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      5 GGGGG 9

RESULT 4
AAQ79367
ID AAQ79367 standard; DNA; 10 BP.
XX
AC AAQ79367;

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XX 25-MAR-2003 (revised)
DT 05-JUN-1995 (first entry)
XX
XX Regulatory element AP2/Rev located at posn. 707 of the extended 3'
DE flanking region of human erythropoietin.
XX
XX Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.
XX
XX Synthetic.
XX
XX WO9423570-A1.
XX
XX 27-OCT-1994.
XX
XX 15-APR-1994; 94WO-US004141.
XX
XX 15-APR-1993; 93US-00046295.
XX 23-JUN-1993; 93US-00082850.
XX
XX (UYNV ) UNIV NEW YORK STATE.
XX
XX Lee-Huang S;
XX
XX WPI; 1994-341353/42.
XX
XX New regulatory regions of human erythropoietin gene - used for studying
PT and treating diseases and for prodn. of transgenic animal models (Eng).
XX
XX Disclosure; Table II, page 14; 81pp; English.
XX
XX AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone
CC hEpsLH. This nucleic acid sequence includes a coding sequence, a 5'
CC flanking region contg. multiple regulatory elements and a 3' flanking
CC region contg. multiple regulatory elements. AAQ79355 consists of the last
CC 1777 bases of AAQ79753. It corresp. to the non-coding 3' flanking region
CC of AAQ79753 and includes all the regulatory elements contained therein.
CC It extends from the 5'-most PstI site 3' of the end of the coding
CC sequence to a BamHI site. It comprises 1777 bp exhibiting many stem-loop
CC structures. It also contains TATA boxes in forward and reverse
CC orientation, and at least about 184 potential transcriptional regulatory
CC elements. AAQ79365-Q79369 list several of these elements and their
CC positions. The nucleotide posns. are measured from first nucleotide at
CC the extended 3' end of hEpsLH as shown in AAQ79355. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX
XX Sequence 10 BP; 0 A; 0 C; 9 G; 1 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 6 GGGGG 10

RESULT 5
AAQ79359/c
ID AAQ79359 standard; DNA; 10 BP.
XX
XX AAQ79359;
AC
XX
XX 25-MAR-2003 (revised)
DT 05-JUN-1995 (first entry)
XX
XX Sequence of AP2 regulatory sequence located at posn. 2621 in hEpsLH.
DE Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.
XX
XX Synthetic.
XX
XX WO9423570-A1.
XX

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XX 27-OCT-1994.
XX
XX 15-APR-1994; 94WO-US004141.
XX
XX 15-APR-1993; 93US-00046295.
XX 23-JUN-1993; 93US-00082850.
XX
XX (UYNV ) UNIV NEW YORK STATE.
XX
XX Lee-Huang S;
XX
XX WPI; 1994-341353/42.
XX
XX New regulatory regions of human erythropoietin gene - used for studying
PT and treating diseases and for prodn. of transgenic animal models (Eng).
XX
XX Disclosure; Table I, p. 12; 81pp; English.
XX
XX AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone
CC hEpsLH. This nucleic acid sequence includes EPO coding sequence, a 5'
CC flanking region contg. multiple regulatory elements and a 3' flanking
CC region contg. multiple regulatory elements. AAQ79354 shows the extended
CC 5' flanking region and includes all the 5' regulatory elements. This
CC 3.6 kb EPO genomic clone from fetal liver reported by others. The
CC flanking region comprises 3892 bp and contains CMAT and TATA boxes and at
CC lease 321 potential transcriptional regulatory elements. AAQ79356-Q79362
CC show several of these elements and their positions. The nucleotide
CC position of these elements is measured from the BamHI site at the 5' end
CC of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 1 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 6 GGGGG 2

RESULT 6
AAQ79358/c
ID AAQ79358 standard; DNA; 10 BP.
XX
XX AAQ79358;
AC
XX
XX 25-MAR-2003 (revised)
DT 05-JUN-1995 (first entry)
XX
XX Sequence of AP2 regulatory sequence located at posn. 896 in hEpsLH.
DE Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.
XX
XX Synthetic.
XX
XX WO9423570-A1.
XX
XX 27-OCT-1994.
XX
XX 15-APR-1994; 94WO-US004141.
XX
XX 15-APR-1993; 93US-00046295.
XX 23-JUN-1993; 93US-00082850.
XX
XX (UYNV ) UNIV NEW YORK STATE.
XX
XX Lee-Huang S;
XX
XX WPI; 1994-341353/42.
XX

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PT New regulatory regions of human erythropoietin gene - used for studying  
 XX and treating diseases and for prodn. of transgenic animal models (Eng).  
 PS Disclosure; Table I, p. 12; 81pp; English.  
 XX  
 CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
 CC hEPsLH. This nucleic acid sequence includes EPO coding sequence, a 5'  
 CC flanking region contg. multiple regulatory elements and a 3' flanking  
 CC region contg. multiple regulatory elements. AAQ79354 shows the extended  
 CC 5' flanking region and includes all the 5' regulatory elements. This  
 CC region, consisting of the first 3892 of AAQ79353, was not found in the  
 CC 3.6 kb EPO genomic clone from fetal liver reported by others. The  
 CC flanking region comprises 3892 bp and contains CAAT and TATA boxes and at  
 CC least 321 potential transcriptional regulatory elements. AAQ79356-Q79362  
 CC show several of these elements and their positions. The nucleotide  
 CC position of these elements is measured from the BamHI site at the 5' end  
 CC of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 10 BP; 0 A; 8 C; 0 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGG 5  
 Db 6 GGGGG 2  
 RESULT 7  
 AAQ71100  
 ID AAQ71100 standard; cDNA; 10 BP.  
 AC AAQ71100;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-APR-1995 (first entry)  
 DE Merlin exon 12 splice donor site.  
 KW Polymerase chain reaction; PCR; amplify; primer; bi-lateral schwannoma;  
 KW sequence-tagged site assay; chromosome 22; NF2; deletion; hearing loss;  
 KW neurofibromatosis; merlin; moesin-erzin-radinin-like protein; D22S28;  
 KW tumour suppressor; activity; meningioma; cytoskeleton; gene therapy;  
 KW merlin-associated tumour; D22S1; posterior capsular lens opacity;  
 KW deafness; balance disorder; paralysis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP613945-A2.  
 XX  
 PD 07-SEP-1994.  
 XX  
 XX 25-FEB-1994; 94EP-00301367.  
 XX  
 PR 25-FEB-1993; 93US-00022034.  
 PR 04-MAR-1993; 93US-00026063.  
 PR 19-AUG-1993; 93US-00108808.  
 PR 22-DEC-1993; 93US-00171718.  
 XX  
 PA (GENO) GEN HOSPITAL CORP.  
 XX  
 XX Trefatter JA, Maccollin MM, Gusella JF;  
 PI WPI; 1994-272992/34.  
 XX  
 DR The tumour suppressor gene merlin - for treatment and diagnosis of  
 PT tumours and neurofibromatosis (NF2).  
 PS Example 6; Page 26; 86pp; English.  
 XX  
 XX The sequences given in AAQ71078-109 represent the splice donor and  
 CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-

CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2  
 CC "gene" has been shown by linkage studies to be assigned to chromosome 22.  
 CC The missing or mutated gene in NF2 patients has been shown to be the  
 CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radinin-  
 CC like protein), which possesses tumour suppressor activity, and whose  
 CC tumour suppressor activity is mediated by inter- actions with the  
 CC cytoskeleton. The merlin gene is found on chromosome 22 between the known  
 CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene  
 CC is either lost or mutated. A mutant merlin protein may be encoded by a  
 CC gene in which a mutation of A to T at the first position of the codon  
 CC encoding amino acid 220 causes the substitution of Tyr for Asn. The  
 CC merlin gene may be used in gene therapy for the treatment of a merlin-  
 CC associated tumour or NF2, or for prevention of schwannoma, meningioma,  
 CC posterior capsular lens opacities, deafness or hearing loss, balance  
 CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGG 5  
 Db 5 GGGGG 9  
 RESULT 8  
 AAQ64610/c  
 ID AAQ64610 standard; cDNA; 10 BP.  
 XX  
 AC AAQ64610;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 15-DEC-1994 (first entry)  
 DE Alzheimer's/Parkinsons mitochondrial DNA mutation detection.  
 XX  
 KW Mitochondrial DNA mutation; associated with Alzheimer's;  
 KW Parkinson's disease; mismatch primers; PCR; amplification;  
 XX polymerase chain reaction; ss.  
 OS Homo sapiens.  
 XX  
 PN WO9409162-A1.  
 XX  
 XX 28-APR-1994.  
 XX  
 XX 20-OCT-1993; 93WO-US010072.  
 XX  
 XX 20-OCT-1992; 92US-00963723.  
 XX  
 XX (UYEM-) UNIV EMORY SCHOOL MEDICINE.  
 XX  
 XX Wallace DC;  
 PI WPI; 1994-151346/18.  
 XX  
 DR Detection of mitochondrial DNA mutation associated with Alzheimer's  
 PT disease and/or Parkinson's disease - for diagnosing or predicting a pre-  
 PT disposition to Alzheimer's disease and/or Parkinson's disease in a  
 PT patient.  
 XX  
 PS Disclosure; Page 36; 83pp; English.  
 XX  
 CC A 12S(956-965) insertion mutation harbours a novel 12S rRNA gene  
 CC insertion. Direct sequence analysis revealed that the insertion consisted  
 CC of approximately five cytosines within AAQ64610. This mitochondrial DNA  
 CC mutation is associated with Alzheimer's and/or Parkinson's diseases. The  
 CC detection of the mutations is useful for diagnosing or predicting a pre-  
 CC disposition to either of the diseases. (Updated on 25-MAR-2003 to correct  
 CC PN field.)  
 XX

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SQ Sequence 10 BP; 0 A; 9 C; 0 G; 1 T; 0 U; 0 Other;
  Query Match      100.0%; Score 5; DB 2; Length 10;
  Best Local Similarity 100.0%; Pred. No. 1.6e+06;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 5 GGGGG 1

RESULT 9
AAT08734
ID AAT08734 standard; DNA; 10 BP.
AC AAT08734;
XX
XX
DT 14-JUN-1996 (first entry)
XX
DE U14snRNA inverted repeat sequence.
XX
XX snRNA; small nucleolar RNA; U14; non-translated sequence; conserved;
KW Box C; Box D; processing; pre-ribosomal RNA; ribosome formation;
KW normal growth phenotype; yeast; plant; maize; potato; 18S rRNA; ss.
XX
OS Synthetic.
XX
PN WO9530747-A1.
XX
PD 16-NOV-1995.
XX
PF 04-MAY-1994; 94WO-EP001409.
XX
PR 04-MAY-1994; 94WO-EP001409.
XX
PA (GENE-) GENE SHEARS PTY LTD.
XX
PI Brown JWS, Leader DJ, Waugh R;
XX
DR WPI; 1995-404114/51.
XX
Nucleic acid contg. plant U14 sequences and their deriva. - for
PT regulating prodn. of ribosomal RNA, also as stabilisers for heterologous
PT RNA.
XX
PS Claim 7; Page 29; 57pp; English.
XX
U14 small nucleolar RNA (snRNA) is present in genomes as a non-
CC translated sequence. U14 sequences contain at the extremities of the
CC coding sequence, a pair of inverted repeats, which usually have a length
CC of between 4 and 20, e.g. 5-12 nucleotides and which are complementary to
CC each other to allow the formation of a stem by base-pairing. The stem
CC structure is thought to protect the U14 gene from digestion by RNase. The
CC present sequence forms a stem structure by annealing to its complementary
CC strand. SnRNAs are involved in processing of pre-ribosomal RNA
CC transcripts and ribosome formation. U14snRNA is required for a normal
CC growth phenotype and for processing of pre-rRNA transcripts in yeast.
CC Plant U14 sequences have been identified and characterised in the present
CC invention, and may be intron encoded
XX
SQ Sequence 10 BP; 1 A; 0 C; 5 G; 4 T; 0 U; 0 Other;
  Query Match      100.0%; Score 5; DB 2; Length 10;
  Best Local Similarity 100.0%; Pred. No. 1.6e+06;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 3 GGGGG 7

RESULT 10
AAAX32616
ID AAX32616 standard; DNA; 10 BP.
AC AAX32616;
XX
XX
DT 23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #16.
XX
XX Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.
XX
PR 28-FEB-1994; 94US-00202927.
XX
PA (MICR-) MICROPROBE CORP.
PA (UYA ) UNIV YALE.
XX
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX
XX WPI; 1995-311501/40.
XX
New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT intramolecular duplex with hairpin loop region, having selective
PT cytotoxicity against some tumour cells.
XX
PS Disclosure; Page 50; 107pp; English.
XX
New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC and which have a steroid structure attached to the 3'-end through a
CC linker attached to the A-ring of the steroid skeleton. In particular, the
CC present sequence has a cholesterol moiety attached by its A-ring to to
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC oligonucleotides form stable duplexes at physiological temperature and
CC have selective cytotoxic activity against certain tumour cell lines,
CC including some with multiple drug resistance
XX
SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;
  Query Match      100.0%; Score 5; DB 2; Length 10;
  Best Local Similarity 100.0%; Pred. No. 1.6e+06;
  Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 6 GGGGG 10

RESULT 11
AAT08758
ID AAT08758 standard; DNA; 10 BP.
XX
XX AAT08758;
AC
XX
DT 14-JUN-1996 (first entry)
XX
DE U14snRNA inverted repeat sequence.
XX
XX snRNA; small nucleolar RNA; U14; non-translated sequence; conserved;
KW Box C; Box D; processing; pre-ribosomal RNA; ribosome formation;
KW normal growth phenotype; yeast; plant; maize; potato; 18S rRNA; ss.
XX
OS Synthetic.
XX
PN WO9530748-A2.
XX

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[illegible]

```
XX SQ Sequence 10 BP; 3 A; 1 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 3 GGGGG 7

RESULT 14
AAQ96686
ID AAQ96686 standard; DNA; 10 BP.
XX AC AAQ96686;
XX DT 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 281.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU000063.
XX PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WI; 1995-293115/38.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU000063.
XX PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WI; 1995-293115/38.
XX PD New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 191; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 2 GGGGG 6

RESULT 15
AAQ96683
ID AAQ96683 standard; DNA; 10 BP.
```

```
XX AAQ96683;
XX AC 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 278.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU000063.
XX PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WI; 1995-293115/38.
XX PD New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
PT LTR region - can be used in a vaccine to inhibit/reduce productive
PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 191; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX SQ Sequence 10 BP; 4 A; 0 C; 6 G; 0 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 5 GGGGG 9

RESULT 16
AAQ96687
ID AAQ96687 standard; DNA; 10 BP.
XX AC AAQ96687;
XX DT 16-OCT-2003 (revised)
DT 22-MAR-1996 (first entry)
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 282.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
```



XX PF 14-FEB-1995; 95WO-AU0000063.  
 XX PR 14-FEB-1994; 94AU-00003864.  
 XX PR 21-FEB-1994; 94AU-00004002.  
 XX PR 23-DEC-1994; 94AU-00000284.  
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 XX (AURE-) AUSTRALIAN RED CROSS SOC.  
 XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 XX WPI; 1995-293115/38.  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX Claim 13; Page 191; 301pp; English.  
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGGG 5  
 Db |||||  
 1 GGGGG 5  
 RESULT 17  
 AAQ96684  
 ID AAQ96684 standard; DNA; 10 BP.  
 XX AC AAQ96684;  
 XX DT 16-OCT-2003 (revised)  
 XX DT 22-MAR-1996 (first entry)  
 XX DE HIV-1 NL4-3 nef gene nucleotide deletion 279.  
 XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 XX Human immunodeficiency virus 1.  
 XX WO9521912-A1.  
 XX 17-AUG-1995.  
 XX PF 14-FEB-1995; 95WO-AU0000063.  
 XX PR 14-FEB-1994; 94AU-00003864.  
 XX PR 21-FEB-1994; 94AU-00004002.  
 XX PR 23-DEC-1994; 94AU-00000284.  
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 XX (AURE-) AUSTRALIAN RED CROSS SOC.  
 XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 XX WPI; 1995-293115/38.  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive

PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX Claim 13; Page 191; 301pp; English.  
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX Sequence 10 BP; 4 A; 0 C; 6 G; 0 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGGG 5  
 Db |||||  
 4 GGGGG 8  
 RESULT 18  
 AAQ96688  
 ID AAQ96688 standard; DNA; 10 BP.  
 XX AC AAQ96688;  
 XX DT 16-OCT-2003 (revised)  
 XX DT 22-MAR-1996 (first entry)  
 XX DE HIV-1 NL4-3 nef gene nucleotide deletion 283.  
 XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 XX Human immunodeficiency virus 1.  
 XX WO9521912-A1.  
 XX 17-AUG-1995.  
 XX PF 14-FEB-1995; 95WO-AU0000063.  
 XX PR 14-FEB-1994; 94AU-00003864.  
 XX PR 21-FEB-1994; 94AU-00004002.  
 XX PR 23-DEC-1994; 94AU-00000284.  
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 XX (AURE-) AUSTRALIAN RED CROSS SOC.  
 XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 XX WPI; 1995-293115/38.  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX Claim 13; Page 191; 301pp; English.  
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;  
 SQ

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
 |||||  
 Db 1 GGGGG 5

## RESULT 19

AAQ93130/c  
 ID AAQ93130 standard; DNA; 10 BP.

XX AC AAQ93130;

XX DT 06-MAR-1996 (first entry)

XX DE Telomerase RNA (telRNA) gene fragment mutated coding sequence.

XX KW Telomerase; telomere; cancer; gene therapy; euploides; mutation; tumour;  
 XX KW treatment; ss.

XX OS Tetrahymena sp.

XX PN EP666313-A2.

XX PD 09-AUG-1995.

XX PF 27-JAN-1995; 95EP-00300539.

XX PR 27-JAN-1994; 94US-00189151.

XX PA (IOWA ) UNIV IOWA STATE RES FOUND INC.

XX PI Henderson E;

XX DR WPI; 1995-270495/36.

XX PT New gene encoding human telomerase RNA, related vectors and transformed  
 XX PT cells - useful esp. for treatment of cancer by gene therapy.

XX PS Example 7; Page 9; 20pp; English.

XX CC AAQ93130 is a mutated telomerase RNA gene fragment which when introduced  
 XX CC to a cell results in rapid cell death. A new telomerase gene or gene  
 XX CC fragment coding for telomerase RNA has been identified. Mutations of this  
 XX CC gene can be used in the treatment of tumours. The DNA can be introduced  
 XX CC into cancerous cells in vivo or in vitro so that the mutated telomerase  
 XX CC competes with endogenous telomerase for formation of active telomeres.  
 XX CC This results in the addition of aberrant telomere sequences to the ends  
 XX CC of chromosomes which causes genetic instability and rapid cell death.  
 XX CC Telomere-specific ribozymes may also be useful to treat or prevent cancer  
 XX CC i.e. it may be present to inactivate any telomerase RNA if a normal cell  
 XX CC undergoes transformation. The method is specific for tumour cells since  
 XX CC telomerase is inactive in normal cells

XX SQ Sequence 10 BP; 4 A; 6 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
 |||||  
 Db 8 GGGGG 4

## RESULT 20

AAQ88461

ID AAQ88461 standard; DNA; 10 BP.

XX AC AAQ88461;

XX

DT 19-DEC-1995 (first entry)

XX DE Human mitochondrial D-loop region DNA probe 6-2.

XX KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;  
 XX KW D-loop region; biological chip; hybridisation fingerprint;  
 XX KW interrogation position; ss.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT modified\_base 10

FT /\*tag= a  
 FT /note= "3'-end of probe is covalently attached to chip  
 FT surface"

XX PN W09511995-A1.

XX PD 04-MAY-1995.

XX PF 26-OCT-1994; 94WO-US012305.

XX PR 26-OCT-1993; 93US-00143312.

XX PR 02-AUG-1994; 94US-00284064.

XX PA (AFFY-) AFFYMAX TECHNOLOGIES NV.

XX PI Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA;  
 XX PI Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shan N, Sheldon EL;

XX DR WPI; 1995-178887/23.

XX PT New arrays of oligo:nucleotide probes - used for comparing known  
 XX PT sequences with variants for detection of mutation(s) and sequencing.

XX PS Disclosure; Page 107; 223pp; English.

XX CC A DNA chip was prepared for analysing sequences contained in a 1.3kb  
 XX CC fragment of human mitochondrial DNA from the D-loop region, the most  
 XX CC polymorphic region of human mitochondrial DNA. The chip comprised a set  
 XX CC of 268 overlapping oligonucleotide probes (see AAQ8421-Q88684) of  
 XX CC varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm  
 XX CC x 1cm array. Each position in the sequence was represented by at least  
 XX CC one probe (usually 2 or more). DNA was amplified from six human donors  
 XX CC and then transcribed to give the 1.3kb RNA transcripts which were  
 XX CC fragmented and hybridised to the chip. For each individual, a unique  
 XX CC hybridisation fingerprint was produced on the chip; all differences could  
 XX CC be correlated with differences in the cloned genomic DNA sequence

XX SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
 |||||

Db 3 GGGGG 7

## RESULT 21

AAQ88437

ID AAQ88437 standard; DNA; 10 BP.

XX AC AAQ88437;

XX DT 19-DEC-1995 (first entry)

XX DE Human mitochondrial D-loop region DNA probe 16-0.

XX KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;  
 XX KW D-loop region; biological chip; hybridisation fingerprint;

```

KW interogation position; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 10
FT /tag= a
FT /note= "3'-end of probe is covalently attached to chip
FT surface"
XX
XX WO9511995-A1.
XX
XX 04-MAY-1995.
XX
XX 26-OCT-1994; 94WO-US012305.
XX
XX 26-OCT-1993; 93US-00143312.
XX 02-AUG-1994; 94US-00284064.
XX
XX (AFY-) AFFYMAX TECHNOLOGIES NV.
XX
XX Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA,
XX Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX WPI; 1995-178887/23.
XX
XX New arrays of oligonucleotide probes - used for comparing known
XX sequences with variants for detection of mutation(s) and sequencing.
XX
XX Disclosure; Page 106; 223pp; English.
XX
XX A DNA chip was prepared for analysing sequences contained in a 1.3kb
XX fragment of human mitochondrial DNA from the D-loop region, the most
XX polymorphic region of human mitochondrial DNA. The chip comprised a set
XX of 268 overlapping oligonucleotide probes (see AA088421-088684) of
XX varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
XX x 1cm array. Each position in the sequence was represented by at least
XX one probe (usually 2 or more). DNA was amplified from six human donors
XX and then transcribed to give the 1.3kb RNA transcripts which were
XX fragmented and hybridised to the chip. For each individual, a unique
XX hybridisation fingerprint was produced on the chip; all differences could
XX be correlated with differences in the cloned genomic DNA sequence
XX
XX Sequence 10 BP; 2 A; 1 C; 7 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GGGGG 5
XX |||||
XX Db 4 GGGGG 8
XX
XX RESULT 22
XX AAQ88493
XX ID AAQ88493 standard; DNA; 10 BP.
XX
XX AC AAQ88493;
XX
XX DT 20-DEC-1995 (first entry)
XX
XX DE Human mitochondrial D-loop region DNA probe 4-4.
XX
XX KW Tiling strategy; immobilised nucleic acid probe array; mitochondrial DNA;
XX D-loop region; biological chip; hybridisation fingerprint;
XX interogation position; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX modified_base 10
XX /tag= a

```

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FT
FT
XX
XX PN WO9511995-A1.
XX
XX PD 04-MAY-1995.
XX
XX PF 26-OCT-1994; 94WO-US012305.
XX
XX PR 26-OCT-1993; 93US-00143312.
XX 02-AUG-1994; 94US-00284064.
XX
XX (AFY-) AFFYMAX TECHNOLOGIES NV.
XX
XX Chee M, Cronin MT, Fodor SP, Gingeras TR, Huang XC, Hubbell EA,
XX Lipshutz RJ, Lobban PE, Miyada CG, Morris MS, Shah N, Sheldon EL;
XX WPI; 1995-178887/23.
XX
XX New arrays of oligonucleotide probes - used for comparing known
XX sequences with variants for detection of mutation(s) and sequencing.
XX
XX Disclosure; Page 107; 223pp; English.
XX
XX A DNA chip was prepared for analysing sequences contained in a 1.3kb
XX fragment of human mitochondrial DNA from the D-loop region, the most
XX polymorphic region of human mitochondrial DNA. The chip comprised a set
XX of 268 overlapping oligonucleotide probes (see AA088421-088684) of
XX varying length (9-14 nucleotides) with varying overlaps arranged in a 1cm
XX x 1cm array. Each position in the sequence was represented by at least
XX one probe (usually 2 or more). DNA was amplified from six human donors
XX and then transcribed to give the 1.3kb RNA transcripts which were
XX fragmented and hybridised to the chip. For each individual, a unique
XX hybridisation fingerprint was produced on the chip; all differences could
XX be correlated with differences in the cloned genomic DNA sequence
XX
XX Sequence 10 BP; 1 A; 1 C; 8 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.6e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 GGGGG 5
XX |||||
XX Db 3 GGGGG 7
XX
XX RESULT 23
XX AAT14138/C
XX ID AAT14138 standard; DNA; 10 BP.
XX
XX AC AAT14138;
XX
XX DT 29-MAY-1996 (first entry)
XX
XX DE Cytokine responsive DNA spacer regulatory element.
XX
XX KW Regulatory element; transcriptional regulatory protein;
XX signalling molecule; DNA spacer; agonist; antagonist; anaemia;
XX gene transcription; inflammation; cytopenia; cancer; ss.
XX
XX OS Synthetic.
XX
XX PN WO9528482-A2.
XX
XX PD 26-OCT-1995.
XX
XX PF 10-APR-1995; 95WO-US004477.
XX
XX PR 14-APR-1994; 94US-00228935.
XX 27-MAR-1995; 95US-00410780.
XX
XX (LIGA-) LIGAND PHARM INC.

```

XX Seidel HM, Lamb IP;  
 XX WPI; 1995-373797/48.  
 XX DNA spacer regulatory elements responsive to cytokine(s) - for detecting  
 PT the presence of transcriptional regulatory protein in a sample.  
 XX Claim 7; Page 125; 135pp; English.  
 XX The present oligonucleotide comprises a regulatory element TT(Nx)AA,  
 CC where x is 4-7, and the regulatory element binds an activated  
 CC transcriptional regulatory protein in response to a signalling mol., i.e.  
 CC a cytokine. This cytokine responsive DNA spacer regulatory element can be  
 CC used to detect the presence of a transcriptional regulatory protein in a  
 CC sample, and in assays for (ant)agonists of gene transcription. The  
 CC identified cpds. may be used to treat cytokine-induced disease states, or  
 CC to ameliorate disease states caused by cytokine deficiency, e.g.  
 CC inflammation, anaemia, cytopenia and (pre)cancerous conditions  
 XX  
 SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
 |||||  
 Db 7 GGGGG 3

RESULT 24  
 AAT05376/c  
 ID AAT05376 standard; DNA; 10 BP.  
 XX  
 AC AAT05376;  
 XX  
 DT 04-JUN-1996 (first entry)  
 XX  
 DE Setoria nodorum RAPD primer OPB-19.  
 XX  
 KW Plant pathogen; fungus; Septoria nodorum; Septoria tritici; Fusarium;  
 KW Pseudocercospora herpotrichoides; Mycosphaerella fijiensis; PCR;  
 KW Mycosphaerella musicola; amplification; primer; ribosomal RNA gene;  
 KW internal transcribed region; strain; capture; colourimetric assay;  
 KW isolate; development; population; random amplified polymorphic DNA; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9529260-A2.  
 XX  
 PD 02-NOV-1995.  
 XX  
 PF 19-APR-1995; 95WO-US004712.  
 XX  
 PR 25-APR-1994; 94US-00233608.  
 XX  
 PA (CIBA ) CTBA GEIGY AG.  
 XX  
 PI Ligon JW, Beck JJ;  
 XX  
 DR WPI; 1995-383005/49.  
 XX

DNA encoding intervening transcribed sequence - used for detection of  
 PT plant fungal pathogens.

PS Claim 9; Page 16; 65pp; English.

CC A novel method for the detection of plant pathogenic strains of fungi  
 CC e.g. Septoria nodorum, S. tritici, Pseudocercospora herpotrichoides,  
 CC Mycosphaerella fijiensis, M. musicola or Fusarium spp. involves the PCR  
 CC amplification of sequences found in the internal transcribed region (ITS)  
 CC of the 18S, 5.8S and 28S ribosomal RNA genes by the primers AAQ94359-93

CC and AAT05357-72. These primers are derived from the ITS sequences of  
 CC these fungi (AAT05394-T05404 and AAQ94398) and are strain specific. The  
 CC amplification products of the reactions using these primers can be used  
 CC with the capture primers AAT05378-93 in colourimetric assays. The primers  
 CC and ITS DNAs can be used for the detection of specific fungal pathogen  
 CC isolates and in monitoring disease development in plant populations. The  
 CC primers AAT05373-7 were obtained from purchased random amplified  
 CC polymorphic DNA (RAPD) primer libraries and used to PCR amplify ITS  
 CC sequences in conjunction with the primers AAQ94390-3. This primer  
 CC amplified a 1.1 kb region from S. nodorum

XX Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
 |||||  
 Db 6 GGGGG 2

RESULT 25  
 AAT04915/c  
 ID AAT04915 standard; cDNA; 10 BP.

XX AC AAT04915;

XX  
 DT 25-MAR-2003 (revised)  
 DT 15-MAY-1996 (first entry)

XX Mammalian stem cell factor (SCF) cDNA oligonucleotide primer 201-7.

XX Stem cell factor; progenitor; haematopoiesis; SCF; anaemia;  
 KW thrombocytopenia; leucopenia; AIDS; immunodeficiency; bone graft;  
 KW transplant; neoplasia; myelosuppression; bone marrow; ss.

XX Synthetic.

XX EP676470-A1.

XX 11-OCT-1995.

XX 04-OCT-1990; 95EP-00105391.

XX 16-OCT-1989; 89US-00422383.

XX 11-JUN-1990; 90US-00537198.

XX 24-AUG-1990; 90US-00573616.

XX 28-SEP-1990; 90WO-US005548.

XX 01-OCT-1990; 90US-00589701.

XX (AMGE-) AMGEN INC.

XX Zsebo KM, Suggs SV, Bosselman RA, Martin FH;

XX WPI; 1995-346090/45.

XX New stem cell factor polypeptide(s) - for stimulating the growth of  
 PT primitive progenitor cells, esp. for treating disorders involving blood  
 PT cells.

XX Example 3; Fig 12C; 127pp; English.

XX AAT04915-T04922 are oligonucleotide primers and probes used for the  
 CC amplification and sequencing of mammalian stem cell factor (SCF). Non-  
 CC naturally occurring SCF and C-terminally truncated polypeptides, having  
 CC amino acid sequences sufficiently duplicative of naturally occurring SCF,  
 CC stimulate growth of primitive progenitors such as haematopoietic  
 CC progenitor cells, neural stem cells and primordial germ stem cells. The  
 CC peptides can be used in a composition for treating leucopenia, anaemia or  
 CC thrombocytopenia, for enhancing engraftment of bone marrow during  
 CC transplantation or for bone marrow recovery after chemotherapy or  
 CC radiation-induced bone marrow aplasia or myelosuppression. They can also

CC be used for treating neoplasia, nerve damage, infertility, intestinal  
 CC damage or myeloproliferative disorders. Antibodies may be raised against  
 CC the peptides for use in detection or neutralisation of SCF in serum. SCF  
 CC may be useful for the treatment of AIDS and severe combined  
 CC immunodeficiency (SCID) states alone or in combination with other factors  
 CC such as IL-7. (Updated on 25-MAR-2003 to correct PF field.)  
 XX  
 SQ Sequence 10 BP; 0 A; 8 C; 1 G; 0 T; 0 U; 1 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
 |||||  
 Db 8 GGGGG 4

## RESULT 26

AAQ81070  
 ID AAQ81070 standard; DNA; 10 BP.

XX AC AAQ81070;

DT 25-MAR-2003 (revised)

DT 21-SEP-1995 (first entry)

XX supF gene triplex forming mutagenic oligonucleotide pso-AG10.

XX supF gene; triplex forming mutagenic oligonucleotide; pso-AG10;

KW 4'-hydroxymethyl-4,5',8-trimethylpsoralenated; site specific; ss.

XX Synthetic.

XX Key Location/Qualifiers  
 FT modified\_base 1  
 FT /\*tag= a  
 FT /note= "4'-hydroxymethyl-4,5', 8-trimethylpsoralenated"

XX WO9501364-A1.

XX PD 12-JAN-1995.

XX PF 24-JUN-1994; 94WO-US007234.

XX PR 25-JUN-1993; 93US-00083088.

XX (UYVA ) UNIV YALE.

XX Glazer PM, Havre PA;

XX WPI; 1995-060943/08.

XX New mutagenic oligo:nucleotide(s) - having a mutagen incorporated in an  
 PT oligo:nucleotide which forms a triplex, for site-directed mutagenesis.  
 XX  
 PS Example 5; Page 5; 72pp; English.

CC AAQ81070 is the supF gene triplex forming mutagenic oligonucleotide pso-  
 CC AG10. It forms a triplex (a triple stranded nucleic acid) with a specific  
 CC site on the supF genome, enabling the covalently bound 4'-hydroxymethyl-  
 CC 4,5',8-trimethylpsoralen group to produce a site specific mutation.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX

SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
 |||||  
 Db 6 GGGGG 10

## RESULT 27

AAT27213

ID AAT27213 standard; DNA; 10 BP.

XX AC AAT27213;

XX DT 10-DEC-1996 (first entry)

XX DE HIV-1 detection probe DNA A(-)1.

XX KW Human immunodeficiency virus; HIV; manufacture; immobilised probe;  
 KW magnetic microparticle; carboxy group; primary amino group;  
 KW hybridisation; ss.

XX OS Synthetic.

XX PN JP08089294-A.

XX PD 09-APR-1996.

XX PF 28-SEP-1994; 94JP-00233448.

XX PR 28-SEP-1994; 94JP-00233448.

XX PA (JAPS ) NIPPON GOSSEI GOMU KK.

XX DR WPI; 1996-233380/24.

XX Powder mfr. for detecting specific nucleic acids, useful for diagnosis -  
 PT comprises fixing single stranded oligo:nucleotide having fixed and  
 PT hybridisable regions to insol. microparticles having superficial carboxyl  
 PT gps.

XX Example 1; Page 6; 8pp; Japanese.

CC The probes AAT27211-4 are examples of probes, used to detect HIV-1  
 CC sequences, which are generated by a novel method of manufacturing an  
 CC immobilised probe. The method involves fixing a nucleic acid probe  
 CC sequence to the surface of an insol. magnetic microparticle via carboxy  
 CC gps. on the surface of the particle. The nucleic acid is single stranded,  
 CC of length 10-150 nucleotides and has a fixed region of 5-30 nucleotides  
 CC contg. prim. amino gps. and a hybridising region comprising 5 similar  
 CC nucleotides positioned away from the terminus of the oligonucleotide

SQ Sequence 10 BP; 0 A; 0 C; 10 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
 |||||

Db 1 GGGGG 5

## RESULT 28

AAT35000

ID AAT35000 standard; DNA; 10 BP.

XX AC AAT35000;

XX DT 25-MAR-2003 (revised)

DT 03-DEC-1996 (first entry)

XX HIV inhibitor #3.

XX HIV; infection inhibitor; triplex forming; purine rich promoter; V3 loop;  
 KW transcription inhibitor; gp120 protein; viral growth; enzyme inhibitor;  
 KW PLAZ; telomere length; glove coating; condom; ss.

XX OS Synthetic.

```

XX  US5523389-A.
XX  04-JUN-1996.
XX  28-SEP-1993; 93US-00128011.
XX  29-SEP-1992; 92US-00954185.
XX  (ISIS-) ISIS PHARM INC.
XX  Imbach JL, Ecker DJ, Wyatt JR;
XX  WPI; 1996-285782/29.
XX  New octa-nucleotide with guanosine quartet and phosphorothioate links -
XX  is inhibitor of HIV infection by binding to the V3 loop.
XX  Disclosure; Col 2; 14pp; English.
XX  AAT34998-T35001 represent HIV inhibitors. Sequences containing only G and
XX  T residues (such as these sequences) are triplex forming
XX  oligonucleotides, and form purine rich promoter elements used to inhibit
XX  transcription. These sequences bind to the HIV gp120 protein at the V3
XX  loop via the internal guanosine quartet. This binding prevents cell-to-
XX  cell and virus-to-cell infection. The sequences may also be used for
XX  inhibiting viral growth, and other viral genes, for inhibiting the enzyme
XX  PLA2, and to modulate telomere length. In some cases these sequences need
XX  to be chemically modified. The chemically modified oligonucleotides
XX  preferably include at least one phosphorothioate linkage. Other modified
XX  intersugar links, or 2'-modified sugar residues can also be used. These
XX  oligonucleotides can be used for coating gloves, condoms, etc, or for
XX  topical application. (Updated on 25-MAR-2003 to correct PF field.)
XX  Sequence 10 BP; 0 A; 0 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 1 GGGGG 5

RESULT 29
AAT35713
ID AAT35713 standard; DNA; 10 BP.
XX
AC AAT35713;
XX
DT 08-OCT-1996 (first entry)
XX
DE Primer UBC515 for V.dahliae RAPD reaction.
XX
KW RAPD; random amplified polymorphic DNA; diagnostic assay; quantitative;
KW PCR; primer; qualitative; soil sample; agricultural field; potatoe;
KW V.albo-atrum; soil fumigation; amplify; polymerase chain reaction; ss.
XX
OS Synthetic.
XX
XX US5527671-A.
XX
XX 18-JUN-1996.
XX
XX 07-NOV-1994; 94US-00335565.
XX
XX 07-NOV-1994; 94US-00335565.
XX
XX (WISC ) WISCONSIN ALUMNI RES FOUND.
XX
XX German TL, Li K, Rouse DI;
XX

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DR WPI; 1996-299849/30.
XX Assay for Verticillium dahliae - by amplification of specific DNA
XX sequence.
XX Example; Col 9; 16pp; English.
XX
XX AAT35710-T35738 represent amplification primers used in a random
XX amplified polymorphic DNA (RAPD) reaction on V.dahliae DNA. These
XX sequences were used to isolate the sequence represented by AAT35706 for
XX use in the diagnostic assays of the invention. The qualitative assays of
XX the invention comprise analysing a sample for the presence of the
XX V.dahliae sequence. Detection of the V.dahliae sequence in the sample
XX shows that the sample is infected by V.dahliae. A quantitative assay of
XX the invention, comprises taking a sample and isolating nucleic acids from
XX it. A sequence that acts as an internal standard (see AAT35707) is added
XX to the isolated nucleic acids. The internal standard competes with the
XX V.dahliae sequence for the PCR primers used in the reaction (such as the
XX sequences represented by AAT35708 and AAT35709). The amplified portion of
XX the internal standard is a different size to the amplified portion of the
XX V.dahliae sequence. The amounts of amplified DNA of each sequence is then
XX compared to indicate the number of V.dahliae present in the sample. The
XX sample used in these assays is normally a soil sample from an
XX agricultural field that is going to be used for growing potatoes. These
XX assays are faster and more accurate than methods based on culturing soil
XX samples in selective media. The assays can also distinguish between
XX V.dahliae and V.albo-atrum. By using these assays, unnecessary soil
XX fumigation can be avoided
XX
XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 1 GGGGG 5

RESULT 30
AAT10084/c
ID AAT10084 standard; DNA; 10 BP.
XX
XX AAT10084;
XX
XX 29-AUG-1996 (first entry)
XX
DE Hammerhead ribozyme RNA complementary oligonucleotide.
XX
XX Hammerhead; ribozyme; enhanced RNA cleavage; cleavage efficiency;
XX viral inactivation; viral RNA transcript; hybridisation; target RNA;
XX complementary oligonucleotide; ss.
XX
XX Synthetic.
XX
XX WO9600232-A1.
XX
XX 04-JAN-1996.
XX
XX 21-JUN-1995; 95WO-AU000359.
XX
XX 24-JUN-1994; 94US-00265484.
XX
XX (GENE-) GENE SHEARS PTY LTD.
XX
XX Keese P, Stapper M, Ferriman R;
XX
XX WPI; 1996-068825/07.
XX
XX Improved catalytic hammer-head ribozyme(s) and enhanced RNA cleavage -
XX useful in activating target sequences in e.g. infectious viruses.
XX

```

PS Example 3; Page 64; 122pp; English.

XX The present oligonucleotide is a complementary oligonucleotide (CO) for the ribozyme given in AAT10062 or AAT10072, which are specific examples of a claimed, highly generic, hammerhead ribozyme with enhanced RNA cleavage. The CO alters the cleavage efficiency of the ribozymes, i.e. the cleavage efficiency of the CO in combination with a ribozyme as a \$ of a control without the CO is 152. The ribozymes of the invention (opt. in conjunction with a CO) have extensive therapeutic and biological applications, e.g. disease causing viruses in man, animals and plants may be inactivated by administering to an infected subject a ribozyme adapted to hybridise to, and cleave RNA transcripts of the virus

XX Sequence 10 BP; 0 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
7 GGGGG 3

Db

RESULT 31

AAT98862

ID AAT98862 standard; DNA; 10 BP.

XX AC AAT98862;

XX AC AAT98862;

DT 20-MAR-1998 (first entry)

XX Core-binding site clone 6-9-1.

DE Protein-binding site isolation; transcription factor modification;

KW DNA-binding protein; inhibitor identification; ss.

KW DNA-binding protein; inhibitor identification; ss.

XX Synthetic.

OS Synthetic.

XX WO9727330-A1.

XX 31-JUL-1997.

XX 24-JAN-1997; 97WO-US001230.

XX 24-JAN-1996; 96US-00590571.

XX (UYVA ) UNIV YALE.

XX Weissman SM, Kulkarni P, Nallur GN;

PI WPI; 1997-393714/36.

DR Identifying protein-binding sites for DNA-binding proteins - using duplexes having 5' and 3' sequences for annealing to amplification primers with an internal potential protein-binding site sequence.

XX Example 3; Page 22; 52pp; English.

XX This sequence represents a core-binding site identified using the method of the invention. This sequence was identified using the 32P-labelled oligonucleotide duplex shown in AAT76581 and the primers shown in AAT76582-776583 in the method of the invention. The method is for simultaneously isolating protein-binding sites for DNA-binding proteins. The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes having 5' and 3' sequences capable of annealing to primers for amplification and an internal sequence having a potential protein-binding site, a non-specific inhibitor and a sample containing DNA-binding proteins; (b) separating unbound ON duplexes from ON duplexes complexed with the DNA-binding proteins; (c) amplifying complexed duplexes to form amplified duplexes; thereby isolating protein-binding sites for the DNA-binding proteins. The methods can be used to identify protein-binding sites which can be used to identify corresponding DNA-binding proteins in an expression library. They can also be used to develop products to inhibit the function of a given DNA-binding protein or for the modification of transcription factors

SQ Sequence 10 BP; 0 A; 5 C; 0 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC an expression library. They can also be used to develop products to inhibit the function of a given DNA-binding protein or for the modification of transcription factors

XX Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||||  
5 GGGGG 9

Db

RESULT 32

AAT98847

ID AAT98847 standard; DNA; 10 BP.

XX AC AAT98847;

XX AC AAT98847;

DT 20-MAR-1998 (first entry)

XX Binding site BSN1 identified using the method of the invention.

DE Protein-binding site isolation; transcription factor modification;

KW DNA-binding protein; inhibitor identification; ss.

KW DNA-binding protein; inhibitor identification; ss.

XX Synthetic.

OS Synthetic.

XX WO9727330-A1.

XX 31-JUL-1997.

XX 24-JAN-1997; 97WO-US001230.

XX 24-JAN-1996; 96US-00590571.

XX (UYVA ) UNIV YALE.

XX Weissman SM, Kulkarni P, Nallur GN;

PI WPI; 1997-393714/36.

DR Identifying protein-binding sites for DNA-binding proteins - using duplexes having 5' and 3' sequences for annealing to amplification primers with an internal potential protein-binding site sequence.

XX Example 3; Page 19; 52pp; English.

XX This sequence represents a binding site identified using the method of the invention. This sequence was identified using the 32P-labelled oligonucleotide duplex shown in AAT76581 and the primers shown in AAT76582-776583 in the method of the invention. The method is for simultaneously isolating protein-binding sites for DNA-binding proteins. The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes having 5' and 3' sequences capable of annealing to primers for amplification and an internal sequence having a potential protein-binding site, a non-specific inhibitor and a sample containing DNA-binding proteins; (b) separating unbound ON duplexes from ON duplexes complexed with the DNA-binding proteins; (c) amplifying complexed duplexes to form amplified duplexes; thereby isolating protein-binding sites for the DNA-binding proteins. The methods can be used to identify protein-binding sites which can be used to identify corresponding DNA-binding proteins in an expression library. They can also be used to develop products to inhibit the function of a given DNA-binding protein or for the modification of transcription factors

SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 GGGGG 5
DB      3 GGGGG 7

RESULT 33
AAT98859
ID AAT98859 standard; DNA; 10 BP.
XX
AC AAT98859;
XX
XX
DT 20-MAR-1998 (first entry)
XX
DE Core-binding site clone 6-6-2.
XX
XX Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
FN WO9727330-A1.
XX
PD 31-JUL-1997.
XX
PF 24-JAN-1997; 97WO-US001230.
XX
PR 24-JAN-1996; 96US-00590571.
XX
PA (UYVA ) UNIV YALE.
XX
PI Weissman SM, Kulkarni P, Nallur GN;
XX
XX WPI; 1997-393714/36.
XX
DR Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 22; 52pp; English.
XX
XX This sequence represents a core-binding site identified using the method
CC of the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 3 A; 0 C; 5 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
DB      4 GGGGG 8

RESULT 34
AAT98864
ID AAT98864 standard; DNA; 10 BP.

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```

XX AAT98864;
XX
XX 20-MAR-1998 (first entry)
XX
XX Core-binding site clone 6-12-2R.
XX
XX Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
XX Synthetic.
XX
OS WO9727330-A1.
XX
FN 31-JUL-1997.
XX
XX 24-JAN-1997; 97WO-US001230.
XX
PR 24-JAN-1996; 96US-00590571.
XX
PA (UYVA ) UNIV YALE.
XX
XX Weissman SM, Kulkarni P, Nallur GN;
XX
XX WPI; 1997-393714/36.
XX
DR Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 22; 52pp; English.
XX
XX This sequence represents a core-binding site identified using the method
CC of the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
DB      3 GGGGG 7

RESULT 35
AAT98851
ID AAT98851 standard; DNA; 10 BP.
XX
AC AAT98851;
XX
XX 20-MAR-1998 (first entry)
XX
XX Binding site BSN14 identified using the method of the invention.
DE Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.

```



XX OS Synthetic.  
 XX PN WO9727330-A1.  
 XX PD 31-JUL-1997.  
 XX PF 24-JAN-1997; 97WO-US001230.  
 XX PR 24-JAN-1996; 96US-00590571.  
 XX PA (UYVA ) UNIV YALE.  
 XX PI Weissman SM, Kulkarni P, Nallur GN;  
 XX DR WPI; 1997-393714/36.  
 XX PT Identifying protein-binding sites for DNA-binding proteins - using  
 PT duplexes having 5' and 3' sequences for annealing to amplification  
 PT primers with an internal potential protein-binding site sequence.  
 XX PS Example 3; Page 19; 52pp; English.  
 XX CC This sequence represents a binding site identified using the method of  
 CC the invention. This sequence was identified using the 32P-labelled  
 CC oligonucleotide duplex shown in Aar76581 and the primers shown in  
 CC Aar76582-T76583 in the method of the invention. The method is for  
 CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
 CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
 CC having 5' and 3' sequences capable of annealing to primers for  
 CC amplification and an internal sequence having a potential protein-binding  
 CC site, a non-specific inhibitor and a sample containing DNA-binding  
 CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
 CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
 CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
 CC binding proteins. The methods can be used to identify protein-binding  
 CC sites which can be used to identify corresponding DNA-binding proteins in  
 CC an expression library. They can also be used to develop products to  
 CC inhibit the function of a given DNA-binding protein or for the  
 CC modification of transcription factors  
 XX SQ Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGG 5  
 Db 1 GGGGG 5  
 RESULT 36  
 AAT70006  
 ID AAT70006 standard; DNA; 10 BP.  
 XX AC AAT70006;  
 XX DT 25-AUG-1997 (first entry)  
 XX DE Triplex-forming oligonucleotide AG10.  
 XX KW Site-directed mutagenesis; triple helix; triplex; psoralen; gene therapy;  
 KW oncogene inactivation; supF gene; ss.  
 XX OS Synthetic.  
 XX PN WO9639195-A2.  
 XX PD 12-DEC-1996.  
 XX PF 04-JUN-1996; 96WO-US008883.  
 XX PP

PR 06-JUN-1995; 95US-00463519.  
 XX (UYVA ) UNIV YALE.  
 XX PI Glazer PM, Havre PA;  
 XX DR WPI; 1997-042873/04.  
 XX PT Triple-helix forming oligonucleotide linked to a mutagen - useful for  
 PT site-specific mutagenesis of target gene, e.g. for gene therapy or to  
 PT inactivate oncogene(s) or viral genes.  
 XX PS Example 1; Fig 1; 68pp; English.  
 XX CC Homopurine oligonucleotide AG10 (AAT70006) can be linked to psoralen at  
 CC its 5' end and used to achieve site-specific, targeted mutagenesis of a  
 CC specific gene. It is based on a homopurine/ homopyrimidine 10-bp motif  
 CC found at bp 167-176 of the supF gene (see also AAT70005), an E. coli  
 CC amber suppressor tyrosine tRNA gene. Targeted mutagenesis was achieved  
 CC by incubating pso-AG10 with supF DNA in vitro to form a triplex at  
 CC positions 167-176 of the supF gene and bring the tethered psoralen into  
 CC proximity with the targeted base pair 167 (see also AAT70008). This  
 CC method of site-directed mutagenesis can be used for gene therapy, to  
 CC inactivate oncogenes or viral genes, to study DNA repair mechanisms and  
 CC to produce transmutated plants and animals  
 XX SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGGG 5  
 Db 6 GGGGG 10  
 RESULT 37  
 AAT70007  
 ID AAT70007 standard; DNA; 10 BP.  
 XX AC AAT70007;  
 XX DT 25-AUG-1997 (first entry)  
 XX DE Oligonucleotide GA10.  
 XX KW Site-directed mutagenesis; triple helix; triplex; psoralen; gene therapy;  
 KW oncogene inactivation; supF gene; ss.  
 XX OS Synthetic.  
 XX PN WO9639195-A2.  
 XX PD 12-DEC-1996.  
 XX PF 04-JUN-1996; 96WO-US008883.  
 XX PR 06-JUN-1995; 95US-00463519.  
 XX PA (UYVA ) UNIV YALE.  
 XX PI Glazer PM, Havre PA;  
 XX DR WPI; 1997-042873/04.  
 XX PT Triple-helix forming oligonucleotide linked to a mutagen - useful for  
 PT site-specific mutagenesis of target gene, e.g. for gene therapy or to  
 PT inactivate oncogene(s) or viral genes.  
 XX PS Example 1; Page 15; 68pp; English.  
 XX CC Oligonucleotide GA10 (AAT70007), the reverse of oligonucleotide AG10

CC (AAT70006), was used in assays for triplex formation with the supF gene  
CC target (see also AAT70005). GA10 failed to bind to supF or to compete with  
CC AG10 for binding. AG10 bound specifically to the supF gene  
XX  
SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGG 5  
Db 1 GGGGG 5  
RESULT 38  
AAT80370  
ID AAT80370 standard; DNA; 10 BP.  
XX  
AC AAT80370;  
XX  
DT 16-OCT-1997 (first entry)  
XX  
DE Oligo HCV-223, multiplex forming oligomer.  
XX  
KW Complementary; 5' untranslated region; UTR; hepatitis C virus; HCV;  
KW inhibition; replication; expression; detection; chronic hepatitis;  
KW acute hepatitis; hepatocarcinoma; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 1..5  
FT /tag= a  
FT /note= "2'-OME RNA"  
FT modified\_base 6..10  
FT /tag= b  
FT /note= "Comprises phosphorothioate linkages"  
XX  
PN W09639500-A2.  
XX  
PD 12-DEC-1996.  
XX  
PF 04-JUN-1996; 96WO-EP002427.  
XX  
PR 06-JUN-1995; 95US-00471968.  
XX  
PA (HOPF ) HOFFMANN LA ROCHE & CO AG F.  
PA (HYBR-) HYBRIDON INC.  
XX  
PI Frank BL, Goodchild J, Hamlin HA, Kiluskie RE, Roberts NA;  
PI Roberts PC, Walther DM, Wolfe JL;  
XX  
DR WPI; 1997-043122/04.  
XX  
PT Oligo: nucleotide(s) complementary to HCV 5' untranslated region - used in  
PT the treatment and detection of HCV infection, esp. hepatitis and hepato-  
PT carcinoma.  
XX  
PS Claim 28; Page 22; 100pp; English.  
XX  
CC The sequences given in AAT80211-382 represent synthetic oligonucleotides  
CC which are complementary to a portion of the 5' untranslated region (UTR)  
CC of hepatitis C virus (HCV). These sequences may be used in a  
CC pharmaceutical composition for the control or prevention of HCV  
CC infection. They may be used to inhibit replication or expression of HCV  
CC or for detecting the presence of HCV in a sample. They may be used to  
CC inhibit HCV replication in a cell and are therefore useful in the  
CC treatment of HCV infections such as chronic and acute hepatitis and  
CC hepatocarcinoma. This sequence forms multiplex binding complexes with  
CC regions of the HCV genome. This sequence forms a duplex at the region -  
CC 218 to -227 and does not form a purine strand triplex  
XX

SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGG 5  
Db 1 GGGGG 5  
RESULT 39  
AAT47062  
ID AAT47062 standard; DNA; 10 BP.  
XX  
AC AAT47062;  
XX  
DT 05-SEP-1997 (first entry)  
XX  
DE Oligonucleotide AG10, which binds triplex target site in supFG1.  
XX  
KW Triplex; supFG1; forming; target site; triple stranded; induction;  
KW mutation; targetted mutagenesis; triple helix; ss.  
XX  
OS Synthetic.  
XX  
PN W09640898-A1.  
XX  
PD 19-DEC-1996.  
XX  
PF 03-JUN-1996; 96WO-US008392.  
XX  
PR 07-JUN-1995; 95US-00476712.  
XX  
PA (UYUA ) UNIV YALE.  
XX  
PI Glazer PM;  
XX  
DR WPI; 1997-052310/05.  
XX  
PT Oligo-nucleotide for targetted mutagenesis of double stranded nucleic  
PT acid mol. - by forming triple stranded nucleic acid mol. with target  
PT region of double stranded nucleic acid mol.  
XX  
PS Example 1; Fig 1; 29pp; English.  
XX  
CC In an example of the invention, the binding of the oligonucleotides AG10  
CC (AAT47062), AG20 (AAT47061) and AG30 (AAT47060) to the supFG1 triplex  
CC target site (AAT47059), was examined using a gel mobility shift assay.  
CC Based on the concentration dependence of the triplex formation, the  
CC equilibrium constants for AG10, AG20 and AG30 were 3x10 power -5, 3x10  
CC power -7 and 2x10 power -8. The oligonucleotides were then tested for  
CC their ability to induce mutations in the pSupFG1 SV40 vector in monkey  
CC COS cells. AG30 generated mutations in the target gene at a frequency of  
CC 0.27%, 13 fold over the spontaneous background in the assay. In contrast,  
CC AG10 and AG20, which show inferior 3rd strand binding to supFG1, were  
CC much less effective in producing mutations. Examples of some of the  
CC mutations induced in the pSupFG1 vector using the oligonucleotides are  
CC given in AAT75067-73  
XX  
SQ Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGGG 5  
Db 6 GGGGG 10  
RESULT 40  
AAV62570/c

```

ID  AAV62570 standard; DNA; 10 BP.
XX
AC  AAV62570;
XX
DT  17-DEC-1998 (first entry)
XX
DE  Septoria nodorum species specific RAPD primer OPB-19.
XX
KW  Internal transcribed spacer; ITS; ribosomal RNA; Fusarium avenaceum;
KW  Fusarium culmorum; Fusarium graminearum; Fusarium moniliforme; plant;
KW  Septoria avenae; Microdochium nivale; Fusarium poae; fungal pathogen;
KW  random amplified polymorphic DNA; PCR; nucleic acid detection; RAPD;
KW  PCR primer; ss.
XX
OS  Synthetic.
OS  Phaeosphaeria nodorum.
XX
PN  US5814453-A.
XX
PD  29-SEP-1998.
XX
PF  02-JUL-1997; 97US-00887480.
XX
PR  19-APR-1995; 95WO-US004712.
PR  15-OCT-1996; 96US-00722187.
XX
PA  (NOVS ) NOVARTIS FINANCE CORP.
XX
PI  Beck JJ;
XX
DR  WPI; 1998-541745/46.
XX
PT  DNA isolated from fungal RNA, and its internal transcribed spacer
PT  sequence - used for detecting fungal pathogens in plant tissue.
XX
PS  Example 7; Col 19; 56pp; English.
XX
CC  Sequences AAV62567 to AAV62571 represent random amplified polymorphic DNA
CC  (RAPD) primers used in the course of the invention for detection of
CC  Septoria species. The invention provides a DNA molecule isolated from the
CC  ribosomal RNA gene region of a fungal pathogen, where the DNA molecule
CC  consists of an internal transcribed spacer (ITS) sequence selected from
CC  ITS1 and ITS2 of Fusarium culmorum, Fusarium graminearum, Fusarium
CC  moniliforme, Septoria avenae or Microdochium nivale. A method for
CC  detecting F. graminearum, F. culmorum, F. moniliforme, F. poae, F.
CC  avenaceum and M. nivale isolates is also provided which comprises
CC  isolating DNA from a plant leaf infected with at least one of the above
CC  pathogens and amplifying parts of the ITS sequence of the pathogen(s) by
CC  PCR using specific primers from within these sequences. The pathogen(s)
CC  are detected by visualising the amplified part of the ITS sequence
XX
SQ  Sequence 10 BP; 3 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 6 GGGGG 2

RESULT 41
AAV45390
ID AAV45390 standard; DNA; 10 BP.
XX
AC AAV45390;
XX
DT 11-JAN-1999 (first entry)
XX
DE Mouse CD3-epsilon enhancer binding site for Ikaros.
XX
KW Ikaros; mIK; transcription factor; mouse; lymphocyte;

cell differentiation; T cell; cancer; immunodeficiency;
Alzheimer's disease; therapy; diagnosis; CD3-epsilon; enhancer; ss.
Mus sp.
CA2194256-A.
05-MAR-1998.
02-JAN-1997; 97CA-02194256.
05-SEP-1996; 96US-00711417.
(GEHO ) GEN HOSPITAL CORP.
Georgopoulos K;
WPI; 1998-378292/33.
New nucleic acid encoding Ikaros protein involved in early
differentiation of lymphocytes - existing in several isoforms, and
related products, used to treat e.g. immune diseases or cancer and to
control cell differentiation.
Disclosure; Page 38; 158pp; English.
This oligonucleotide from the mouse CD3-epsilon gene enhancer was
identified as a potential high affinity binding site for Ikaros proteins
(see AAW70963-71). It partially includes the core motif GGGAA found in
consensus recognition sequences for murine Ikaros isoforms mIk-1, mIk-2
and mIk-3 (see AAV52830-32). High affinity binding sites for Ikaros have
been found in enhancer and promoter regions of the regulatory domains of
the TCR and antigen complex, the CD3 genes, the SL3 and HIV long terminal
repeat and in the regulatory domains of other T cell restricted antigens
(see AAV45358-402) by gel retardation assay. Ikaros is involved in early
differentiation of lymphocytes. The invention provides Ikaros nucleic
acids (see AAV42805-11 and AAV42840) and polypeptides, vectors and host
cells. These are used to treat T and B cell diseases, to control
expression of heterologous genes placed under control of an Ikaros-
responsive element, to treat nervous system diseases and to modulate cell
division, amplification or differentiation, especially in haematopoietic
cells
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 3 GGGGG 7

RESULT 42
AAV67001
ID AAV67001 standard; cDNA; 10 BP.
XX
AC AAV67001;
XX
DT 14-JAN-1999 (first entry)
XX
DE CD3-epsilon enhancer oligonucleotide #3.
XX
KW CD3-delta gene; Ikaros gene; T cell; progenitor stem cell; leukaemia;
KW differentiation marker; immune system; corpus striatum; AIDS;
KW Alzheimer's disease; ss.
XX
OS Mus sp.
OS Synthetic.
XX
PN US5824770-A.
XX

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PD 20-OCT-1998.
XX
XX 05-JUN-1995; 95US-00465590.
XX
XX 14-SEP-1992; 92US-00946233.
PR 14-SEP-1993; 93US-00121438.
XX
XX 02-MAY-1994; 94US-00238212.
XX
XX (GCHO ) GEN HOSPITAL CORP.
XX
XX Georgopoulos K;
XX
XX WPI; 1998-582621/49.
XX
XX Ikaros poly:peptide(s) - useful for treating disorders of immune system
XX or corpus striatum.
XX
XX Disclosure; Col 27; 111pp; English.
XX
XX The present invention describes a purified peptide having at least one of
XX the following properties: (a) it stimulates transcription of a DNA
XX sequence under the control of a delta A element, an NFkB element or an
XX Ikaros binding oligonucleotide consensus sequence; (b) it binds to any of
XX a delta A element, an NFkB element or an Ikaros binding oligonucleotide
XX consensus sequence; (c) it competitively inhibits the binding of a
XX naturally occurring Ikaros isoform to any of a delta A element, an NFkB
XX element or an Ikaros binding oligonucleotide consensus sequence; (d) it
XX competitively inhibits Ikaros binding to Ikaros responsive elements; or
XX (e) it inhibits protein-protein interactions of transcriptional complexes
XX formed with naturally occurring Ikaros isoforms. The proteins, provided
XX that they stimulate gene transcription under the control of delta A
XX elements, NFkB elements and/or Ikaros-binding oligonucleotides, bind to
XX delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,
XX competitively inhibit binding of naturally occurring Ikaros isoforms to
XX delta A elements, NFkB elements and/or Ikaros-binding oligonucleotides,
XX competitively inhibit Ikaros binding to Ikaros-responsive elements and/or
XX inhibit protein-protein interactions of transcriptional complexes with
XX naturally occurring Ikaros isoforms, can be used to treat immune system
XX disorders, e.g. leukaemia or AIDS, or corpus striatum disorders, e.g.
XX Alzheimer's disease. AAV6975 to AAV67118 represent oligonucleotides
XX given in the present invention
XX
XX Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 3 GGGGG 7

RESULT 43
AAZ86960
ID AAZ86960 standard; DNA; 10 BP.
XX
XX AAZ86960;
AC
XX
XX 16-MAY-2000 (first entry)
DT
XX
XX PCR primer for detection of genetic uniformity of a plant clone.
DE
XX
XX PCR primer; genetic uniformity; plant clone body; detection; ss.
KW
XX
XX Synthetic.
OS
XX
XX JPI0262667-A.
FN
XX
XX 06-OCT-1998.
PD
XX
XX 19-MAR-1997; 97JJP-00106563.
PF
XX
XX

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PR 19-MAR-1997; 97JJP-00106563.
XX
XX (SAOK ) NIPPON SEISHI KK.
XX
XX WPI; 1998-587287/50.
DR
XX
XX New primer - used for the detection of genetic uniformity of a clone
XX plant body.
XX
XX Example 1; Page 5; 7pp; Japanese.
XX
XX This sequence represents an example of the PCR primer of the invention.
XX The primers of the invention consist of 10 bases and have the formula: 5'
XX -NNNN XY XY XY-3'; where: N, X and Y = optional nucleic acid monomers;
XX and N and X as well as N and Y may be nucleic acids having a same base
XX but X and Y are nucleic acids having different bases. The primers are
XX used to distinguish between plant clone bodies at the DNA level, with
XX high sensitivity
XX
XX Sequence 10 BP; 3 A; 0 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 44
AAV32461/C
ID AAV32461 standard; RNA; 10 BP.
XX
XX AAV32461;
AC
XX
XX 11-SEP-1998 (first entry)
DT
XX
XX Oligonucleotide (ac)9T.
DE
XX
XX Phosphoramidite monomer; PM; nucleophile; coupling activator; tetrazole;
XX phosphorodiester linkage; N-methylimidazole; NMI; 4,5-dicyanoimidazole;
XX DNA/RNA hybrid; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH modified_base 1..9
FT /*tag= a
FT /note= "Each nucleotide is a 2'-Aminocytidine"
FT misc_difference 10
FT /*tag= b
FT /note= "deoxythymidine"
FT
XX
XX WO9816540-A1.
PN
XX
XX 23-APR-1998.
PD
XX
XX 08-OCT-1997; 97WO-US015744.
PF
XX
XX 15-OCT-1996; 96US-00730556.
PR
XX
XX 25-SEP-1997; 97US-00937867.
PR
XX
XX (NEXS-) NEXSTAR PHARM INC.
PA
XX
XX Vargeese C, Pieken W, Carter JD, Yegge J;
XX
XX WPI; 1998-261034/23.
DR
XX
XX Preparation of oligonucleotides from phosphoramidite monomers - using
XX coupling activator which is less acidic than tetrazole, e.g., 4,5-
XX dicyanoimidazole or 2-nitroimidazole.
XX
XX

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PS Example 6; Page 18; 49pp; English.
CC The invention provides a method for oligonucleotide synthesis from
CC phosphoramidite monomers (PMs) which involves reacting a PM and a
CC nucleophile in the presence of a coupling activator. The coupling
CC activator chosen is less acidic than, and at least as nucleophilic as,
CC tetrazole. The present oligonucleotide (AC)9T was prepared using either
CC tetrazole, N-methylimidazole (NMI) or 4,5-dicyanimidazole as the
CC coupling activator. The method, which claims to give improved coupling
CC efficiency may be used for the production of oligonucleotides
XX
SQ Sequence 10 BP; 0 A; 9 C; 0 G; 0 T; 0 U; 1 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
DB 9 GGGGG 5

RESULT 45
ID AAV56865/c
XX AAV56865 standard; DNA; 10 BP.
AC AAV56865;
XX
XX
DT 02-DEC-1998 (first entry)
DE Regulatory element containing oligonucleotide #24.
XX
XX Cytokine-responsive regulatory; primer; promoter; detection; isolation;
KW transcriptional control; STAT protein; screening; agonist; ss.
XX
XX Synthetic.
XX
XX US5814517-A.
PN
XX
PD 29-SEP-1998.
XX
XX 27-MAR-1995; 95US-00410779.
XX
XX 14-APR-1994; 94US-00228935.
XX
XX (LIGA-) LIGAND PHARM INC.
PA
XX
XX Lamb IP, Seidel HM;
XX
XX WPI; 1998-541763/46.
XX
XX DNA constructs containing cytokine-responsive regulatory elements -
XX useful in assays for transcription-regulating proteins or gene
XX transcription agonists or antagonists.
XX
XX Claim 11; Col 11; 58pp; English.
XX
XX AAV56842-V56976 and AAV1601-V61631 are oligonucleotides used in the
XX production of constructs comprising a cytokine-responsive regulatory
XX element linked to a promoter which is linked to a heterologous coding
XX sequence so that the coding sequence is under the transcriptional control
XX of the regulatory element and the promoter, where the regulatory element
XX has a nucleotide sequence selected from TTCNNGAA, TTANYTAA, and TTCNYTAA
XX where N is A, T, C or G, and Y = 3 or 4. The constructs can be used to
XX detect or isolate transcription-regulating proteins, e.g. STAT proteins,
XX in a sample by contacting the sample with the construct so that the
XX protein binds to the regulatory element, and detecting or separating
XX the resulting complex. The cells can be used in screening assays for agonists
XX of gene transcription, in which the level of expression of the coding
XX sequence is measured in the presence and absence of a test compound or in
XX the presence of the corresponding cytokine
XX
SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
DB 9 GGGGG 5

RESULT 46
ID AAV50112/c
XX AAV50112 standard; DNA; 10 BP.
AC AAV50112;
XX
XX 21-OCT-1998 (first entry)
DE Yeast tag for NORP gene locus NORP2.
XX
XX Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW eukaryotic cell; antifungal; SAGE tag; gene expression;
XX serial analysis of gene expression; probe; ss.
XX
XX Saccharomyces cerevisiae.
XX Synthetic.
XX
XX WO9832847-A2.
PN
XX
XX 30-JUL-1998.
PD
XX
XX 22-JAN-1998; 98WO-US001216.
PF
XX
XX 23-JAN-1997; 97US-0035917P.
PR
XX
XX (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
PA
XX
XX Velculescu VE, Vogelstein B, Kinzler KW;
XX
XX WPI; 1998-427943/36.
XX
XX Yeast transcriptome - useful for modulating eukaryotic cell, for
XX screening antifungal agents, and for identifying genes in cell cycle
XX progression.
XX
XX Claim 1; Page 23; 44pp; English.
XX
XX Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
XX involved in cell cycle progression selected from the group of
XX nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
XX tags for highly expressed genes and NORF genes are given in AAV50051 to
XX AAV50345. The present invention describes: (1) a method of using yeast
XX genes to modulate the cell cycle which comprises administering to a cell
XX an isolated DNA molecule comprising a yeast gene which is involved in
XX cell cycle progression selected from differentially expressed genes (SAGE
XX tags given in AAV50051 to AAV50345); (2) a method for screening candidate
XX antifungal drugs which comprises contacting a test substance with a yeast
XX cell and monitoring expression of a yeast gene which is involved in cell
XX cycle progression; (3) a method of identifying human genes which are
XX involved in cell cycle progression which comprises hybridizing a probe
XX comprising at least 10 contiguous nucleotides of a yeast gene which is
XX differentially expressed between at least 2 phases selected from the log
XX phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
XX the phase in the cell cycle, where the probe comprises at least 14
XX contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
XX AAV50345), or as an array of probes on a solid support
XX
XX Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 GGGGG 5
Db      10 GGGGG 6

RESULT 47
AAV50068/c
ID AAV50068 standard; DNA; 10 BP.
XX
AC AAV50068;
XX
XX 21-OCT-1998 (first entry)
XX
DE Yeast tag for highly expressed gene locus NORF2.
XX
XX Yeast; Saccharomyces cerevisiae; transcriptome; cell cycle; regulation;
KW eukaryotic cell; antifungal; SAGE tag; gene expression;
KW serial analysis of gene expression; probe; ss.
XX
OS Saccharomyces cerevisiae.
OS Synthetic.
XX
PN WO9832847-A2.
XX
XX 30-JUL-1998.
XX
XX 22-JAN-1998; 98WO-US001216.
XX
XX 23-JAN-1997; 97US-0035917P.
XX
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Velculescu VE, Vogelstein B, Kinzler KW;
XX
XX WPI; 1998-427943/36.
XX
PT Yeast transcriptome - useful for modulating eukaryotic cell, for
PT screening antifungal agents, and for identifying genes in cell cycle
PT progression.
XX
PS Claim 11; Page 21; 44pp; English.
XX
CC Yeast transcriptome is encoded by a DNA molecule comprising a yeast gene
CC involved in cell cycle progression selected from the group of
CC nonannotated ORF (NORF) genes. SAGE (serial analysis gene expression)
CC tags for highly expressed genes and NORF genes are given in AAV50051 to
CC AAV50345. The present invention describes: (1) a method of using yeast
CC genes to modulate the cell cycle which comprises administering to a cell
CC an isolated DNA molecule comprising a yeast gene which is involved in
CC cell cycle progression selected from differentially expressed genes (SAGE
CC tags given in AAV50051 to AAV50345); (2) a method for screening candidate
CC antifungal drugs which comprises contacting a test substance with a yeast
CC cell and monitoring expression of a yeast gene which is involved in cell
CC cycle progression; (3) a method of identifying human genes which are
CC involved in cell cycle progression which comprises hybridizing a probe
CC comprising at least 10 contiguous nucleotides of a yeast gene which is
CC differentially expressed between at least 2 phases selected from the log
CC phase, the S phase and the G2/M phase; and (4) a probe for ascertaining
CC the phase in the cell cycle, where the probe comprises at least 14
CC contiguous nucleotides of a NORF gene (SAGE tags given in AAV50051 to
CC AAV50345), or as an array of probes on a solid support
XX
SQ Sequence 10 BP; 0 A; 7 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      10 GGGGG 6

RESULT 48
AAV35941/c
ID AAV35941 standard; DNA; 10 BP.
XX
XX AAV35941;
XX
XX 26-AUG-1998 (first entry)
XX
DE Primer used in RAPD assay of the invention.
XX
XX Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
KW muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
OS Synthetic.
OS Sus sp.
XX
PN WO9815837-A1.
XX
XX 16-APR-1998.
XX
XX 07-OCT-1997; 97WO-GB002741.
XX
XX 07-OCT-1996; 96GB-00020904.
XX
XX 18-FEB-1997; 97GB-00003350.
XX
XX 20-MAR-1997; 97GB-00005796.
XX
XX 09-SEP-1997; 97GB-00019002.
XX
PA (MEAT-) MEAT & LIVESTOCK COMMISSION.
XX
PI Maltin CA, Steven J, Warkup CC;
XX
XX WPI; 1998-240968/21.
XX
XX Assay for alleles or muscle fibre composition characteristic of Duroc
XX type pigs - comprises determination of genotype or muscle fibre
XX properties, used to identify animals for breeding programs and to assess
XX meat quality.
XX
PS Example 3; Page 33; 56pp; English.
XX
CC PCR primers AAV35877-996 were used in a rapid amplification of
CC polymorphic DNA (RAPD) reaction in the assay of the invention. This assay
CC is used to determine if an animal has an allele for, or muscle fibre
CC composition (MFC) characteristic of, the Duroc pig. Duroc pigs produce
CC meat of superior quality (particularly tenderness) but are normally less
CC efficient feed converters and fatter than other types. The assay
CC comprises analysing a tissue sample to determine if the genotype
CC comprises the allele, and genetic features typical of animals with Duroc-
CC type MFC are present. The method is used to select animals that have
CC Duroc characteristics for use in breeding programmes (to develop the
CC animals with Duroc pig characteristics), and to assess meat quality
XX
SQ Sequence 10 BP; 1 A; 6 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
Db      10 GGGGG 6

RESULT 49
AAV04582
ID AAV04582 standard; DNA; 10 BP.
XX
XX AAV04582;
XX
XX 07-APR-1999 (first entry)
XX
XX Inverted repeat from snoRNA forming a stem structure.
XX

```

KW Small nucleolar RNA gene; snRNA; maize; promoter; RNA production;  
KW RNA stability; small non-translated RNA; intergenic region;  
XX inverted repeat; ds.  
XX Unidentified.  
XX OS  
XX PN EP887405-A1.  
XX PD 30-DEC-1998.  
XX PF 25-JUN-1997; 97EP-00401480.  
XX PR 25-JUN-1997; 97EP-00401480.  
XX PA (GENE-) GENE SHEARS PTY LTD.  
XX PI Brown JWS, Leader DJ;  
XX WPI; 1999-047872/05.  
XX DR  
XX PT Producing stabilised RNA molecules - using a DNA precursor comprising  
XX plant small nucleolar RNA stabilising sequences.  
XX PS Disclosure; Page 6; 98pp; English.  
XX CC The present sequence represents an inverted repeat from small nucleolar  
CC RNA (snRNA) sequences. The present sequence forms a stem structure in  
CC the protein binding sites of snRNAs, and prevents overdigestion by 3',  
CC and 5' exonucleases. Plant snRNA genes enable production of multiple  
CC stabilised RNA from a single promoter in a splicing-independent manner,  
CC and allow the production of RNA from intron or non-intron sequences. The  
CC present sequence is used in the method of the invention. The  
CC specification describes a method for producing small non-translated RNA  
CC molecules, which comprises introducing a precursor DNA containing one or  
CC a cluster of coding sequences into a plant or yeast cell. Each coding  
CC sequence comprises a non-translated RNA sequence to be stabilised, which  
CC is capable of functionally interacting with a cellular component and  
CC stabilising sequences comprising at least one protein binding site. The  
CC stabilised RNA units are transcribed by the cell's endogenous processing  
CC machinery. The process is useful for qualitatively and quantitatively  
CC enhancing the production and stability of RNA molecules, especially non-  
CC translated RNA e.g. ribozymes and antisense RNA. The nucleic acid  
CC molecules are useful as probes or primers for identification of snRNA  
CC sequences and intergenic regions  
XX SQ Sequence 10 BP; 1 A; 0 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 3 GGGGG 7  
RESULT 50  
AA04583/c  
ID AAX04583 standard; DNA; 10 BP.  
XX AC AAX04583;  
XX DT 07-APR-1999 (first entry)  
XX DE Inverted repeat from snRNA forming a stem structure.  
XX KW Small nucleolar RNA gene; snRNA; maize; promoter; RNA production;  
KW RNA stability; small non-translated RNA; intergenic region;  
XX inverted repeat; ds.  
XX OS Unidentified.  
XX PN EP887405-A1.

XX 30-DEC-1998.  
XX PF 25-JUN-1997; 97EP-00401480.  
XX PR 25-JUN-1997; 97EP-00401480.  
XX PA (GENE-) GENE SHEARS PTY LTD.  
XX PI Brown JWS, Leader DJ;  
XX WPI; 1999-047872/05.  
XX DR  
XX PT Producing stabilised RNA molecules - using a DNA precursor comprising  
XX plant small nucleolar RNA stabilising sequences.  
XX PS Disclosure; Page 6; 98pp; English.  
XX CC The present sequence represents an inverted repeat from small nucleolar  
CC RNA (snRNA) sequences. The present sequence forms a stem structure in  
CC the protein binding sites of snRNAs, and prevents overdigestion by 3',  
CC and 5' exonucleases. Plant snRNA genes enable production of multiple  
CC stabilised RNA from a single promoter in a splicing-independent manner,  
CC and allow the production of RNA from intron or non-intron sequences. The  
CC present sequence is used in the method of the invention. The  
CC specification describes a method for producing small non-translated RNA  
CC molecules, which comprises introducing a precursor DNA containing one or  
CC a cluster of coding sequences into a plant or yeast cell. Each coding  
CC sequence comprises a non-translated RNA sequence to be stabilised, which  
CC is capable of functionally interacting with a cellular component and  
CC stabilising sequences comprising at least one protein binding site. The  
CC stabilised RNA units are transcribed by the cell's endogenous processing  
CC machinery. The process is useful for qualitatively and quantitatively  
CC enhancing the production and stability of RNA molecules, especially non-  
CC translated RNA e.g. ribozymes and antisense RNA. The nucleic acid  
CC molecules are useful as probes or primers for identification of snRNA  
CC sequences and intergenic regions  
XX SQ Sequence 10 BP; 1 A; 0 C; 5 G; 4 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 3 GGGGG 7  
RESULT 50  
AA04583/c  
ID AAX04583 standard; DNA; 10 BP.  
XX AC AAX04583;  
XX DT 07-APR-1999 (first entry)  
XX DE Inverted repeat from snRNA forming a stem structure.  
XX KW Small nucleolar RNA gene; snRNA; maize; promoter; RNA production;  
KW RNA stability; small non-translated RNA; intergenic region;  
XX inverted repeat; ds.  
XX OS Unidentified.  
XX PN EP887405-A1.

XX 30-DEC-1998.  
XX PF 25-JUN-1997; 97EP-00401480.  
XX PR 25-JUN-1997; 97EP-00401480.  
XX PA (GENE-) GENE SHEARS PTY LTD.  
XX PI Brown JWS, Leader DJ;  
XX WPI; 1999-047872/05.  
XX DR  
XX PT Producing stabilised RNA molecules - using a DNA precursor comprising  
XX plant small nucleolar RNA stabilising sequences.  
XX PS Disclosure; Page 6; 98pp; English.  
XX CC The present sequence represents an inverted repeat from small nucleolar  
CC RNA (snRNA) sequences. The present sequence forms a stem structure in  
CC the protein binding sites of snRNAs, and prevents overdigestion by 3',  
CC and 5' exonucleases. Plant snRNA genes enable production of multiple  
CC stabilised RNA from a single promoter in a splicing-independent manner,  
CC and allow the production of RNA from intron or non-intron sequences. The  
CC present sequence is used in the method of the invention. The  
CC specification describes a method for producing small non-translated RNA  
CC molecules, which comprises introducing a precursor DNA containing one or  
CC a cluster of coding sequences into a plant or yeast cell. Each coding  
CC sequence comprises a non-translated RNA sequence to be stabilised, which  
CC is capable of functionally interacting with a cellular component and  
CC stabilising sequences comprising at least one protein binding site. The  
CC stabilised RNA units are transcribed by the cell's endogenous processing  
CC machinery. The process is useful for qualitatively and quantitatively  
CC enhancing the production and stability of RNA molecules, especially non-  
CC translated RNA e.g. ribozymes and antisense RNA. The nucleic acid  
CC molecules are useful as probes or primers for identification of snRNA  
CC sequences and intergenic regions  
XX SQ Sequence 10 BP; 4 A; 5 C; 0 G; 1 T; 0 U; 0 Other;  
Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGGG 5  
Db 8 GGGGG 4  
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Job time : 258.4 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 04:56:02 ; Search time 2222.4 Seconds  
(without alignments)  
81.983 Million cell updates/sec

Title: GGGGG  
Perfect score: 5  
Sequence: 1 99999 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 156772

Minimum DB seq length: 10  
Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : EST:\*

1: gb\_est1: \*  
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5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gse1: \*  
9: gb\_gse2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 20	5	100.0	13	5	BM395395 50072-2-8
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 preparation can be found in Chilcoat and Turkewitz (2001)  
 Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

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Qy 1 GGGGG 5

Db 10 GGGGG 6

## RESULT 2

BM396043

LOCUS BM396043 10 bp mRNA linear EST 17-JAN-2002  
 DEFINITION 5009-0-15-H12.t.2 Chilcoat/Turkewitz cDNA (large fraction)

ACCESSION BM396043

VERSION BM396043.1

KEYWORDS EST.

## SOURCE

Tetrahymena thermophila

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 10)

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,

Frankel, J. and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

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Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

## FEATURES

source

1..10

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preparation can be found in Chilcoat and Turkewitz (2001)

Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

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Qy 1 GGGGG 5

Db 5 GGGGG 9

## RESULT 3

CL435808/c

LOCUS CL435808 10 bp DNA linear GSS 18-MAR-2004  
 DEFINITION PST1453-NR.seq MCB1 Mus musculus genomic clone PST1453-NR.seq

similar to Racgap1, genomic survey sequence.

ACCESSION CL435808

VERSION CL435808.1

KEYWORDS GSS.

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 10)

Hicks, G.G.

www.EScells.ca

Unpublished (2002)

Contact: Hicks GG

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ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada

Tel: 204 787 2133

Fax: 204 787 2190

Email: hicks@cc.umanitoba.ca

U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional

sequence information and target gene cloning can be generated. ES

cell line harboring insertion mutation of target gene is available.

Sequence analysis available from

http://140.193.242.7/esdb/public\_search\_frame.php?PST=PST1453-NR.se

q

Class: Gene Trap.

Location/Qualifiers

1..10

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## ORIGIN

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 8 GGGGG 4

## RESULT 4

CL436345

LOCUS

DEFINITION

PST2785-NR.Seg MCB1 Mus musculus genomic clone PST2785-NR.Seg

similar to Sfr1, genomic survey sequence.

ACCESSION

CL436345

VERSION

CL436345.1

KEYWORDS

GSS.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 10)

Hicks, G.G.

www.EScells.ca

Unpublished (2002)

Contact: Hicks GG

Mammalian Functional Genomics Centre

Manitoba Institute of Cell Biology, University of Manitoba

ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada

Tel: 204 787 2133

Fax: 204 787 2190

Email: hicks@cc.umanitoba.ca

U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional

sequence information and target gene cloning can be generated. ES

cell line harboring insertion mutation of target gene is available.

Sequence analysis available from

http://140.193.242.7/esdb/public\_search\_frame.php?PST=PST2785-NR.Se

q

Class: Gene Trap.

Location/Qualifiers

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source
1..10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST2785-NR.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosV1"

ORIGIN
Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 5
CL438120/c
LOCUS          CL438120
DEFINITION    PST6843-NL.Seq MICB1 Mus musculus genomic clone PST6843-NL.Seq,
genomic survey sequence.
ACCESSION     CL438120
VERSION       CL438120.1 GI:45574363
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hicks,G.G.
www.Escells.ca
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST6843-NL.Se
q
Class: Gene Trap.
Location/Qualifiers
1..10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST6843-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosV1"

FEATURES
source
1..10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST6843-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosV1"

ORIGIN
Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 6
CL439043
LOCUS          CL439043
DEFINITION    PST8576-NR.Seq MICB1 Mus musculus genomic clone PST8576-NR.Seq,
genomic survey sequence.
ACCESSION     CL439043
VERSION       CL439043.1 GI:45576187
KEYWORDS      GSS.
SOURCE        Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Hicks,G.G.
www.Escells.ca
Unpublished (2002)
Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, University of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional
sequence information and target gene cloning can be generated. ES
cell line harboring insertion mutation of target gene is available.
Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST8576-NR.Se
q
Class: Gene Trap.
Location/Qualifiers
1..10
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST8576-NR.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeosV1"

ORIGIN
Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 7
AJ657108
LOCUS          AJ657108
DEFINITION    AJ657108 KN277 Sus scrofa cDNA clone C0005196_K06, mRNA sequence.
ACCESSION     AJ657108
VERSION       AJ657108.1 GI:49341140
KEYWORDS      EST.
SOURCE        Sus scrofa (pig)
ORGANISM      Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
Contact: Anderson SI
Genomics and Bioinformatics
```

Roslin Institute  
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross\_match with the -minscore 20 and -minmatch 12 options. Vector:pBluescriptII(SK+) R. Site1: EcoRI R. Site2: NotI 5' Seq Primer M13F Normalised library constructed from pooled early embryos, from 8- cell stage to blastocysts. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.

## FEATURES

source

1. .11  
Location/Qualifiers  
/organism="Sus scrofa"  
/mol\_type="mRNA"  
/db\_xref="taxon:9823"  
/clone="C0005196\_K06"  
/tissue\_type="embryo"  
/clone\_lib="KN277"  
/note="Vector: pBluescriptII(SK+); Site 1: EcoRI; Site 2: NotI; Single pass sequencing. Normalised library constructed from pooled early embryos, from 8-cell stage to blastocysts."

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 1 GGGGG 5

## RESULT 8

BM395228/c

LOCUS

50072-2-8-B05.r.1 Chilcoat/Turkewitz cDNA (large fraction).  
Tetrahymena thermophila cDNA, mRNA sequence.

## ACCESSION

BM395228

## KEYWORDS

EST.

## SOURCE

Tetrahymena thermophila

Tetrahymena thermophila

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;

Hymenostomatida; Tetrahymenina; Tetrahymena.

1 (bases 1 to 11)

Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,

Frankel, J., and Klobutcher, L.

EST from Tetrahymena thermophila, strain CU428.1, growing cells

Unpublished (2002)

Contact: Turkewitz AP

Molecular Genetics and Cell Biology

University of Chicago

920 E. 58th Street, Chicago, IL 60637, USA

Tel: 773 702 4374

Fax: 773 702 3172

Email: apturkew@midway.uchicago.edu

Seq primer: T3.

## FEATURES

source

1. .11  
Location/Qualifiers  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library preparation can be found in Chilcoat and Turkewitz (2001) Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 9 GGGGG 5

## RESULT 9

CF543031

LOCUS

DEFINITION

CF543031 11 bp mRNA linear EST 22-SEP-2003

SO15532-024-030-P02-SP6 MP12-ADIS-024-leaf Beta vulgaris cDNA clone

024-030-P02 5-PRIME, mRNA sequence.

## ACCESSION

CF543031

## VERSION

CF543031.1

## KEYWORDS

Beta vulgaris

## SOURCE

Beta vulgaris

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

1 (bases 1 to 11)

## AUTHORS

Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,

Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.

and Radelof, U.

Construction of a 'unigene' cDNA clone set by oligonucleotide

fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

## JOURNAL

MEDLINE

22362189

## COMMENT

12472698

Contact: Weishaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 11 Std Error: 0.00

Plate: 30 row: P column: 02

Seq primer: SP6.

## FEATURES

source

1. .11  
Location/Qualifiers  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding line)"  
/db\_xref="GABI:936732"  
/db\_xref="taxon:161934"  
/clone="024-030-P02"  
/tissue\_type="leaf"  
/lab\_host="EMPH108"  
/clone\_lib="MP12-ADIS-024-leaf"  
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Binbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-SalI-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-BEET project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database:http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 7; Length 11;  
Best Local Similarity 100.0%; Pred. No. 9.6e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 1 GGGGG 5

## RESULT 10

BQ585390/c

LOCUS

BQ585390 12 bp mRNA linear EST 06-DEC-2002

```

DEFINITION S011420-024-001-G08-SP6R MP1Z-ADIS-024-inflorescence Beta vulgaris
ACCESSION BQ585330
VERSION BQ585330.1 GI:261114972
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1 (bases 1 to 12)
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
TITLE 1 (bases 1 to 12)
AUTHORS Drwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
JOURNAL Construction of a 'unigene' cDNA clone set by oligonucleotide
MEDLINE fingerprinting allows access to 25 000 potential sugar beet genes
PUBMED Plant J. 32 (5), 845-857 (2002)
COMMENT Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 12 Std Error: 0.00
Plate: 1 row: G column: 08
Seq primer: SP6r; ATTAGGTGACACTATAGAGA.
FEATURES
source
location/Qualifiers
1..12
/organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:181317"
/db_xref="taxon:161934"
/cclone="024-001-G08"
/tissue_type="inflorescence"
/lab_host="EMDH108"
/cclone_lib="MP1Z-ADIS-024-inflorescence"
/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinfanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match 100.0%; Score 5; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGG 5
Db 12 GGGGG 8
RESULT 11
CA851641/
LOCUS D15H12_024 16.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION cDNA clone D15H12 5', mRNA sequence.
ACCESSION CA851641
VERSION CA851641.1 GI:33388434
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

```

```

rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 12)
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean
JOURNAL infected by the soybean cyst nematode
COMMENT Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
FEATURES
source
location/Qualifiers
1..12
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/cclone="D15H12"
/tissue_type="Roots"
/dev_stage="Seedlings"
/cclone_lib="cDNA Peking library 2, 4 day SCN3"
/notes="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."
ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGG 5
Db 11 GGGGG 7
RESULT 12
CA851649/
LOCUS D16A08 B20 02.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION cDNA clone D16A08 5', mRNA sequence.
ACCESSION CA851649
VERSION CA851649.1 GI:33388442
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 12)
AUTHORS Alkharouf,N.W., Khan,R. and Matthews,B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean
JOURNAL infected by the soybean cyst nematode
COMMENT Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.
FEATURES
source
location/Qualifiers
1..12
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/cclone="D16A08"
/tissue_type="Roots"

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/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 12 GGGGG 8

RESULT 13
AJ600541
LOCUS
DEFINITION
17 pUC8 PstI Rice Etiolated Leaf Genomic Library Oryza sativa
(indica cultivar-group) genomic clone RG143, genomic survey
sequence.
ACCESSION
AJ600541
VERSION
AJ600541.1 GI:3435350
KEYWORDS
GSS.
SOURCE
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaeae; Oryza.
REFERENCE
1 (bases 1 to 12)
McCouch, S.R., Kochert, G., Yu, Z.H., Wang, Z.Y., Khush, G.S.,
Coffman, W.R. and Tanksley, S.D.
Molecular mapping of rice chromosomes
Theor. Appl. Genet. 76, 815-829 (1988)
Contact: Susan R. McCouch
Cornell University
Dept. Plant Breeding, Ithaca, NY 14853-1901, USA
Tel: 607 255 0420
Fax: 607 255 6683
Email: srm4@cornell.edu
For mapping information, additional citations and other related
information concerning this probe, please refer to the RiceGenes
database at
http://ars-genome.cornell.edu/cgi-bin/WebAce/webace?db=ricegenes&
class=MarkerObject&RG143
DNA Sequencing was done by the DOE Plant
Research Lab, Michigan State University. Informatics was done at
the Computational Biology Centers, University of Minnesota.
PCR Primers
FORWARD: M13 Forward
BACKWARD: M13 Reverse
Insert Length: 1 Std Error: 0.00
Seq primer: M13 -21 dye primer
Class: RFLP probe.
Location/Qualifiers
1..12
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="IR36"
/db_xref="RiceGenes:RG143"
/db_xref="taxon:39946"
/clone="RG143"
/clone_lib="pUC8 PstI Rice Etiolated Leaf Genomic Library"
/note="Vector: pUC8; Total leaf DNA was digested with the
restriction enzyme PstI. DHS-alpha bacterial cells were
then transformed with ligated plasmid. Random genomic
clones were given consecutive numbers (RG-#) as they were
prepared. The same numbers were then used to designate
loci in the genome as detected by genetic mapping."

ORIGIN
Query Match      100.0%; Score 5; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

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Qy 1 GGGGG 5
    |||||
Db 7 GGGGG 11

RESULT 14
AJ600541
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, right border, clone
508E06, genomic survey sequence.
ACCESSION
AJ600541
VERSION
AJ600541.1 GI:37950169
KEYWORDS
GSS; right border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
1
Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
22363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 12)
Balzergue, S.
Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
1..12
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassilewskija"
/db_xref="taxon:3702"
/clone="508E06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1..12
/note="T-DNA flanking sequence
right border"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 5 GGGGG 9

RESULT 15
AJ600549
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, right border, clone
508F08, genomic survey sequence.
ACCESSION
AJ600549
VERSION
AJ600549.1 GI:37950177


```

```

KEYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (chale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE
AUTHORS
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepointec, B., Caboche, M. and Lecharny, A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE
22363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 12)
AUTHORS
Balzerque, S.
TITLE
Direct Submission
JOURNAL
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program "Genoplante" (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
Location/Qualifiers
source
1..12
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassilewskija"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1..12
/note="T-DNA flanking sequence
right border"
ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
|||||
Db 5 GGGGG 9

RESULT 16
BG810452/c 13 bp mRNA linear EST 22-MAY-2001
LOCUS
DEFINITION
mgct006xc07f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe
grisea cDNA clone mgct006xc07f 5', mRNA sequence.
ACCESSION
BG810452
VERSION
BG810452.1 GI:14181432
KEYWORDS
EST.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 13)
AUTHORS
Choi, W. and Dean, R.A.
TITLE
Construction and sequence analysis of an appressorium stage cDNA
library in the rice blast fungus, Magnaporthe grisea
JOURNAL
Unpublished (2001)
COMMENT
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University

GSS; right border; T-DNA flanking sequence.
Arabidopsis thaliana (chale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE
AUTHORS
Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepointec, B., Caboche, M. and Lecharny, A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE
22363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 12)
AUTHORS
Balzerque, S.
TITLE
Direct Submission
JOURNAL
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program "Genoplante" (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
Location/Qualifiers
source
1..12
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassilewskija"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1..12
/note="T-DNA flanking sequence
right border"
ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
|||||
Db 5 GGGGG 9

RESULT 16
BG810452/c 13 bp mRNA linear EST 22-MAY-2001
LOCUS
DEFINITION
mgct006xc07f Magnaporthe grisea Appressorium Stage cDNA Magnaporthe
grisea cDNA clone mgct006xc07f 5', mRNA sequence.
ACCESSION
BG810452
VERSION
BG810452.1 GI:14181432
KEYWORDS
EST.
SOURCE
Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM
Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 13)
AUTHORS
Choi, W. and Dean, R.A.
TITLE
Construction and sequence analysis of an appressorium stage cDNA
library in the rice blast fungus, Magnaporthe grisea
JOURNAL
Unpublished (2001)
COMMENT
Contact: Ralph A. Dean
Fungal Genomics Laboratory
North Carolina State University

Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: T3 primer (AATTAACCTCCTCAAGGG).
Location/Qualifiers
source
1..13
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="70-15"
/db_xref="taxon:148305"
/clone_lib="mgct006xc07f"
/dev_stage="Germinated conidia on appressorium-inductive
surface"
/clone_lib="Magnaporthe grisea Appressorium Stage cDNA"
/note="Vector: pBlueScript SK(+). Vector: Site 1: EcoRI;
Site 2: XhoI; The appressorium formation-specific cDNA
library was constructed from conidia germinated for 5-8 hr
on an inductive surface. The library contains over 55,000
clones with average insert size of 1.5 kbp."
ORIGIN
Query Match 100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
|||||
Db 11 GGGGG 7

RESULT 17
BG926067/c 13 bp mRNA linear EST 06-NOV-2001
LOCUS
DEFINITION
HNC23-1-E8.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
sequence.
ACCESSION
BG926067
VERSION
BG926067.1 GI:14320590
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 13)
AUTHORS
Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,
Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
Lark, W.W.
TITLE
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
JOURNAL
Osteoarthr. Cartil. 9 (7), 641-653 (2001)
MEDLINE
21482651
PUBMED
11597177
COMMENT
Contact: Sanjay Kumar
Email: sanjay.kumar-l@sk.com
Seq primer: T7.
Location/Qualifiers
source
1..13
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT 1; Site_1: SalI; Site_2: NotI;
Directional"
ORIGIN

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Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      7 GGGGG 3

RESULT 18
BM394028/c
LOCUS      BM394028      13 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION      50072-2-12-E02.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM394028
VERSION
KEYWORDS
SOURCE
ORGANISM      Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz A.P., Karrer K.M., Jahn C., Orlas E., Kirk K.E.,
Frankel J. and Klobutcher L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 3172
Fax: 773 702 3174
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
      source
      1..13
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: BlueScript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      7 GGGGG 3

RESULT 19
BM395265/c
LOCUS      BM395265      13 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION      50072-2-8-C08.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM395265
VERSION
KEYWORDS
SOURCE
ORGANISM      Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz A.P., Karrer K.M., Jahn C., Orlas E., Kirk K.E.,
Frankel J. and Klobutcher L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 3172
Fax: 773 702 3174
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
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      1..13
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: BlueScript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      11 GGGGG 7

RESULT 19
BM395265/c
LOCUS      BM395265      13 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION      50072-2-8-C08.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM395265
VERSION
KEYWORDS
SOURCE
ORGANISM      Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz A.P., Karrer K.M., Jahn C., Orlas E., Kirk K.E.,
Frankel J. and Klobutcher L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 3172
Fax: 773 702 3174
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
      source
      1..13
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: BlueScript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      13 GGGGG 9

RESULT 20
BM395395/c
LOCUS      BM395395      13 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION      50072-2-8-H07.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM395395
VERSION
KEYWORDS
SOURCE
ORGANISM      Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz A.P., Karrer K.M., Jahn C., Orlas E., Kirk K.E.,
Frankel J. and Klobutcher L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 3172
Fax: 773 702 3174
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
      source
      1..13
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: BlueScript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      12 GGGGG 8

RESULT 20
BM395395/c
LOCUS      BM395395      13 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION      50072-2-8-H07.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM395395
VERSION
KEYWORDS
SOURCE
ORGANISM      Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz A.P., Karrer K.M., Jahn C., Orlas E., Kirk K.E.,
Frankel J. and Klobutcher L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 3172
Fax: 773 702 3174
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
      source
      1..13
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: BlueScript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      13 GGGGG 9

```

```

Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
      source
      1..13
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: BlueScript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      12 GGGGG 8

RESULT 20
BM395395/c
LOCUS      BM395395      13 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION      50072-2-8-H07.r.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION      BM395395
VERSION
KEYWORDS
SOURCE
ORGANISM      Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS      Turkewitz A.P., Karrer K.M., Jahn C., Orlas E., Kirk K.E.,
Frankel J. and Klobutcher L.
TITLE      EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL      Unpublished (2002)
COMMENT      Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
      source
      1..13
      /organism="Tetrahymena thermophila"
      /mol_type="mRNA"
      /strain="CU428.1"
      /db_xref="taxon:5911"
      /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
      /note="Vector: BlueScript2 SK+; Details on library
      preparation can be found in Chilcoat and Turkewitz (2001)
      Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
      |||||
Db      13 GGGGG 9

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RESULT 21
BQ595080
LOCUS      13 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION Beta vulgaris
ACCESSION BQ595080
VERSION   BQ595080.1 GI:26124663
KEYWORDS  EST.
SOURCE    Beta vulgaris
ORGANISM  Beta vulgaris
REFERENCE
AUTHORS   Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
          Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
          and Radloff,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
          fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
MEDLINE   22362189
PUBMED    12472698
COMMENT   Contact: Weishaar B
          ADIS DNA core facility at MPIZ
          Max-Planck-Institute for Plant Breeding Research
          Carl-von-Linne Weg 10, 50829 Koeln, Germany
          Fax: 00492215062851
          Email: weishaar@mpiz-koeln.mpg.de
          Insert Length: 13 Std Error: 0.00
          Plate: 23 row: M column: 14
          Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES
source
1. .13
   /organism="Beta vulgaris"
   /mol_type="mRNA"
   /cultivar="KWS2320 (double haploid, monogerm breeding
   line)"
   /db_xref="taxon:161934"
   /clone="024-023-M14"
   /lab_host="EMDH10B"
   /tissue_type="developing root"
   /clone_lib="MPIZ-ADIS-024-developing root"
   /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
   cDNA library from sugar beet. Library provided by KWS
   Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
   b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
   orientation:
   SP6-Sali-CCACGGGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
   Sequencing granted in the context of the GABI-Beet
   project, local PI: Dr. Katharina Schneider, coordinator:
   Prof. Christian Jung; Sequence submission managed by
   RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      100.0%; Score 5; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 22
AJ587920
LOCUS      13 bp      DNA      linear      GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
          340A06, genomic survey sequence.
ACCESSION AJ587920
VERSION   AJ587920.1 GI:37937544
KEYWORDS  GSS; left border; T-DNA flanking sequence.

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```

SOURCE
ORGANISM  Arabidopsis thaliana (thale cress)
          Arabidopsis thaliana
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
          rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
AUTHORS   1 Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
          Chauvin,S., Bechtold,N., Cruaud,C., Derose,R., Pelletier,G.,
          Lepiniec,L., Caboche,M. and Leclarny,A.
          T-DNA integration into the Arabidopsis genome depends on sequences
          of pre-insertion sites
JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE   22363535
PUBMED    12446565
REFERENCE
2 (bases 1 to 13)
AUTHORS   Balzerque,S.
TITLE     Direct Submission
JOURNAL   Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
          Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT   PCR was performed on DNA from transformants of Arabidopsis thaliana
          plants from INRA (Versailles). The DNA fragment(s) resulting from
          the PCR were directly sequenced from the left or the right border
          to determine the genomic sequence flanking the insertion. T-DNA
          derived sequences were removed. Information to order the
          corresponding mutant line and a link to a database providing a
          graphical display of the insertion site are available at
          http://dbgap.versailles.inra.fr/publiclines/. This sequence has
          been generated in the framework of the French plant genomics
          program 'Genoplante' (http://www.genoplante.com and
          http://genoplante-info.inbio.gen.fr).
FEATURES
source
1. .13
   /organism="Arabidopsis thaliana"
   /mol_type="genomic DNA"
   /cultivar="Wassilewskija"
   /db_xref="taxon:3702"
   /clone_lib="340A06"
   /clone="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1. .13
             /note="T-DNA flanking sequence
             left border"
ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 4 GGGGG 8

RESULT 23
BM392794
LOCUS      14 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION BM392794
VERSION   BM392794.1 GI:18192847
KEYWORDS  EST.
SOURCE    Tetrahymena thermophila
ORGANISM  Tetrahymena thermophila
          Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
          Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
AUTHORS   1 Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
          Frankel,J. and Klobutcher,L.
          EST from Tetrahymena thermophila, strain CU428.1, growing cells
          Unpublished (2002)
JOURNAL   Contact: Turkewitz AP
          Molecular Genetics and Cell Biology
          University of Chicago
          920 E. 58th Street, Chicago, IL 60637, USA

```

```

Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
    source
        Location/Qualifiers
            1..14
                /organism="Tetrahymena thermophila"
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                /strain="CU428.1"
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                /clone_lib="Chilcoat/Turkewitz cDNA (small fraction)"
                /note="Vector: BlueScript2 SK+; Details on library
                preparation can be found in Chilcoat and Turkewitz (2001)
                Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
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    Best Local Similarity 100.0%; Pred. No. 9.5e+06;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 24
BM394089
LOCUS      50072-2-12-H08.f.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM394089
VERSION     1
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
    ORGANISM
        Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /note="Vector: BlueScript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
            Proc. Natl. Acad. Sci USA, 98: 8709-8713."
    AUTHORS  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
    TITLE    EST from Tetrahymena thermophila, strain CU428.1, growing cells
    JOURNAL  Unpublished (2002)
    COMMENT  Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
    FEATURES
        source
            Location/Qualifiers
                1..14
                    /organism="Tetrahymena thermophila"
                    /mol_type="mRNA"
                    /strain="CU428.1"
                    /db_xref="taxon:5911"
                    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                    /note="Vector: BlueScript2 SK+; Details on library
                    preparation can be found in Chilcoat and Turkewitz (2001)
                    Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
    Query Match      100.0%; Score 5; DB 4; Length 14;
    Best Local Similarity 100.0%; Pred. No. 9.5e+06;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 25
BM395308
LOCUS      50072-2-8-E04.f.2 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM395308
VERSION     1
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
    ORGANISM
        Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /note="Vector: BlueScript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
            Proc. Natl. Acad. Sci USA, 98: 8709-8713."
    AUTHORS  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
    TITLE    EST from Tetrahymena thermophila, strain CU428.1, growing cells
    JOURNAL  Unpublished (2002)
    COMMENT  Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
    FEATURES
        source
            Location/Qualifiers
                1..14
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                    /mol_type="mRNA"
                    /strain="CU428.1"
                    /db_xref="taxon:5911"
                    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                    /note="Vector: BlueScript2 SK+; Details on library
                    preparation can be found in Chilcoat and Turkewitz (2001)
                    Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
    Query Match      100.0%; Score 5; DB 4; Length 14;
    Best Local Similarity 100.0%; Pred. No. 9.5e+06;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 8 GGGGG 12

RESULT 26
BM395363/c
LOCUS      50072-2-8-G05.r.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM395363
VERSION     1
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
    ORGANISM
        Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /note="Vector: BlueScript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
            Proc. Natl. Acad. Sci USA, 98: 8709-8713."
    AUTHORS  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
    TITLE    EST from Tetrahymena thermophila, strain CU428.1, growing cells
    JOURNAL  Unpublished (2002)
    COMMENT  Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
    FEATURES
        source
            Location/Qualifiers
                1..14
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                    /strain="CU428.1"
                    /db_xref="taxon:5911"
                    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                    /note="Vector: BlueScript2 SK+; Details on library
                    preparation can be found in Chilcoat and Turkewitz (2001)
                    Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
    Query Match      100.0%; Score 5; DB 4; Length 14;
    Best Local Similarity 100.0%; Pred. No. 9.5e+06;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 8 GGGGG 12

RESULT 27
BM395363
LOCUS      50072-2-8-G05.r.1 Chilcoat/Turkewitz cDNA (large fraction)
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM395363
VERSION     1
KEYWORDS    EST.
SOURCE      Tetrahymena thermophila
    ORGANISM
        Tetrahymena thermophila
            Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
            Hymenostomatida; Tetrahymenina; Tetrahymena.
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /note="Vector: BlueScript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
            Proc. Natl. Acad. Sci USA, 98: 8709-8713."
    AUTHORS  Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
            Frankel,J. and Klobutcher,L.
    TITLE    EST from Tetrahymena thermophila, strain CU428.1, growing cells
    JOURNAL  Unpublished (2002)
    COMMENT  Contact: Turkewitz AP
            Molecular Genetics and Cell Biology
            University of Chicago
            920 E. 58th Street, Chicago, IL 60637, USA
            Tel: 773 702 4374
            Fax: 773 702 3172
            Email: apturkew@midway.uchicago.edu
            Seq primer: T3.
    FEATURES
        source
            Location/Qualifiers
                1..14
                    /organism="Tetrahymena thermophila"
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                    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                    /note="Vector: BlueScript2 SK+; Details on library
                    preparation can be found in Chilcoat and Turkewitz (2001)
                    Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
    Query Match      100.0%; Score 5; DB 4; Length 14;
    Best Local Similarity 100.0%; Pred. No. 9.5e+06;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 8 GGGGG 12

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/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 14 GGGGG 10

## RESULT 27

BQ585808  
LOCUS  
DEFINITION  
S014470-024-014-A01-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
024-014-A01 5-PRIME, mRNA sequence.

ACCESSION  
VERSION  
BQ585808.1 GI:26115390  
KEYWORDS  
EST.

SOURCE  
Beta vulgaris

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

## AUTHORS

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

## JOURNAL

22362189

## MEDLINE

12472698

## COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 14 row: A column: 01  
Seq primer: SP6; CATACGATTAGTGACACTATAG.

## FEATURES

Location/Qualifiers

1..14  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
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line)"  
/db\_xref="GABI:187232"  
/db\_xref="taxon:161934"  
/clone="024-014-A01"  
/tissue\_type="leaf"  
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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database:http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 5 GGGGG 9

## RESULT 28

BQ593114  
LOCUS  
DEFINITION  
E012797-024-027-N23-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-027-N23 5-PRIME, mRNA sequence.

ACCESSION  
VERSION  
BQ593114.1 GI:36122697

## KEYWORDS

## SOURCE

Beta vulgaris

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

## AUTHORS

1 (bases 1 to 14)  
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

## TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)

## JOURNAL

## MEDLINE

## PUBMED

## COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MP1Z  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 14 Std Error: 0.00  
Plate: 27 row: N column: 23  
Seq primer: SP6; CATACGATTAGTGACACTATAG.

## FEATURES

Location/Qualifiers

1..14  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
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line)"  
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/db\_xref="taxon:161934"  
/clone="024-027-N23"  
/tissue\_type="developing root"  
/lab\_host="EMDH108"  
/clone\_lib="MP1Z-ADIS-024-developing root"  
/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 1 GGGGG 5

## RESULT 29

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BX679320/c
LOCUS BX679320 14 bp mRNA linear EST 28-OCT-2003
DEFINITION BX679320 RS Pinus pinaster cDNA clone RS22H11, mRNA sequence.
ACCESSION BX679320
VERSION BX679320.1 GI:38013250
KEYWORDS EST.
SOURCE Pinus pinaster
ORGANISM Pinus pinaster
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
TITLE 1 (bases 1 to 14)
JOURNAL Identification of water-deficit responsive genes in Maritime pine
COMMENT (Pinus pinaster Ait.) using an EST approach
Unpublished (2002)
Contact: Frigerio JM
Genetique et Amelioration 69
INRA
Route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierrot.inra.fr
Email: Frigerio@pierrot.inra.fr
Seq primer: T3.

FEATURES
source
1..14
/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RS22H11"
/tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_lib="RS"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library
was made from the roots of 6 weeks old seedlings grown in
hydroponic conditions. A three weeks drought stress
treatment was applied by lowering the osmotic potential of
the nutrient solution to -0.45 MPa using 170 g/l of
polyethylene glycol as an osmoticum. A mixture of
genotypes were used. Oligo-dT primed cDNA was
directionally cloned into the EcoRI-XhoI lambda-ZAP vector
arms and mass-excised to form a pBluescript phagemid"

ORIGIN
Query Match 100.0%; Score 5; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 14 GGGGG 10

RESULT 30
CA850835 14 bp mRNA linear EST 01-AUG-2003
LOCUS D07A10_A22 01.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION cDNA clone D07A10 5', mRNA sequence.
ACCESSION CA850835
VERSION CA850835.1 GI:33387628
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean
JOURNAL infected by the soybean cyst nematode
COMMENT Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)

BX679320/c
LOCUS BX679320 14 bp mRNA linear EST 28-OCT-2003
DEFINITION BX679320 RS Pinus pinaster cDNA clone RS22H11, mRNA sequence.
ACCESSION BX679320
VERSION BX679320.1 GI:38013250
KEYWORDS EST.
SOURCE Pinus pinaster
ORGANISM Pinus pinaster
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
TITLE 1 (bases 1 to 14)
JOURNAL Identification of water-deficit responsive genes in Maritime pine
COMMENT (Pinus pinaster Ait.) using an EST approach
Unpublished (2002)
Contact: Frigerio JM
Genetique et Amelioration 69
INRA
Route d'Arcachon 33612 Cestas CEDEX France
Email: Frigerio@pierrot.inra.fr
Email: Frigerio@pierrot.inra.fr
Seq primer: T3.

FEATURES
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1..14
/organism="Pinus pinaster"
/mol_type="mRNA"
/db_xref="taxon:71647"
/clone="RS22H11"
/tissue_type="root"
/dev_stage="6 weeks old seedling"
/lab_host="SOLR"
/clone_lib="RS"
/note="Vector: Uni-ZAP XR; ecotype: Landes; The library
was made from the roots of 6 weeks old seedlings grown in
hydroponic conditions. A three weeks drought stress
treatment was applied by lowering the osmotic potential of
the nutrient solution to -0.45 MPa using 170 g/l of
polyethylene glycol as an osmoticum. A mixture of
genotypes were used. Oligo-dT primed cDNA was
directionally cloned into the EcoRI-XhoI lambda-ZAP vector
arms and mass-excised to form a pBluescript phagemid"

ORIGIN
Query Match 100.0%; Score 5; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 14 GGGGG 10

RESULT 30
CA850835 14 bp mRNA linear EST 01-AUG-2003
LOCUS D07A10_A22 01.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max
DEFINITION cDNA clone D07A10 5', mRNA sequence.
ACCESSION CA850835
VERSION CA850835.1 GI:33387628
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Alkharouf, N.W., Khan, R. and Matthews, B.F.
TITLE Analysis of expressed sequence tags from roots of resistant soybean
JOURNAL infected by the soybean cyst nematode
COMMENT Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)

```

US Department of Agriculture (USDA), ARS, PSI  
 Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
 USA  
 Tel: 301 504 5750  
 Fax: 301 504 5728  
 Email: alkharouf@ars.usda.gov.  
 Location/Qualifiers  
 1..14  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Kennebec"  
 /db\_xref="taxon:3847"  
 /clone="D07A10"  
 /tissue\_type="Roots"  
 /dev\_stage="Seedlings"  
 /clone\_lib="cDNA Peking library 2, 4 day SCN3"  
 /note="Vector: pBluescript SK-; cDNA clones from mRNA  
 extracted from Peking roots 2 and 4 days past invasion."

## ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 14;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
 Db 8 GGGGG 12

## RESULT 31

CK258733 14 bp mRNA linear EST 30-JUL-2004  
 LOCUS CK258733  
 DEFINITION CK258733 potato callus cDNA library, normalized and full-length  
 SOLANUM TUBEROSUM cDNA clone POCDF73 5' end, mRNA sequence.

ACCESSION CK258733

VERSION CK258733.1 GI:39815713

KEYWORDS EST.

SOURCE SOLANUM TUBEROSUM (potato)

ORGANISM SOLANUM TUBEROSUM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 asterids; lamiales; Solanales; Solanaceae; Solanum.

1 (bases 1 to 14)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from potato callus tissue

Unpublished (2003)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from the University of Arizona Genomics

Institute via http://genome.arizona.edu/orders/

Seq primer: ATT TAG GTG ACA CTA TAG.

## FEATURES

source

1..14

/organism="Solanum tuberosum"

/mol\_type="mRNA"

/cultivar="Kennebec"

/db\_xref="taxon:4113"

/clone="POCDF73"

/tissue\_type="callus"

/lab\_host="DH10B-Tona"

/clone\_lib="potato callus cDNA library, normalized and

full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: RNA was isolated from Solanum tuberosum var.

Kennebec callus tissue grown on solid media."

## ORIGIN

Query Match 100.0%; Score 5; DB 7; Length 14;

Best Local Similarity 100.0%; Pred. No. 9.5e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 32
LOCUS CK258733/c
DEFINITION EST742370 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone FOCDF73 5' end, mRNA sequence.
ACCESSION CK258733
VERSION CK258733.1 GI:39815713
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE 1 (bases 1 to 14)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
TITLE Generation of ESTs from potato callus tissue
JOURNAL Unpublished (2003)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/.
Seq primer: ART TAG GTG ACA CTA TAG.
FEATURES
source
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/organism="Solanum tuberosum"
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/clone="POCDF73"
/tissue_type="callus"
/lab_host="DH10B-Tona"
/clone_lib="potato callus cDNA library, normalized and
full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."
ORIGIN
Query Match 100.0%; Score 5; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 13 GGGGG 9

RESULT 33
AJ587271
LOCUS AJ587271
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
257804, genomic survey sequence.
ACCESSION AJ587271
VERSION AJ587271.1 GI:37936860
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechold, N., Cruaud, C., Derose, R., Pelletier, G.,
Lepiniec, L., Caboche, M. and Lecharny, A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 14)
AUTHORS Balzergue, S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (e) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
source
1..14
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassiliewskaja"
/db_xref="taxon:3702"
/clone="257B04"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1..14
/notes="T-DNA flanking sequence
left border"
ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 7 GGGGG 11

RESULT 34
LOCUS AW248644
DEFINITION 2820747.3prime NIH_MGC_7 Homo sapiens cDNA clone IMAGE:2820747 3',
mRNA sequence.
ACCESSION AW248644
VERSION AW248644.1 GI:6591637
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 15)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Other ESTs: 2820747.5prime
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LLNL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information can
be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality
Scores: PHRED from University of Washington Genome Center. Vector
Trimming: cross match from University of Washington Genome Center
PHRAP suite, Poly-T Identification: patMatch.pl from Berkeley
Drosophila Genome Project. University of Washington Genome Center:
http://www.genome.washington.edu Low Quality Sequence: 6 contiguous
PHRED high quality bases following vector sequence. Very Low
Quality Sequence: Trace file contained 15 contiguous distinct peaks

```



following vector sequence. Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this cDNA insert was polyadenylated.  
 Plate: LLCMS row: A column: 4  
 High quality sequence stop: 6.

## FEATURES

source

```

1. .15
  Location/Qualifiers
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:2820747"
    /issue_type="small cell carcinoma"
    /cell_line="WG3"
    /lab_host="DH10B (phage-resistant)"
    /clone_lib="NIH MGC_7"
    /note="Organ: lung; Vector: pOTB7; Site_1: XhoI; Site_2:
    EcoRI; cDNA made by oligo-dT priming. Directionally
    cloned into EcoRI/XhoI sites using the following 5'
    adaptor: GGCACGAG(G). Size-selected >500bp for average
    insert size 1.8kb. Library constructed by Ling Hong in
    the laboratory of Gerald M. Rubin (University of
    California, Berkeley) using ZAP-cDNA synthesis kit
    (Stratagene) and Superscript II RT (Life Technologies)."
```

## ORIGIN

```

Query Match      100.0%; Score 5; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGGG 5

Db 11 GGGGG 15

## RESULT 35

```

BM395188
LOCUS      50072-2-7-H12.f.2 Chilcoat/Turkewitz cDNA (large fraction) EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM395188
VERSION     BM395188.1 GI:18195241
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
```

```

REFERENCE  1 (bases 1 to 15)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J., and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
```

## FEATURES

source

```

1. .15
  Location/Qualifiers
    /organism="Tetrahymena thermophila"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
    /note="Vector: Bluescript2 SK+; Details on library
    preparation can be found in Chilcoat and Turkewitz
    Proc. Natl. Acad. Sci USA, 98: 8709-8713."
```

## ORIGIN

```

Query Match      100.0%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
```

```

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGGG 5
Db 1 GGGGG 5
```

## RESULT 36

```

BM395189/c
LOCUS      50072-2-7-H12.r.1 Chilcoat/Turkewitz cDNA (large fraction) EST 17-JAN-2002
DEFINITION Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION  BM395189
VERSION     BM395189.1 GI:18195242
KEYWORDS   EST.
SOURCE     Tetrahymena thermophila
ORGANISM   Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
```

```

REFERENCE  1 (bases 1 to 15)
AUTHORS   Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J., and Klobutcher,L.
TITLE     EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL   Unpublished (2002)
COMMENT   Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
```

## FEATURES

source

```

1. .15
  Location/Qualifiers
    /organism="Tetrahymena thermophila"
    /mol_type="mRNA"
    /strain="CU428.1"
    /db_xref="taxon:9606"
    /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
    /note="Vector: Bluescript2 SK+; Details on library
    preparation can be found in Chilcoat and Turkewitz
    Proc. Natl. Acad. Sci USA, 98: 8709-8713."
```

## ORIGIN

```

Query Match      100.0%; Score 5; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGGG 5

Db 12 GGGGG 8

## RESULT 37

```

BQ588758
LOCUS      E012534-024-014-P24-SP6 MP1Z-ADIS-024-storage root Beta vulgaris EST 06-DEC-2002
DEFINITION cDNA clone 024-014-P24 5-PRIME, mRNA sequence.
ACCESSION  BQ588758
VERSION     BQ588758.1 GI:26118341
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
```

```

REFERENCE  1 (bases 1 to 15)
AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruuck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radeloff,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL   Plant J. 32 (5), 845-857 (2002)
```

```

MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaa@mpi-z-koeln.mpg.de
            Insert Length: 15 Std Error: 0.00
            Plate: 14 row: P column: 24
            Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES     Location/Qualifiers
            1..15
            /organism="Beta vulgaris"
            /mol_type="mRNA"
            /cultivar="KWS2320 (double haploid, monogerm breeding
            line)"
            /db_xref="GABI:187217"
            /db_xref="taxon:161934"
            /clone="024-014-P24"
            /tissue_type="storage root"
            /lab_host="EMDH10B"
            /clone_lib="MPIZ-ADIS-024-storage root"
            /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Binbeck, Germany, contact:
            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      100.0%; Score 5; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 5 GGGGG 9

RESULT 38
BQ590018
LOCUS      BQ590018 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012843-024-019-G23-T7 MPIZ-ADIS-024-storage root Beta vulgaris
            cDNA clone 024-019-G23 3-PRIME, mRNA sequence.
ACCESSION  BQ590018
VERSION    BQ590018.1 GI:26119601
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 15)
            Hewig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
            Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
            Plant J. 32 (5), 845-857 (2002)
JOURNAL    22362189
MEDLINE    12472698
PUBMED     12472698
COMMENT    Contact: Weishaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaa@mpi-z-koeln.mpg.de
            Insert Length: 15 Std Error: 0.00

MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weishaa@mpi-z-koeln.mpg.de
            Insert Length: 15 Std Error: 0.00
            Seq primer: T7; GTAATACGACTCCTATAGGCG.
FEATURES     Location/Qualifiers
            1..15
            /organism="Beta vulgaris"
            /mol_type="mRNA"
            /cultivar="KWS2320 (double haploid, monogerm breeding
            line)"
            /db_xref="GABI:190101"
            /db_xref="taxon:161934"
            /clone="024-019-G23"
            /tissue_type="storage root"
            /lab_host="EMDH10B"
            /clone_lib="MPIZ-ADIS-024-storage root"
            /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Binbeck, Germany, contact:
            b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match      100.0%; Score 5; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 39
CA794555
LOCUS      CA794555 15 bp mRNA linear EST 05-DEC-2002
DEFINITION Cac BL_1497 Cac BL (Bean and Leaf from Amelonado type Cacao)
            Theobroma cacao cDNA clone Cac_BL_1497 5', mRNA sequence.
ACCESSION  CA794555
VERSION    CA794555.1 GI:26051631
KEYWORDS   EST.
SOURCE     Theobroma cacao (cacao)
ORGANISM   Theobroma cacao
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
            Theobroma.
REFERENCE  1 (bases 1 to 15)
            Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
            Retzel,E.R. and Jones,C.A.
            Gene discovery and microarray analysis of cacao (Theobroma cacao
            L.) varieties
            Planta 216 (2), 255-264 (2002)
JOURNAL    2237596
MEDLINE    12447539
PUBMED     12447539
COMMENT    Contact: Jones, Paul
            Masterfoods
            3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
            Tel: +44 1664 416644
            Email: Paul.Jones@eu.affem.com
            Seq primer: T3.
FEATURES     Location/Qualifiers
            1..15
            /organism="Theobroma cacao"
            /mol_type="mRNA"
            /strain="Amelonado type"
            /db_xref="taxon:3641"
            /clone="Cac_BL_1497"
            /tissue_type="Mature leaf and mature bean"
            /cell_type="Whole organ"
            /dev_stage="maturity"

```

```

/lab_host="XL-1 Blue MRF"
/clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
Cacao)"
/note="Vector: pBK-CMV; Bean and leaf tissue from an
Amelonado type Cacao tree."

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 8 GGGGG 12

RESULT 40
CK283790
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 15)
Alkharouf,N.W., Khan,R. and Matthews,B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharouf@ba.ars.usda.gov.
Location/Qualifiers
1..15
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clone="D08F09"
/tissue_type="Roots"
/dev_stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pBluescript SK-; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days past invasion."

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 41
CK283790
LOCUS
DEFINITION
ACCESSION

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Nicotiana.
1 (bases 1 to 15)
Buell,C.R., Hart,A., Zisemann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST746511
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq Primer: GTA ATA CGA CTC ACT ATA GGG C.
Location/Qualifiers
1..15
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMAJ54"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Xanthomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match      100.0%; Score 5; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 7 GGGGG 11

RESULT 42
CK283790/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 15)
Buell,C.R., Hart,A., Zisemann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST746511

```

```

CK283790.1 GI:39856749
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 15)
Buell,C.R., Hart,A., Zisemann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST746511
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq Primer: GTA ATA CGA CTC ACT ATA GGG C.
Location/Qualifiers
1..15
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMAJ54"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Xanthomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match      100.0%; Score 5; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 7 GGGGG 11

RESULT 43
CK283790
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 15)
Buell,C.R., Hart,A., Zisemann,V., Karamycheva,S.A., Day,B.,
Staskawicz,B., Jin,H. and Baker,B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST746511

```

Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via <http://genome.arizona.edu/orders/>.  
Seq primer: GTA ATA CGA CTC ACT ATA GGG C.

#### FEATURES

Location/Qualifiers

1..15  
/organism="Nicotiana benthamiana"  
/mol\_type="mRNA"  
/db\_xref="taxon:4100"  
/clone="NBMAJ54"  
/tissue\_type="abiotic and biotic stress-treated leaves,  
callus tissue and root tissue"  
/lab\_host="DH10B-Tona"  
/clone\_lib="Nicotiana benthamiana mixed tissue cDNA  
library, normalized, full-length"  
/note="Vector: pCMVSPORT6.1; Site\_1: EcoRI; Site\_2: NotI;  
supplier: RNA was isolated from Nicotiana benthamiana  
tissues that include callus, roots from liquid culture  
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),  
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
Xanthomonas campestris pv campestris 12 hr, 18hr;  
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
campestris pv vesicatoria 18hr). RNA was isolated from  
these tissues and pooled in approximately equal molar  
amounts."

#### ORIGIN

Query Match 100.0%; Score 5; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 6 GGGGG 2

RESULT 43  
AA937364  
LOCUS  
DEFINITION  
oj08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595 3'  
similar to SW:ACRO\_FABIT P48038 ACROSIN PRECURSOR ;contains MS1.b2  
MS1 repetitive element ;, mRNA sequence.

ACCESSION AA937364

VERSION AA937364.1 GI:3095475

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

unknown library type

Trace considered overall poor quality

Insert Length: 1265 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1491595"

/tissue\_type="metastatic melanoma to bowel"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP Mel3"  
/note="Organ: bowel (skin primary); Vector: pCMV-SPORT4;  
Site 1: SalI; Site 2: NotI; Cloned unidirectionally.  
Primer: Oligo dT. Average insert size 0.9 kb. Life  
Technologies catalog #: 10981-017"

#### ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 4 GGGGG 8

#### RESULT 44

AA939272/c

LOCUS

DEFINITION  
oq31b06.s1 NCI CGAP GC4 Homo sapiens cDNA clone IMAGE:1587923 3'  
similar to SW:CA34\_HUMAN Q01955 PROCOLLAGEN ALPHA 3(IV) CHAIN  
PRECURSOR. ;contains OPR.b3 MS1 repetitive element ;, mRNA  
sequence.

ACCESSION AA939272

VERSION AA939272.1 GI:3099185

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1587923"

/tissue\_type="pooled germ cell tumors"

/lab\_host="DH10B"

/clone\_lib="NCI-CGAP GC4"

/note="Vector: p7T3D-Fac (Pharmacia) with a modified  
polylinker; 1st strand cDNA was prepared from 3 pooled

germ cell tumors, and was then primed with a Not I -

oligo(dT) primer. Double-stranded cDNA was ligated to Eco

RI adaptors (Pharmacia), digested with Not I and cloned

into the Not I and Eco RI sites of the modified p7T3

vector. Library is normalized. Library was constructed by

Bento Soares and M. Fatima Bonaldo."

#### ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

```

Db          6 GGGGG 2

RESULT 45
AA968729
LOCUS
DEFINITION
16 bp mRNA linear EST 27-AUG-1998
or69h11.s1 NCI CGAP GC3 Homo sapiens cDNA clone IMAGE:1601157 3'
similar to SW:PRPE_HUMAN P2811 BASIC PROLINE-RICH PEPTIDE P-E
;contains element MSRI repetitive element ;, mRNA sequence.
AA968729
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 514 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1601157"
/sex="female, pooled"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "

FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1601157"
/sex="female, pooled"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
|||||
Db 2 GGGGG 6

RESULT 46
AA1075064
LOCUS
DEFINITION
16 bp mRNA linear EST 27-AUG-1998
ou61g11.x1 NCI CGAP Br2 Homo sapiens cDNA clone IMAGE:1632356 3'
similar to TR:Q24346 Q24348 FIBRILLARIN ;, mRNA sequence.
AA1075064
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1601157"
/sex="female, pooled"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC3"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. Library was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN
Query Match 100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
|||||
Db 2 GGGGG 6

RESULT 47
AA1094839
LOCUS
DEFINITION
16 bp mRNA linear EST 18-AUG-1998
ga22c08.x1 NCI CGAP Brn23 Homo sapiens cDNA clone IMAGE:1687502 3'
similar to TR:O00599 O00599 CON1.;contains element MSRI repetitive
element ;, mRNA sequence.
AA1094839
ACCESSION
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTCAP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

```

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.  
 DNA Sequencing by: Greg Lennon, Ph.D.  
 Clone Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: [www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.

## FEATURES

source

```

1. .16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1687502"
/tissue_type="glioblastoma (pooled)"
/lab_host="DH10B"
/clone_lib="NCI CGAP_Brn23"
/notes="Organ: Brain; Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified p7T73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."
```

## ORIGIN

```

Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GGGGG 5

Db 6 GGGGG 2

## RESULT 48

```

AI209036
LOCUS      16 bp mRNA linear EST 19-OCT-1998
DEFINITION gq18g10.x1 Soares_placenta_8to9weeks_2NbHP8to9w Homo sapiens cDNA
            clone IMAGE:1759938 3' similar to TR:Q64371 Q64371 PR-VBETAL.
            ;contains element MER22 repetitive element ;, mRNA sequence.
```

## ACCESSION

AI209036

## KEYWORDS

EST. AI209036.1 GI:3770978

## SOURCE

```

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

## REFERENCE

1 (bases 1 to 16)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium ([info@image.llnl.gov](mailto:info@image.llnl.gov)) for further information.

Trace considered overall poor quality

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1759938"

```

/dev_stage="two placentae: one from 8 weeks and another
from 9 weeks post conception"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares_placenta_8to9weeks_2NbHP8to9w"
/notes="Organ: placenta; Vector: p7T73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACCAATCTGAAGTGGAGCGCGCATATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p7T73 vector
(Pharmacia). Library constructed by Bento Soares and
M.Fatima Bonaldo."
```

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 9.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 5 GGGGG 9

## RESULT 49

AI262040

## LOCUS

```

DEFINITION AI262040
            16 bp mRNA linear EST 28-JAN-1999
            qk24h08.x1 NCI CGAP Kid3 Homo sapiens cDNA clone IMAGE:1869951 3'
            similar to SW:Call_BOVIN P02453 COLLAGEN ALPHA 1(I) CHAIN ;, mRNA
            sequence.
```

## ACCESSION

AI262040

## KEYWORDS

EST. AI262040.1 GI:3870243

## SOURCE

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 16)

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)

Trace considered overall poor quality

Insert Length: 1352 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1869951"

/lab\_host="DH10B"

/clone\_lib="NCI CGAP\_Kid3"

/notes="Organ: kidney; Vector: p7T73D-Pac (Pharmacia) with

a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st

strand cDNA was primed with a Not I - oligo(dT) primer,

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Not I and cloned into the Not

I and Eco RI sites of the modified p7T73 vector. mRNA

source: 2 pooled kidneys. Library went through one round

of normalization. Library constructed by Bento Soares and

```

ORIGIN
M. Fatima Bonaldo. "

Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      2 GGGGG 6

RESULT 50
AI274782/c
LOCUS      AI274782
DEFINITION qv67h03.x1 NCI_CGAP Ut1 Homo sapiens cDNA clone IMAGE:1986677 3'
            similar to WP:F59E12.9 Cell1534 ;contains element MSRI repetitive
            element ;, mRNA sequence.
ACCESSION  AI274782
VERSION     AI274782.1 GI:3897056
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 16)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1556 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1986677"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI_CGAP Ut1"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"

FEATURES
source

ORIGIN

Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      16 GGGGG 12

Search completed: January 7, 2005, 11:01:51
Job time : 2234.4 secs

```

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 05:37:38 ; Search time 58 Seconds  
(without alignments)  
61.275 Million cell updates/sec

Title: GGGGG

Perfect score: 5

Sequence: 1 99999 5

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 896372

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/prodata/1/ina/5A-COMB.seq:\*

2: /cgn2\_6/prodata/1/ina/5B-COMB.seq:\*

3: /cgn2\_6/prodata/1/ina/6A-COMB.seq:\*

4: /cgn2\_6/prodata/1/ina/6B-COMB.seq:\*

5: /cgn2\_6/prodata/1/ina/PCTUS-COMB.seq:\*

6: /cgn2\_6/prodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	100.0	10	1	US-08-151-574-51
2	5	100.0	10	1	US-08-151-574-52
3	5	100.0	10	1	US-07-963-723A-3
4	5	100.0	10	1	US-08-229-515A-17
5	5	100.0	10	1	US-08-229-515A-18
6	5	100.0	10	1	US-08-128-011-3
7	5	100.0	10	1	US-08-335-565A-6
8	5	100.0	10	1	US-08-235-503B-12
9	5	100.0	10	1	US-07-860-445-18
10	5	100.0	10	1	US-08-233-608-45
11	5	100.0	10	1	US-08-307-713-18
12	5	100.0	10	1	US-08-197-463-4
13	5	100.0	10	1	US-08-202-927-16
14	5	100.0	10	1	US-08-335-354A-3
15	5	100.0	10	1	US-08-335-354A-4
16	5	100.0	10	1	US-08-645-865-17
17	5	100.0	10	1	US-08-645-865-18
18	5	100.0	10	1	US-08-171-718-41
19	5	100.0	10	1	US-08-665-511-18
20	5	100.0	10	1	US-08-467-126-2
21	5	100.0	10	1	US-08-887-480-45
22	5	100.0	10	1	US-08-410-779B-24
23	5	100.0	10	1	US-08-465-590-35
24	5	100.0	10	2	US-08-441-887A-40
25	5	100.0	10	2	US-08-441-887A-64
26	5	100.0	10	2	US-08-441-887A-96
27	5	100.0	10	2	US-08-173-489C-223
28	5	100.0	10	2	US-08-173-489C-224
29	5	100.0	10	2	US-08-590-571-28
30	5	100.0	10	2	US-08-590-571-33
31	5	100.0	10	2	US-08-590-571-44
32	5	100.0	10	2	US-08-590-571-47
33	5	100.0	10	2	US-08-590-571-49
34	5	100.0	10	2	US-08-419-448-51
35	5	100.0	10	2	US-08-419-448-52
36	5	100.0	10	2	US-08-821-205-3
37	5	100.0	10	2	US-08-821-205-4
38	5	100.0	10	2	US-08-482-651-57
39	5	100.0	10	2	US-08-595-043A-66
40	5	100.0	10	2	US-08-595-043A-67
41	5	100.0	10	2	US-08-403-888A-145
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## ALIGNMENTS

RESULT 1  
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; Patent No. 5436156  
; GENERAL INFORMATION:  
; APPLICANT: Robert F.M. Van Gorcom  
; APPLICANT: Willem Van Hartingsveldt  
; APPLICANT: Petrus A. Van Paridon  
; APPLICANT: Annemarie E. Veenstra  
; APPLICANT: Rudolf G.M. Luttin  
; APPLICANT: Gerardus Seltin  
; TITLE OF INVENTION: Cloning and Expression of Microbial  
; TITLE OF INVENTION: Phytase  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Morrison & Foerster  
; STREET: 545 Middlefield Road, Suite 200  
; CITY: Menlo Park  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94025-3471  
; COMPUTER READABLE FORM:  
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; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; SOFTWARE:  
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; APPLICATION NUMBER: US/08/151,574  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/688,578



```
;
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
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; TOPOLOGY: linear
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; Qy 1 GGGGG 5
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; RESULT 5
; US-08-229-515A-18
; Sequence 18, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDDIN
; ADDRESSEE: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
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; COMPUTER READABLE FORM:
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
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; RESULT 6
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; Patent No. 5523389
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Wyatt, Jacqueline R.
; APPLICANT: Imbach, Jean Louis
; TITLE OF INVENTION: Inhibitors of Human Immunodeficiency
; TITLE OF INVENTION: Virus
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5523389ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
;
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; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaumont, Rebecca R.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET NUMBER: ISIS-1161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
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; RESULT 7
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; Sequence 6, Application US/08335565A
; Patent No. 5527671
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GENERAL INFORMATION:  
; APPLICANT: Li, Kening  
; APPLICANT: Rouse, Douglas L.  
; APPLICANT: German, Thomas L.  
; TITLE OF INVENTION: ASSAY FOR VERTICILLIUM DAHLIAE  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Quarles and Brady  
; STREET: 1 South Pinckney St., PO BOX 2113  
; CITY: Madison  
; STATE: WI  
; COUNTRY: USA  
; ZIP: 53701-2113  
; COMPUTER READABLE FORM:  
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; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,565A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seay, Nicholas J.  
; REGISTRATION NUMBER: 27,386  
; REFERENCE/DOCKET NUMBER: 960296.93065  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 608-251-5000  
; TELEFAX: 608-251-9166  
; INFORMATION FOR SEQ ID NO: 6:  
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; Sequence 12, Application US/08235503B  
; Patent No. 5563036  
; GENERAL INFORMATION:  
; APPLICANT: Peterson, Michael G  
; APPLICANT: Baichwal, Vijay R  
; APPLICANT: Scrulovici, Berta  
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY  
; NUMBER OF SEQUENCES: 75  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
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; APPLICATION NUMBER: US/08/235,503B  
; FILING DATE: 29-APR-1994  
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
; NAME: Oseman, Richard A  
; REGISTRATION NUMBER: 36,627  
; REFERENCE/DOCKET NUMBER: A-59332/RAO  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 12:  
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DB 8 GGGGG 4  
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; Sequence 18, Application US/07860445  
; Patent No. 5573905  
; GENERAL INFORMATION:  
; APPLICANT: Lerner, Richard  
; APPLICANT: Janda, Kim  
; APPLICANT: Brenner, Sydney  
; TITLE OF INVENTION: ENCODED COMBINATORIAL CHEMICAL LIBRARIES  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: The Scripps Research Institute, Office of  
; ADDRESSEE: Patent Counsel  
; STREET: 10666 No. 5573905th Torrey Pines Road, TPC 8  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
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; SOFTWARE: PatentIn Release #1.0, Version #1.25  
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; APPLICATION NUMBER: US/07/860,445  
; FILING DATE: 19920330  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitting, Thomas  
; REGISTRATION NUMBER: 34,163  
; REFERENCE/DOCKET NUMBER: TSR5023P  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-554-2937  
; TELEFAX: 619-554-6312  
; INFORMATION FOR SEQ ID NO: 18:  
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Best Local Similarity 100.0%; Pred. No. 1.8e+05;
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; Patent No. 5585238
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,608
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-19
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-233-608-45

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      6 GGGGG 2

RESULT 11
US-08-307-713-18
; Sequence 18, Application US/08307713
; Patent No. 5604122
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: IMPROVEMENTS IN OR RELATING TO DNA CLONING
```

```
; TITLE OF INVENTION: TECHNIQUES AND PRODUCTS FOR USE THEREWITH
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leydig, Voit & Mayer, Ltd.
; STREET: 180 No. 5604122th Stetson, Two Prudential Plaza,
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/307,713
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB93/00584
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206210.8
; FILING DATE: 21-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilyk Jr., John
; REGISTRATION NUMBER: 30763
; REFERENCE/DOCKET NUMBER: 62920
; TELEPHONE: (312) 616-5600
; TELEFAX: (312) 616-5700
; TELEX: 25-3533
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: YES
US-08-307-713-18

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      1 GGGGG 5

RESULT 12
US-08-197-463-4/c
; Sequence 4, Application US/08197463
; Patent No. 5627047
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael
; APPLICANT: Besnard, Francois
; APPLICANT: Nakatani, Yoshihiro
; TITLE OF INVENTION: Astrocyte-Specific Transcription
; TITLE OF INVENTION: of Human Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Koslasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/769,626  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330  
REFERENCE/DOCKET NUMBER: 1173-362P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: protein\_bind  
LOCATION: 1..10  
OTHER INFORMATION: /function= "transcription enhancer"  
OTHER INFORMATION: /bound\_moiety= "AP-2"  
OTHER INFORMATION: /standard\_name= "AP-2 site"  
US-08-197-463-4

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 10 GGGGG 6

RESULT 13  
US-08-202-927-16  
Sequence 16, Application US/08202927  
Patent No. 5646126  
GENERAL INFORMATION:  
APPLICANT: Cheng, Yung-Chi  
APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Meyer Jr., Rich B.  
APPLICANT: Pai, Balakrishna S.  
APPLICANT: Reed, Michael W.  
APPLICANT: Zhou, James H.  
TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klein & Szekeres  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675

REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
a cholesterol moiety which has its A ring linked to  
the 3'-phosphate through a carbonyl group attached  
to the ring nitrogen of a moiety derived from  
4-hydroxy-2-hydroxymethylpyrrolidine (see  
formula 3)."  
US-08-202-927-16

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 6 GGGGG 10

RESULT 14  
US-08-335-354A-3/c  
Sequence 3, Application US/08335354A  
Patent No. 5652358  
GENERAL INFORMATION:  
APPLICANT: Pfeleiderer, Wolfgang  
APPLICANT: Schnell, Ralf  
APPLICANT: Matysiak, Stephan  
TITLE OF INVENTION: Solid-Phase Synthesis Of  
Oligoribonucleotides.  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
Dunner  
STREET: 1300 I Street, N.W., Suite 700  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/335,354A  
FILING DATE: 03-NOV-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: GR P 43 43 126.7  
FILING DATE: 17-DEC-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Horton, Ken  
REGISTRATION NUMBER: 39,481  
REFERENCE/DOCKET NUMBER: 02481.1413-00000  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-408-4000  
TELEFAX: 202-408-4400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-335-354A-3

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      10 GGGGG 6

RESULT 15
US-08-335-354A-4
; Sequence 4, Application US/08335354A
; Patent No. 5652358
; GENERAL INFORMATION:
; APPLICANT: Pfeleiderer, Wolfgang
; APPLICANT: Schnell, Ralf
; APPLICANT: Matysiak, Stephan
; TITLE OF INVENTION: Solid-Phase Synthesis Of
; TITLE OF INVENTION: Oligoribonucleotides.
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/335,354A
; FILING DATE: 03-NOV-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: GR P 43 43 126.7
; FILING DATE: 17-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Horton, Ken
; REGISTRATION NUMBER: 39,481
; REFERENCE/DOCKET NUMBER: 02481.1413-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (genomic)
US-08-335-354A-4

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      1 GGGGG 5

RESULT 16
US-08-645-865-17
; Sequence 17, Application US/08645865
```

```
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-645-865-17

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db      4 GGGGG 8

RESULT 17
US-08-645-865-18
; Sequence 18, Application US/08645865
; Patent No. 5654406
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/645,865
; FILING DATE: 14 MAY 1996
; CLASSIFICATION: 435
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404-688-0770
; TELEFAX: 404-688-9880
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-645-865-18
;
; Query Match 100.0%; Score 5; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.8e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GGGGG 5
; DB 3 GGGGG 7
;
; RESULT 18
; US-08-171-718-41
; Sequence 41, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808
; FILING DATE: 19-AUG-1993
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-645-865-18
;
; Query Match 100.0%; Score 5; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.8e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GGGGG 5
; DB 3 GGGGG 7
;
; RESULT 19
; US-08-665-511-18
; Sequence 18, Application US/08665511
; Patent No. 5723598
; GENERAL INFORMATION:
; APPLICANT: Lerner, Richard
; APPLICANT: Janda, Kim
; APPLICANT: Brenner, Sydney
; TITLE OF INVENTION: ENCODED COMBINATORIAL CHEMICAL LIBRARIES
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: The Scripps Research Institute, Office of
; ADDRESSEE: Patent Counsel
; STREET: 10666 No. 5723598th Torrey Pines Road, TPC 8
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/665,511
; FILING DATE: 18-JUN-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/860445
; FILING DATE: 30-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: TSR5023P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-554-2937
; TELEFAX: 619-554-6312
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5'6')
; OTHER INFORMATION: /note= "Coding sequence located at
; OTHER INFORMATION: indicated position"
; US-08-665-511-18
;
; Query Match 100.0%; Score 5; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 1.8e+05;
; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 1 GGGGG 5
; DB 4 GGGGG 8
```

RESULT 20  
US-08-467-126-2  
; Sequence 2, Application US/08467126  
; Patent No. 5776744  
; GENERAL INFORMATION:  
; APPLICANT: GLAZER, PETER M.  
; APPLICANT: GEORGE, JAY  
; APPLICANT: LIN, L. MICHAEL  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
; EFFECTING HOMOLOGOUS RECOMBINATION  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ONCORPHARM, INC.  
; STREET: 200 PERRY PARKWAY  
; CITY: GAITHERSBURG  
; STATE: MARYLAND  
; COUNTRY: USA  
; ZIP: 20877  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: DISKETTE-3.50 INCH, 1.44 Mb  
; MEDIUM TYPE: STORAGE  
; COMPUTER: APPLE MACINTOSH POWERBOOK 520  
; OPERATING SYSTEM: MACINTOSH  
; SOFTWARE: WORD PERFECT 3.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/467,126  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: KARTA, GLENN E.  
; REGISTRATION NUMBER: 30,649  
; REFERENCE/DOCKET NUMBER: PA-0030  
; TELEPHONE: 301-527-2058  
; TELEFAX: 301-208-6997  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-467-126-2

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGG 5  
Db 6 GGGGG 10

RESULT 21  
US-08-887-480-45/c  
; Sequence 45, Application US/08887480  
; Patent No. 5814453  
; GENERAL INFORMATION:  
; APPLICANT: Beck, James J  
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the  
; TITLE OF INVENTION: Polymerase Chain Reaction  
; NUMBER OF SEQUENCES: 96  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5814453artis Corporation  
; STREET: 520 White Plains Road  
; CITY: Tarrytown  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10591  
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/887,480  
; FILING DATE:  
; CLASSIFICATION: 435  
; APPLICATION NUMBER: US 08/722,187  
; FILING DATE: 15-OCT-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 45:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
; DESCRIPTION: Oligonucleotide primer OPE-19  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-887-480-45

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGGG 5  
Db 6 GGGGG 2

RESULT 22  
US-08-410-779B-24/c  
; Sequence 24, Application US/08410779B  
; Patent No. 5814517  
; GENERAL INFORMATION:  
; APPLICANT: SEIDEL, H. MARTI  
; APPLICANT: LAMB, I. PETER  
; TITLE OF INVENTION: DNA SPACER REGULATORY ELEMENTS  
; RESPONSIVE TO CYTOKINES AND METHODS FOR THEIR USE  
; NUMBER OF SEQUENCES: 166  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LIGAND PHARMACEUTICALS INCORPORATED  
; STREET: 9393 TOWNE CENTRE DRIVE  
; CITY: SAN DIEGO  
; STATE: CALIFORNIA  
; COUNTRY: US  
; ZIP: 92121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/410,779B  
; FILING DATE: 27-MAR-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/228,935  
; FILING DATE: 14-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JURGENSEN, THOMAS E  
; REGISTRATION NUMBER: 34,195  
; REFERENCE/DOCKET NUMBER: 016-0013A.US  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 550-7675  
TELEFAX: (619) 535-3906  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "OTHER NUCLEIC ACID,  
SYNTHETIC DNA"  
US-08-410-779B-24

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
DB 7 GGGGG 3

RESULT 23  
US-08-465-590-35  
Sequence 35, Application US/08465590  
Patent No. 5824770  
GENERAL INFORMATION:  
APPLICANT: Georgopoulos, Katia A.  
TITLE OF INVENTION: IKAROS: A T CELL PATHWAY REGULATORY GENE  
NUMBER OF SEQUENCES: 164  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD  
STREET: 60 STATE STREET, Suite 510  
CITY: BOSTON  
STATE: MASSACHUSETTS  
COUNTRY: USA  
ZIP: 02109

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: ASCII (text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,590  
FILING DATE: 05-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/238,212  
FILING DATE: 02-MAY-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/121,438  
FILING DATE: 14-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/946,233  
FILING DATE: 14-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Myers, Paul L.  
REGISTRATION NUMBER: 35,695  
REFERENCE/DOCKET NUMBER: MPG-006C2DV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617)227-7400  
TELEFAX: (617)227-5941  
INFORMATION FOR SEQ ID NO: 35:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cdna  
US-08-465-590-35

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
DB 3 GGGGG 7

RESULT 24  
US-08-441-887A-40  
Sequence 40, Application US/08441887A  
Patent No. 5837832  
GENERAL INFORMATION:  
APPLICANT: Chee, Mark  
APPLICANT: Cronin, Maureen T.  
APPLICANT: Fodor, Stephanie P.A.  
APPLICANT: Huang, Xiaohua X.  
APPLICANT: Hubbell, Earl A.  
APPLICANT: Lipshutz, Robert J.  
APPLICANT: Lobban, Peter E.  
APPLICANT: Morris, Macdonald S.  
APPLICANT: Sheldon, Edward L.  
TITLE OF INVENTION: Arrays of Nucleic Acid Probes on  
Biological Chips  
NUMBER OF SEQUENCES: 360  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, 8th Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/441.887A  
FILING DATE: 16-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/143,312  
FILING DATE: 26-OCT-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/082,937  
FILING DATE: 25-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Liebeschuetz, Joseph O.  
REGISTRATION NUMBER: 37,505  
REFERENCE/DOCKET NUMBER: 018547-004160US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-326-2400  
TELEFAX: 650-326-2422  
INFORMATION FOR SEQ ID NO: 40:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (probe)  
US-08-441-887A-40

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
DB 4 GGGGG 8

RESULT 25  
US-08-441-887A-64

; Sequence 64, Application US/08441887A  
; Patent No. 5837832

; GENERAL INFORMATION:

; APPLICANT: Chee, Mark

; APPLICANT: Cronin, Maureen T.

; APPLICANT: Fodor, Stephen P.A.

; APPLICANT: Huang, Xiaohua X.

; APPLICANT: Hubbell, Earl A.

; APPLICANT: Lipshutz, Robert J.

; APPLICANT: Lobban, Peter E.

; APPLICANT: Morris, Macdonald S.

; APPLICANT: Sheldon, Edward L.

; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on

; TITLE OF INVENTION: Biological Chips

; NUMBER OF SEQUENCES: 360

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/441,887A

; FILING DATE: 16-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/143,312

; FILING DATE: 26-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/082,937

; FILING DATE: 25-JUN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebeschuetz, Joseph O.

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 018547-004160US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-326-2400

; TELEFAX: 650-326-2422

; INFORMATION FOR SEQ ID NO: 64:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (probe)

; US-08-441-887A-64

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 3 GGGGG 7

RESULT 26

US-08-441-887A-96

; Sequence 96, Application US/08441887A

; Patent No. 5837832

; GENERAL INFORMATION:

; APPLICANT: Chee, Mark

; APPLICANT: Cronin, Maureen T.

; APPLICANT: Fodor, Stephen P.A.

; APPLICANT: Huang, Xiaohua X.

; APPLICANT: Hubbell, Earl A.

; APPLICANT: Lipshutz, Robert J.

; APPLICANT: Lobban, Peter E.

; APPLICANT: Morris, Macdonald S.

; APPLICANT: Sheldon, Edward L.

; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on

; TITLE OF INVENTION: Biological Chips

; NUMBER OF SEQUENCES: 360

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/441,887A

; FILING DATE: 16-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/143,312

; FILING DATE: 26-OCT-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/082,937

; FILING DATE: 25-JUN-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebeschuetz, Joseph O.

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 018547-004160US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-326-2400

; TELEFAX: 650-326-2422

; INFORMATION FOR SEQ ID NO: 96:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (probe)

; US-08-441-887A-96

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.8e+05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 3 GGGGG 7

RESULT 27

US-08-173-489C-223

; Sequence 223, Application US/08173489C

; Patent No. 5861244

; GENERAL INFORMATION:

; APPLICANT: WANG, C. -G.

; APPLICANT: HEPBURN, A. G.

; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA

; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.

; NUMBER OF SEQUENCES: 365

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,

; STREET: 510 EAST 73RD STREET,

; CITY: NEW YORK

; STATE: NEW YORK

; COUNTRY: USA

; ZIP: 10021.

; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: U9518-6  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 223:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double stranded  
TOPOLOGY: linear  
MOLECULE TYPE: Genomic DNA  
DESCRIPTION: 23S rRNA gene from Escherichia coli  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Escherichia coli  
STRAIN: MR5600  
PUBLICATION INFORMATION:  
AUTHORS: Brantlant, C, Krol, A, Machatt, M, A,  
AUTHORS: Pouyet, J, Ebel, J P, Edwards, K, Koessel,  
AUTHORS: H.  
TITLE: Primary and secondary  
structures of Escherichia coli MRE 600 23S  
TITLE: ribosomal RNA Comparison with models of  
TITLE: secondary structure for maize chloroplast 23S  
TITLE: rRNA and for large portions of mouse and human  
TITLE: 16S mitochondrial rRNAs  
JOURNAL: Nucleic Acids Research  
VOLUME: 9  
PAGES: 4303-4324  
DATE: 1981  
RELEVANT RESIDUES IN SEQ ID NO: 223 :FROM 1 TO 10  
US-08-173-489C-223

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
DB 4 GGGGG 8

RESULT 28  
US-08-173-489C-224/C  
Sequence 224, Application US/08173489C  
Patent No. 5861244  
GENERAL INFORMATION:  
APPLICANT: WANG, C. -G.  
APPLICANT: HEPBURN, A. G.  
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA  
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.  
NUMBER OF SEQUENCES: 365  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,  
STREET: 510 EAST 73RD STREET,  
CITY: NEW YORK  
STATE: NEW YORK

COUNTRY: USA  
ZIP: 10021.  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44Mb storage  
COMPUTER: IBM PC/XT/AT  
OPERATING SYSTEM: MS-DOS version 6.2  
SOFTWARE: Wordperfect Version 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/173,489C  
FILING DATE: 22 DEC 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/968,436  
FILING DATE: 29 OCT 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Handelman, Joseph H.  
REGISTRATION NUMBER: 26,179  
REFERENCE/DOCKET NUMBER: U9518-6  
TELEPHONE: (attorney) (212) 708-1880  
TELEFAX: (attorney) (212) 246-8959  
INFORMATION FOR SEQ ID NO: 224:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 bases  
TYPE: nucleic acid  
STRANDEDNESS: single stranded  
TOPOLOGY: linear  
MOLECULE TYPE: Other nucleic acid  
DESCRIPTION: third strand derived from E. coli 23S  
HYPOTHETICAL: yes  
ANTI-SENSE: no  
PUBLICATION INFORMATION:  
RELEVANT RESIDUES IN SEQ ID NO: 224 :FROM 1 TO 10  
US-08-173-489C-224

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
DB 9 GGGGG 5

RESULT 29  
US-08-590-571-28  
Sequence 28, Application US/08590571  
Patent No. 5861246  
GENERAL INFORMATION:  
APPLICANT: Sherman Weissman and Girish N. Nallur  
TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,571  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-590-571-28
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 3 GGGGG 7

RESULT 30
US-08-590-571-33
; Sequence 33, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Mallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/590,571
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-590-571-33
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 31
US-08-590-571-44
; Sequence 44, Application US/08590571
```

```
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Mallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/590,571
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-590-571-44
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 4 GGGGG 8

RESULT 22
US-08-590-571-47
; Sequence 47, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Mallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/590,571
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
```



REFERENCE/DOCKET NUMBER: Yale  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-590-571-47

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 5 GGGGG 9

## RESULT 33

US-08-590-571-49  
Sequence 49, Application US/08590571  
Patent No. 5861246

GENERAL INFORMATION:  
APPLICANT: Sherman Weisman and Girish N. Nallur  
TITLE OF INVENTION: MULTIPLE SELECTION PROCESS  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Yahwak & Associates  
STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: Macintosh

OPERATING SYSTEM: MS-DOS

SOFTWARE: Microsoft Word 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,571

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: George M. Yahwak

REGISTRATION NUMBER: 26,824

REFERENCE/DOCKET NUMBER: Yale

TELEPHONE: (203)268-1951

TELEFAX: (203)268-1951

INFORMATION FOR SEQ ID NO: 49:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-590-571-49

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 3 GGGGG 7

## RESULT 34

US-08-419-448-51

Sequence 51, Application US/08419448  
Patent No. 5863533  
GENERAL INFORMATION:  
APPLICANT: Robert F.M. Van Gorcom  
APPLICANT: Willem Van Hartingsveldt  
APPLICANT: Petrus A. Van Paridon  
APPLICANT: Annemarie E. Veenstra  
APPLICANT: Rudolf G.M. Luttin  
APPLICANT: Gerardus Selten  
TITLE OF INVENTION: Cloning and Expression of Microbial  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20006-1888

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/419,448

FILING DATE: 10-APR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 24615-20026.10

TELEPHONE: 202-887-1500

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (synthetic)

HYPOTHETICAL: NO

US-08-419-448-51

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||||  
Db 6 GGGGG 10

## RESULT 35

US-08-419-448-52/c

Sequence 52, Application US/08419448

Patent No. 5863533

GENERAL INFORMATION:

APPLICANT: Robert F.M. Van Gorcom

APPLICANT: Willem Van Hartingsveldt

APPLICANT: Petrus A. Van Paridon

APPLICANT: Annemarie E. Veenstra

APPLICANT: Rudolf G.M. Luttin

APPLICANT: Gerardus Selten

TITLE OF INVENTION: Cloning and Expression of Microbial

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 2000 Pennsylvania Ave. N.W., Suite 5500

CITY: Washington

STATE: D.C.

; COUNTRY: USA  
; ZIP: 20006-1888  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/419,448  
; FILING DATE: 10-APR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Murashige, Kate H.  
; REGISTRATION NUMBER: 29,959  
; REFERENCE/DOCKET NUMBER: 24615-20026.10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-1500  
; INFORMATION FOR SEQ ID NO: 52:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (synthetic)  
; HYPOTHETICAL: NO  
US-08-419-448-52

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 9 GGGGG 5

RESULT 36  
US-08-821-205-3/c  
; Sequence 3, Application US/08821205  
; Patent No. 5866700  
; GENERAL INFORMATION:  
; APPLICANT: Pfeleiderer, Wolfgang  
; APPLICANT: Schnell, Ralf  
; APPLICANT: Matysiak, Stephan  
; TITLE OF INVENTION: Solid-Phase Synthesis Of  
; TITLE OF INVENTION: Oligoribonucleotides.  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/821,205  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,354  
; FILING DATE: 03-NOV-1994  
; APPLICATION NUMBER: GR P 43 43 126.7  
; FILING DATE: 17-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Horton, Ken  
; REGISTRATION NUMBER: 39,481  
; REFERENCE/DOCKET NUMBER: 02481.1413-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4400  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-821-205-4

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;

; REFERENCE/DOCKET NUMBER: 02481.1413-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-821-205-3

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 10 GGGGG 6

RESULT 37  
US-08-821-205-4  
; Sequence 4, Application US/08821205  
; Patent No. 5866700  
; GENERAL INFORMATION:  
; APPLICANT: Pfeleiderer, Wolfgang  
; APPLICANT: Schnell, Ralf  
; APPLICANT: Matysiak, Stephan  
; TITLE OF INVENTION: Solid-Phase Synthesis Of  
; TITLE OF INVENTION: Oligoribonucleotides.  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &  
; ADDRESSEE: Dunner  
; STREET: 1300 I Street, N.W., Suite 700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005-3315  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/821,205  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/335,354  
; FILING DATE: 03-NOV-1994  
; APPLICATION NUMBER: GR P 43 43 126.7  
; FILING DATE: 17-DEC-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Horton, Ken  
; REGISTRATION NUMBER: 39,481  
; REFERENCE/DOCKET NUMBER: 02481.1413-00000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-408-4000  
; TELEFAX: 202-408-4400  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-821-205-4

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;

```
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 38
US-08-482-651-57/c
; Sequence 57, Application US/08482651
; Patent No. 5874409
; GENERAL INFORMATION:
; APPLICANT: Victoria, Edward J.
; TITLE OF INVENTION: apl IMMUNOREACTIVE PEPTIDES, CONJUGATES
; TITLE OF INVENTION: THEREOF AND METHODS OF TREATMENT FOR apl ANTIBODY-MEDIATED
; TITLE OF INVENTION: PATHOLOGIES
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/482,651
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Park, Freddie K.
; REGISTRATION NUMBER: 35,636
; REFERENCE/DOCKET NUMBER: 25231-20061.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-482-651-57

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 8 GGGGG 4

RESULT 39
US-08-595-043A-66/c
; Sequence 66, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 8 GGGGG 4

RESULT 40
US-08-595-043A-67
; Sequence 67, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

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ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-595-043A-66

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 10 GGGGG 6

RESULT 40
US-08-595-043A-67
; Sequence 67, Application US/08595043A
; Patent No. 5935824
; GENERAL INFORMATION:
; APPLICANT: SGARLATO, GREGORY D.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL
; STREET: 220 MONTGOMERY STREET, SUITE 2200
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,043A
; FILING DATE: 31-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CARROLL, PETER G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: SGAR-00371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```

US-08-595-043A-67

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 5 GGGGG 9

RESULT 41

US-08-403-888A-145  
; Sequence 145, Application US/08403888A  
; Patent No. 5952490  
; GENERAL INFORMATION:  
; APPLICANT: Hanecak et al.  
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core  
; TITLE OF INVENTION: Sequence  
; NUMBER OF SEQUENCES: 146  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490-19 LLP  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 6.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/403.888A  
; FILING DATE: 12-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/954.185  
; FILING DATE: 29-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Paul K. Legaard  
; REGISTRATION NUMBER: 38,534  
; REFERENCE/DOCKET NUMBER: ISIS-1229  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 145:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

US-08-403-888A-145

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 1 GGGGG 5

RESULT 42

US-08-481-658B-19/c  
; Sequence 19, Application US/08481658B  
; Patent No. 5955075  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481.658B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-435-2034  
; TELEFAX: 415-435-0727  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: AP-2 transcription factor  
US-08-481-658B-19

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 6 GGGGG 2

RESULT 43

US-08-481-658B-20/c  
; Sequence 20, Application US/08481658B  
; Patent No. 5955075  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/481.658B  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,190

FILING DATE: 15-JUN-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lauder, Leona L.  
 REGISTRATION NUMBER: 30,863  
 REFERENCE/DOCKET NUMBER: D-0021.3E  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-435-2034  
 TELEFAX: 415-435-0727  
 INFORMATION FOR SEQ ID NO: 20:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 10 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 DESCRIPTION: initiator (Inr) element  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 US-08-481-658B-20

Query Match	100.0%	Score 5;	DB 2;	Length 10;
Best Local Similarity	100.0%	Pred. No. 1.8e+05;		
Matches 5; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```

RESULT 44
US-08-722-187-45/c
; Sequence 45, Application US/08722187
; Patent No. 5955274
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,187

```

```

;      HYPOTHETICAL: NO
;      ANTI-SENSE: NO
US-08-722-187-45

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. NO. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY      1 GGGGG 5
        |||||
Db      6 GGGGG 2

RESULT 45
US-08-476-712-1
; Sequence 1, Application US/08476712
; Patent No. 596246
; GENERAL INFORMATION:

```

```

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. NO. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGGG 5
        |||||
Db       6 GGGGG 10

```

RESULT 46  
US-08-47/-504A-19/c  
Sequence 19, Application US/08477504A  
Patent No. 5972353  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein

NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,504A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCES/DOCKET NUMBER: D-0021.3D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: AP-2 transcription factor  
US-08-477-504A-19

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 6 GGGGG 2

RESULT 47  
US-08-477-504A-20/C  
Sequence 20, Application US/08477504A  
Patent No. 5972353  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/477,504A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCES/DOCKET NUMBER: D-0021.3D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
DESCRIPTION: initiator (Inr) element  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-477-504A-20

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.8e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 8 GGGGG 4

RESULT 48  
US-08-486-756A-19/c  
Sequence 19, Application US/08486756A  
Patent No. 5981711  
GENERAL INFORMATION:  
APPLICANT: Zavada, Jan  
APPLICANT: Pastorekova, Silvia  
APPLICANT: Pastorek, Jaromir  
TITLE OF INVENTION: MN Gene and Protein  
NUMBER OF SEQUENCES: 86  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Leona L. Lauder  
STREET: 6 Mariposa Court  
CITY: Tiburon  
STATE: California  
COUNTRY: USA  
ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,756A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCES/DOCKET NUMBER: D-0021.3C  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-435-2034  
TELEFAX: 415-435-0727  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

```
;
; DESCRIPTION: AP-2 transcription factor
US-08-486-756A-19
;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5
Db 6 GGGGG 2

RESULT 49
US-08-486-756A-20/c
; Sequence 20, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
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; OPERATING SYSTEM: PC-DOS/MS-DOS
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; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 20:
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; TYPE: nucleic acid
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; MOLECULE TYPE: DNA (genomic)
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US-08-486-756A-20

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; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
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; FILING DATE: 07-JUN-1995
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; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 146	5	100.0	10	15	US-10-330-627-582	Sequence 582, App	c 219	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
147	5	100.0	10	15	US-10-330-627-622	Sequence 622, App	c 220	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
c 148	5	100.0	10	15	US-10-330-627-699	Sequence 699, App	c 221	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
c 149	5	100.0	10	15	US-10-330-627-700	Sequence 700, App	c 222	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
c 150	5	100.0	10	15	US-10-330-627-744	Sequence 744, App	c 223	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
c 151	5	100.0	10	15	US-10-330-627-820	Sequence 820, App	c 224	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
c 152	5	100.0	10	15	US-10-330-627-825	Sequence 825, App	c 225	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
c 153	5	100.0	10	15	US-10-330-627-842	Sequence 842, App	c 226	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
c 154	5	100.0	10	15	US-10-330-627-842	Sequence 842, App	c 227	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
155	5	100.0	10	15	US-10-330-627-906	Sequence 906, App	c 228	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
c 156	5	100.0	10	15	US-10-330-627-993	Sequence 993, App	c 229	5	100.0	10	16	US-10-330-333-4	Sequence 3, Appli
c 157	5	100.0	10	15	US-10-330-627-1020	Sequence 1020, Ap	c 230	5	100.0	10	16	US-10-330-627-1020	Sequence 1020, Ap
158	5	100.0	10	15	US-10-330-627-1029	Sequence 1029, Ap	c 231	5	100.0	10	16	US-10-330-627-1029	Sequence 1029, Ap

232	5	100.0	10	18	US-10-816-220-163	Sequence 163, App	305	5	100.0	11	17	US-10-297-969-13	Sequence 13, Appl
c 233	5	100.0	10	18	US-10-816-220-163	Sequence 163, App	c 306	5	100.0	11	17	US-10-297-969-17	Sequence 16, Appl
234	5	100.0	10	18	US-10-650-650-49	Sequence 49, Appl	307	5	100.0	11	17	US-10-297-969-16	Sequence 17, Appl
c 235	5	100.0	10	18	US-10-477-044-11	Sequence 11, Appl	308	5	100.0	11	17	US-10-687-588-3	Sequence 3, Appl
236	5	100.0	10	18	US-10-487-934-70	Sequence 70, Appl	c 309	5	100.0	11	17	US-10-612-224-128	Sequence 128, App
c 237	5	100.0	10	18	US-10-487-934-112	Sequence 112, App	c 310	5	100.0	11	17	US-10-700-118-25	Sequence 25, Appl
c 238	5	100.0	10	18	US-10-487-934-113	Sequence 113, App	311	5	100.0	11	17	US-10-450-797-4	Sequence 4, Appl
239	5	100.0	10	18	US-10-487-934-137	Sequence 137, App	312	5	100.0	11	17	US-10-450-797-30	Sequence 30, Appl
c 240	5	100.0	10	18	US-10-487-934-155	Sequence 155, App	313	5	100.0	11	17	US-10-450-797-49	Sequence 49, Appl
c 241	5	100.0	10	18	US-10-487-934-156	Sequence 156, App	314	5	100.0	11	17	US-10-450-797-75	Sequence 75, Appl
c 242	5	100.0	10	18	US-10-487-934-157	Sequence 157, App	315	5	100.0	11	17	US-10-450-797-81	Sequence 81, Appl
c 243	5	100.0	10	18	US-10-487-934-164	Sequence 164, App	316	5	100.0	11	17	US-10-450-797-88	Sequence 88, Appl
c 244	5	100.0	10	18	US-10-487-934-209	Sequence 209, App	c 317	5	100.0	11	17	US-10-450-797-159	Sequence 159, App
245	5	100.0	10	18	US-10-487-934-282	Sequence 282, App	318	5	100.0	11	17	US-10-450-797-205	Sequence 205, App
c 246	5	100.0	10	18	US-10-487-934-286	Sequence 286, App	319	5	100.0	11	17	US-10-450-797-296	Sequence 296, App
c 247	5	100.0	10	18	US-10-602-494-358	Sequence 358, App	320	5	100.0	11	17	US-10-450-797-312	Sequence 312, App
c 248	5	100.0	10	18	US-10-602-494-376	Sequence 376, App	321	5	100.0	11	17	US-10-450-797-368	Sequence 368, App
249	5	100.0	11	8	US-08-887-505-162	Sequence 162, App	c 322	5	100.0	11	17	US-10-450-797-396	Sequence 396, App
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251	5	100.0	11	9	US-09-796-071-36	Sequence 36, Appl	324	5	100.0	11	17	US-10-450-797-481	Sequence 481, App
252	5	100.0	11	9	US-09-783-338A-1	GENERAL INFORMA	c 325	5	100.0	11	17	US-10-450-797-529	Sequence 529, App
253	5	100.0	11	9	US-09-783-338A-5	Sequence 5, Appl	c 326	5	100.0	11	17	US-10-450-797-607	Sequence 607, App
c 254	5	100.0	11	9	US-09-813-031-12	Sequence 12, Appl	c 327	5	100.0	11	17	US-10-450-797-624	Sequence 624, App
255	5	100.0	11	9	US-09-813-031-20	Sequence 20, Appl	c 328	5	100.0	11	17	US-10-450-797-768	Sequence 768, App
256	5	100.0	11	9	US-09-861-975B-8	Sequence 8, Appl	329	5	100.0	11	17	US-10-450-797-831	Sequence 831, App
c 257	5	100.0	11	9	US-09-813-990A-12	Sequence 12, Appl	330	5	100.0	11	17	US-10-450-797-844	Sequence 844, App
c 258	5	100.0	11	9	US-09-813-990A-20	Sequence 20, Appl	c 331	5	100.0	11	17	US-10-450-797-877	Sequence 877, App
c 259	5	100.0	11	9	US-09-879-813-42	Sequence 42, Appl	332	5	100.0	11	17	US-10-450-797-970	Sequence 970, App
260	5	100.0	11	9	US-09-945-901-9	Sequence 9, Appl	c 333	5	100.0	11	17	US-10-450-797-1009	Sequence 1009, App
261	5	100.0	11	9	US-09-961-700A-51	Sequence 51, Appl	334	5	100.0	11	17	US-10-450-797-1022	Sequence 1022, App
c 262	5	100.0	11	10	US-09-974-974-10	Sequence 10, Appl	c 335	5	100.0	11	17	US-10-450-797-1167	Sequence 1167, App
c 263	5	100.0	11	10	US-09-918-715-48	Sequence 48, Appl	c 336	5	100.0	11	17	US-10-450-797-1183	Sequence 1183, App
c 264	5	100.0	11	10	US-09-918-715-118	Sequence 118, App	337	5	100.0	11	17	US-10-450-797-1217	Sequence 1217, App
265	5	100.0	11	10	US-09-943-115A-56	Sequence 56, Appl	338	5	100.0	11	17	US-10-450-797-1287	Sequence 1287, App
c 266	5	100.0	11	10	US-09-943-115A-61	Sequence 61, Appl	c 339	5	100.0	11	17	US-10-450-797-1338	Sequence 1338, App
267	5	100.0	11	10	US-09-249-155-130	Sequence 130, App	c 340	5	100.0	11	17	US-10-450-797-1406	Sequence 1406, App
268	5	100.0	11	10	US-09-249-155-144	Sequence 144, App	341	5	100.0	11	17	US-10-616-228-36	Sequence 36, Appl
269	5	100.0	11	10	US-09-249-155-147	Sequence 147, App	c 342	5	100.0	11	18	US-10-474-794-48	Sequence 48, Appl
270	5	100.0	11	10	US-09-249-155-236	Sequence 236, App	c 343	5	100.0	11	18	US-10-474-794-118	Sequence 118, App
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c 272	5	100.0	11	11	US-09-775-479-18	Sequence 18, Appl	345	5	100.0	11	18	US-10-114-908-50	Sequence 50, Appl
c 273	5	100.0	11	13	US-10-007-747-9	Sequence 9, Appl	346	5	100.0	11	18	US-10-149-109A-150	Sequence 150, App
274	5	100.0	11	14	US-10-038-937-9	Sequence 9, Appl	c 347	5	100.0	11	18	US-10-149-109A-151	Sequence 151, App
c 275	5	100.0	11	14	US-10-060-795B-19	Sequence 19, Appl	c 348	5	100.0	11	18	US-10-898-106-46	Sequence 46, Appl
c 276	5	100.0	11	14	US-10-060-795B-25	Sequence 25, Appl	c 349	5	100.0	12	9	US-09-365-029-55	Sequence 55, Appl
c 277	5	100.0	11	14	US-10-067-956-46	Sequence 46, Appl	c 350	5	100.0	12	9	US-09-365-029-56	Sequence 56, Appl
c 278	5	100.0	11	15	US-10-146-595-42	Sequence 42, Appl	351	5	100.0	12	9	US-09-861-975B-9	Sequence 9, Appl
c 279	5	100.0	11	15	US-10-055-732-7	Sequence 7, Appl	c 352	5	100.0	12	9	US-09-922-261-31	Sequence 31, Appl
c 280	5	100.0	11	15	US-10-046-671B-46	Sequence 46, Appl	c 353	5	100.0	12	9	US-09-835-371-35	Sequence 35, Appl
281	5	100.0	11	15	US-10-046-671B-58	Sequence 58, Appl	c 354	5	100.0	12	9	US-09-835-371-36	Sequence 36, Appl
c 282	5	100.0	11	15	US-10-046-671B-58	Sequence 58, Appl	c 355	5	100.0	12	9	US-09-841-157A-12	Sequence 12, Appl
283	5	100.0	11	15	US-10-046-671B-59	Sequence 59, Appl	356	5	100.0	12	9	US-09-841-157A-15	Sequence 15, Appl
c 284	5	100.0	11	15	US-10-046-671B-59	Sequence 59, Appl	c 357	5	100.0	12	10	US-09-835-370-35	Sequence 35, Appl
285	5	100.0	11	15	US-10-214-417A-45	Sequence 45, Appl	c 358	5	100.0	12	10	US-09-835-370-36	Sequence 36, Appl
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287	5	100.0	11	15	US-10-407-637-5	Sequence 5, Appl	360	5	100.0	12	10	US-09-888-326-823	Sequence 823, App
288	5	100.0	11	15	US-10-407-637-7	Sequence 7, Appl	361	5	100.0	12	10	US-09-776-479-795	Sequence 795, App
289	5	100.0	11	15	US-10-396-122-102	Sequence 102, App	c 362	5	100.0	12	10	US-09-776-479-812	Sequence 812, App
290	5	100.0	11	15	US-10-314-322-130	Sequence 130, App	c 363	5	100.0	12	10	US-09-964-895-21	Sequence 21, Appl
291	5	100.0	11	15	US-10-314-322-134	Sequence 134, App	364	5	100.0	12	11	US-09-776-479-795	Sequence 795, App
292	5	100.0	11	15	US-10-314-322-140	Sequence 140, App	c 365	5	100.0	12	11	US-09-776-479-812	Sequence 812, App
293	5	100.0	11	15	US-10-314-322-147	Sequence 147, App	366	5	100.0	12	14	US-10-059-888-25	Sequence 25, Appl
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c 296	5	100.0	11	15	US-10-314-322-306	Sequence 306, App	369	5	100.0	12	14	US-10-017-995-795	Sequence 795, App
297	5	100.0	11	15	US-10-314-322-307	Sequence 307, App	c 370	5	100.0	12	14	US-10-017-995-812	Sequence 812, App
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c 304	5	100.0	11	17	US-10-297-969-12	Sequence 12, Appl	377	5	100.0	12	15	US-10-224-523-32	Sequence 32, Appl

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C 389	5	100.0	12	15	US-10-091-281-374	Sequence 374, App	C 462	5	100.0	12	18	US-10-257-017B-276248	Sequence 276248,
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C 392	5	100.0	12	15	US-10-314-578-912	Sequence 812, App	C 465	5	100.0	12	18	US-10-257-017B-276737	Sequence 276737,
C 393	5	100.0	12	16	US-10-182-329-53	Sequence 53, Appl	C 466	5	100.0	12	18	US-10-257-017B-276885	Sequence 276885,
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C 404	5	100.0	12	18	US-10-849-072-9	Sequence 9, Appli	C 477	5	100.0	12	18	US-10-257-017B-279348	Sequence 279348,
C 405	5	100.0	12	18	US-10-849-072-16	Sequence 16, Appl	C 478	5	100.0	12	18	US-10-257-017B-279496	Sequence 279496,
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C 409	5	100.0	12	18	US-10-816-220-161	Sequence 161, App	C 482	5	100.0	12	18	US-10-257-017B-280162	Sequence 280162,
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C 421	5	100.0	12	18	US-10-257-017B-268908	Sequence 268908,	C 494	5	100.0	12	18	US-10-257-017B-281833	Sequence 281833,
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C 428	5	100.0	12	18	US-10-257-017B-270978	Sequence 270978,							
C 429	5	100.0	12	18	US-10-257-017B-271220	Sequence 271220,							
C 430	5	100.0	12	18	US-10-257-017B-271230	Sequence 271230,							
C 431	5	100.0	12	18	US-10-257-017B-271435	Sequence 271435,							
C 432	5	100.0	12	18	US-10-257-017B-271478	Sequence 271478,							
C 433	5	100.0	12	18	US-10-257-017B-271572	Sequence 271572,							
C 434	5	100.0	12	18	US-10-257-017B-271660	Sequence 271660,							
C 435	5	100.0	12	18	US-10-257-017B-271978	Sequence 271978,							
C 436	5	100.0	12	18	US-10-257-017B-272337	Sequence 272337,							
C 437	5	100.0	12	18	US-10-257-017B-272442	Sequence 272442,							
C 438	5	100.0	12	18	US-10-257-017B-272443	Sequence 272443,							
C 439	5	100.0	12	18	US-10-257-017B-272520	Sequence 272520,							
C 440	5	100.0	12	18	US-10-257-017B-272684	Sequence 272684,							
C 441	5	100.0	12	18	US-10-257-017B-272840	Sequence 272840,							
C 442	5	100.0	12	18	US-10-257-017B-272846	Sequence 272846,							
C 443	5	100.0	12	18	US-10-257-017B-272871	Sequence 272871,							
C 444	5	100.0	12	18	US-10-257-017B-272941	Sequence 272941,							
C 445	5	100.0	12	18	US-10-257-017B-272942	Sequence 272942,							
C 446	5	100.0	12	18	US-10-257-017B-273098	Sequence 273098,							
C 447	5	100.0	12	18	US-10-257-017B-273173	Sequence 273173,							
C 448	5	100.0	12	18	US-10-257-017B-273469	Sequence 273469,							
C 449	5	100.0	12	18	US-10-257-017B-273502	Sequence 273502,							
C 450	5	100.0	12	18	US-10-257-017B-274041	Sequence 274041,							

RESULT 1  
US-08-887-505-160  
; Sequence 160, Application US/08887505  
; Publication No. US20020081577A1  
; GENERAL INFORMATION:  
; APPLICANT: Kilkuskie, Robert E.  
; APPLICANT: Frank, Bruce L.  
; APPLICANT: Goodchild, John  
; APPLICANT: Wolfe, Jia L.  
; APPLICANT: Roberts, Peter C.  
; APPLICANT: Hamlin, Jr., Henry A.  
; APPLICANT: Roberts, No. US20020081577A1 A.  
; APPLICANT: Walther, Debra M.  
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR  
; TITLE OF INVENTION: HEPATITIS C VIRUS  
; NUMBER OF SEQUENCES: 172  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hale and Dorr LLP

```

; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,505
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,968
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kerner, Ann-Louise
; REGISTRATION NUMBER: 33,523
; REFERENCE/DOCKET NUMBER: HY2-040CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; TELEFAX: (617) 526-5000
; INFORMATION FOR SEQ ID NO: 160:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA/RNA
; HYPOTHETICAL: NO
; ANTI-SENSE: YES
; US-08-887-505-160

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```

Query Match          100.0%; Score 5; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

```

```

RESULT 2
US-09-005-243-31/c
; Sequence 31, Application US/09005243
; Patent No. US20020018763A1
; GENERAL INFORMATION:
; APPLICANT: Zeebo, Kristina M.
; APPLICANT: Boesselman, Robert A.
; APPLICANT: Suggs, Sidney V.
; APPLICANT: Martin, Francis H.
; TITLE OF INVENTION: Stem Cell Factor
; NUMBER OF SEQUENCES: 104
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005,243
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/449,653

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; FILING DATE: 24-MAY-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/982,255
; FILING DATE: 25-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/589,701
; FILING DATE: 01-OCT-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/573,616
; FILING DATE: 24-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/537,198
; FILING DATE: 11-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/422,383
; FILING DATE: 16-OCT-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 01017/34465
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-005-243-31

```

```

Query Match          100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGGG 5
    |||||
Db 7 GGGGG 3

```

```

RESULT 3
US-09-783-338A-2
; Sequence 2, Application US/09783338A
; Patent No. US2002028922A1
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter M.
; APPLICANT: Havre, Pamela A.
; TITLE OF INVENTION: Chemically Modified Oligonucleotide for
; Site-Directed Mutagenesis
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 1100 Peachtree Street, Suite 2800
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-4530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/783,338A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/083,088
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:

```

NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: YU109  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-815-6508  
TELEFAX: (404)-815-6555  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-783-338A-2  
Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
Qy 1 GGGGG 5  
Db 6 GGGGG 10  
RESULT 4  
US-09-783-338A-3  
Sequence 3, Application US/09783338A  
Patent No. US2002028922A1  
GENERAL INFORMATION:  
APPLICANT: Glazer, Peter M.  
ADDRESS: Havre, Pamela A.  
STREET: 1100 Peachtree Street, Suite 2800  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30309-4530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/783,338A  
FILING DATE: 14-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/083,088  
FILING DATE: 25-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Pabst, Patrea L.  
REGISTRATION NUMBER: 31,284  
REFERENCE/DOCKET NUMBER: YU109  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (404)-815-6508  
TELEFAX: (404)-815-6555  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-783-338A-3  
Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;  
Gaps 0;  
Qy 1 GGGGG 5  
Db 1 GGGGG 5  
RESULT 5  
US-09-224-683-31/c  
Sequence 31, Application US/09224683  
Patent No. US20020031491A1  
GENERAL INFORMATION:  
APPLICANT: Zsebo, Kristina M.  
APPLICANT: Bosselman, Robert A.  
APPLICANT: Suggs, Sidney V.  
APPLICANT: Martin, Francis H.  
TITLE OF INVENTION: Stem Cell Factor: Composition Claims  
NUMBER OF SEQUENCES: 104  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/224,683  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/005,893  
FILING DATE: 12-JAN-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/449,653  
FILING DATE: 24-MAY-1995  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/982,255  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/589,701  
FILING DATE: 01-OCT-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/573,616  
FILING DATE: 24-AUG-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/537,198  
FILING DATE: 11-JUN-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/422,383  
FILING DATE: 16-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 01017/35136  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-224-683-31

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 7 GGGGG 3

RESULT 6
US-09-989-789-96
; Sequence 96, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 96
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-96

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 6 GGGGG 10

RESULT 7
US-09-989-789-97
; Sequence 97, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-97

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 8
US-09-989-789-604
; Sequence 604, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 604
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-604

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 9
US-09-989-789-634
; Sequence 634, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 634
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-634

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5

RESULT 10
US-09-989-789-635
; Sequence 635, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 635
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-635

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
Db 1 GGGGG 5
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; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 635
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-635

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 11
US-09-989-789-1271
; Sequence 1271, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1271
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1271

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 12
US-09-989-789-1272
; Sequence 1272, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1272
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1272

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 13
US-09-989-789-1317
; Sequence 1317, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1317
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1317

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 14
US-09-989-789-1345
; Sequence 1345, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1345
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1345

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5
```

```
; OTHER INFORMATION: DNA
US-09-989-789-1272

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 13
US-09-989-789-1317
; Sequence 1317, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1317
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1317

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 14
US-09-989-789-1345
; Sequence 1345, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1345
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1345

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5
```



```
RESULT 15
US-09-989-789-1637
; Sequence 1637, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1637
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1637

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      1 GGGGG 5

RESULT 16
US-09-989-789-1660
; Sequence 1660, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1660
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1660

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      1 GGGGG 5

RESULT 17
US-09-989-789-1668
; Sequence 1668, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
```

```
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1668

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      3 GGGGG 7

RESULT 18
US-09-852-261-8/c
; Sequence 8, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-09-852-261-8

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
Db      6 GGGGG 2

RESULT 19
US-09-816-763-28/c
; Sequence 28, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
```

;  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor  
; OTHER INFORMATION: EGR-2  
US-09-816-763-28

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 8 GGGGG 4

RESULT 20  
US-09-772-719-19/c  
; Sequence 19, Application US/09772719  
; Patent No. US20020137910A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: AP-2 transcription factor  
US-09-772-719-19

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 6 GGGGG 2

RESULT 21  
US-09-772-719-20/c  
; Sequence 20, Application US/09772719  
; Patent No. US20020137910A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: initiator (Inr) element  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-09-772-719-20

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 8 GGGGG 4

RESULT 22  
US-09-846-033B-139  
; Sequence 139, Application US/09846033B  
; Publication No. US2003004404A1  
; GENERAL INFORMATION:  
; APPLICANT: Rebar, Edward  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Liu, Qiang  
; APPLICANT: Liu, Pei-Qi  
; APPLICANT: Wolffe, Alan  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric  
; APPLICANT: Sangamo BioSciences, Inc.

;  
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc  
; FILE REFERENCE: 019496-005820US  
; CURRENT APPLICATION NUMBER: US/09/846,033B  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 09/733,604  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 09/736,083  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 139  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: target  
US-09-846-033B-139

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||  
Db 1 GGGGG 5

RESULT 23  
US-09-846-033B-141  
; Sequence 141, Application US/09846033B  
; Publication No. US2003004404A1  
; GENERAL INFORMATION:  
; APPLICANT: Rebar, Edward  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Liu, Qiang  
; APPLICANT: Liu, Pei-Qi  
; APPLICANT: Wolffe, Alan  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric  
; APPLICANT: Sangamo BioSciences, Inc.  
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc  
; FILE REFERENCE: 019496-005820US  
; CURRENT APPLICATION NUMBER: US/09/846,033B  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 09/733,604  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 09/736,083  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 141  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: target  
US-09-846-033B-141

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||  
Db 6 GGGGG 10

RESULT 24  
US-09-846-033B-143  
; Sequence 143, Application US/09846033B  
; Publication No. US2003004404A1

;  
; GENERAL INFORMATION:  
; APPLICANT: Rebar, Edward  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Liu, Qiang  
; APPLICANT: Liu, Pei-Qi  
; APPLICANT: Wolffe, Alan  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric  
; APPLICANT: Sangamo BioSciences, Inc.  
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc  
; FILE REFERENCE: 019496-005820US  
; CURRENT APPLICATION NUMBER: US/09/846,033B  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 09/733,604  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 09/736,083  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 143  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: target  
US-09-846-033B-143

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
|||  
Db 4 GGGGG 8

RESULT 25  
US-09-846-033B-144  
; Sequence 144, Application US/09846033B  
; Publication No. US2003004404A1  
; GENERAL INFORMATION:  
; APPLICANT: Rebar, Edward  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Liu, Qiang  
; APPLICANT: Liu, Pei-Qi  
; APPLICANT: Wolffe, Alan  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric  
; APPLICANT: Sangamo BioSciences, Inc.  
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc  
; FILE REFERENCE: 019496-005820US  
; CURRENT APPLICATION NUMBER: US/09/846,033B  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 09/733,604  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 09/736,083  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 144  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: target  
US-09-846-033B-144

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 26
US-09-846-033B-145
; Sequence 145, Application US/09846033B
; Publication No. US20030044404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo BioSciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 145
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-145

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 1 GGGGG 5

RESULT 27
US-09-846-033B-146
; Sequence 146, Application US/09846033B
; Publication No. US20030044404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo BioSciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 146
; LENGTH: 10
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-146

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 3 GGGGG 7

RESULT 28
US-09-846-033B-240
; Sequence 240, Application US/09846033B
; Publication No. US20030044404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo BioSciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-240

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5
    |||||
Db 4 GGGGG 8

RESULT 29
US-09-971-894-39
; Sequence 39, Application US/09971894
; Publication No. US20030044804A1
; GENERAL INFORMATION:
; APPLICANT: Kashi, Yechezkel
; APPLICANT: Gur-Arie, Riva
; APPLICANT: Cohen, Cyril
; APPLICANT: Eitan, Yuval
; APPLICANT: Shelef, Leora
; APPLICANT: Hallerman, Eric
; TITLE OF INVENTION: ABUNDANT, WELL DISTRIBUTED AND HYPERPOLYMORPHIC SIMPLE SEQUENCE R
; FILE REFERENCE: 01/22569
; CURRENT APPLICATION NUMBER: US/09/971,894
; CURRENT FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: US 09/472,035
; PRIOR FILING DATE: 1999-12-27
```

; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 39  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
US-09-971-894-39

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||  
Db 1 GGGGG 5

RESULT 30  
US-09-967-237-20/c  
; Sequence 20, Application US/09967237  
; Publication No. US20030049828A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; FILE REFERENCE: D-0021.5B-2  
; CURRENT APPLICATION NUMBER: US/09/967,237  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 09/178,115  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: HUMAN  
US-09-967-237-20

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||  
Db 8 GGGGG 4

RESULT 31  
US-09-990-186-96  
; Sequence 96, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 96  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
US-09-990-186-96

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||  
Db 1 GGGGG 5

QY 1 GGGGG 5  
|||  
Db 6 GGGGG 10

RESULT 32  
US-09-990-186-97  
; Sequence 97, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 97  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
US-09-990-186-97

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||  
Db 3 GGGGG 7

RESULT 33  
US-09-990-186-604  
; Sequence 604, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 604  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
US-09-990-186-604

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGG 5  
|||  
Db 1 GGGGG 5

RESULT 34  
US-09-990-186-634  
; Sequence 634, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 634  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-634

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 1 GGGGG 5

RESULT 35  
US-09-990-186-635  
; Sequence 635, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 635  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-635

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 1 GGGGG 5

RESULT 36  
US-09-990-186-1271  
; Sequence 1271, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1271  
; LENGTH: 10  
; TYPE: DNA

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1271

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 1 GGGGG 5

RESULT 37  
US-09-990-186-1272  
; Sequence 1272, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1272  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1272

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 1 GGGGG 5

RESULT 38  
US-09-990-186-1317  
; Sequence 1317, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1317  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1317

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

```
Db      1 GGGGG 5
|||||
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1345
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1345

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
|||||
Db      1 GGGGG 5

RESULT 40
US-09-990-186-1637
; Sequence 1637, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1637
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1637

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
|||||
Db      1 GGGGG 5

RESULT 41
US-09-990-186-1660
; Sequence 1660, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1660
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1660

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
|||||
Db      1 GGGGG 5

RESULT 42
US-09-990-186-1668
; Sequence 1668, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1668

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
|||||
Db      3 GGGGG 7

RESULT 43
US-09-979-593-43
; Sequence 43, Application US/09979593
; Publication No. US20030082555A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie B
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MMH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
```

```
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1660
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1660

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
|||||
Db      3 GGGGG 7

RESULT 42
US-09-990-186-1668
; Sequence 1668, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1668

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGGG 5
|||||
Db      3 GGGGG 7

RESULT 43
US-09-979-593-43
; Sequence 43, Application US/09979593
; Publication No. US20030082555A1
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y
; APPLICANT: Denton, R. Rex
; APPLICANT: Kliem, Stefanie B
; APPLICANT: Lee, Helen H
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE
; FILE REFERENCE: MMH-0425 PCT ICAM2
; CURRENT APPLICATION NUMBER: US/09/979,593
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/14714
; PRIOR FILING DATE: 2001-05-07
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; PRIOR APPLICATION NUMBER: 60/201,946  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-979-593-43

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 1 GGGGG 5

## RESULT 44

US-09-989-994-96  
; Sequence 96, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 96  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-96

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 6 GGGGG 10

## RESULT 45

US-09-989-994-97  
; Sequence 97, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 97  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-97

Query Match 100.0%; Score 5; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 3 GGGGG 7

## RESULT 46

US-09-989-994-604  
; Sequence 604, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 604  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-604

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 1 GGGGG 5

## RESULT 47

US-09-989-994-634  
; Sequence 634, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 634  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-634

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5  
Db 1 GGGGG 5

## RESULT 48

US-09-989-994-635  
; Sequence 635, Application US/09989994



; Publication No. US20030104526A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,994

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 635

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-994-635

Query Match

Best Local Similarity 100.0%; Score 5; DB 10; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 1 GGGGG 5

RESULT 49

US-09-989-994-1271

; Sequence 1271, Application US/09989994

; Publication No. US20030104526A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,994

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1271

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-994-1271

Query Match

Best Local Similarity 100.0%; Score 5; DB 10; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 1 GGGGG 5

RESULT 50

US-09-989-994-1272

; Sequence 1272, Application US/09989994

; Publication No. US20030104526A1

; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

; FILE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.20 / S11-US2

; CURRENT APPLICATION NUMBER: US/09/989,994

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1272

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA

US-09-989-994-1272

Query Match

Best Local Similarity 100.0%; Score 5; DB 10; Length 10;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGGG 5

Db 1 GGGGG 5

Search completed: January 7, 2005, 11:31:30

Job time : 272.2 secs

**This Page Blank (uspto)**

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GGGTG

Perfect score: 5

Sequence: 1 ggggtg 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_to.\*

11: gb\_ats.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	100.0	10	6	A52270 Sequence 60
2	5	100.0	10	6	A52271 Sequence 61
3	5	100.0	10	6	A98816 Sequence 16
C 4	5	100.0	10	6	AR013952 Sequence
C 5	5	100.0	10	6	AR016043 Sequence
C 6	5	100.0	10	6	AR016245 Sequence
C 7	5	100.0	10	6	AR017948 Sequence
C 8	5	100.0	10	6	AR020527 Sequence
C 9	5	100.0	10	6	AR030206 Sequence
10	5	100.0	10	6	AR030234 Sequence
11	5	100.0	10	6	AR035526 Sequence
12	5	100.0	10	6	AR050986 Sequence
C 13	5	100.0	10	6	AR059204 Sequence
C 14	5	100.0	10	6	AR069288 Sequence
15	5	100.0	10	6	AR069301 Sequence
16	5	100.0	10	6	AR074300 Sequence
C 17	5	100.0	10	6	AR074448 Sequence
C 18	5	100.0	10	6	AR074449 Sequence
C 19	5	100.0	10	6	AR075515 Sequence

C 20	5	100.0	10	6	AR081128	Sequence
C 21	5	100.0	10	6	AR081129	Sequence
C 22	5	100.0	10	6	AR085325	Sequence
C 23	5	100.0	10	6	AR085326	Sequence
C 24	5	100.0	10	6	AR088073	Sequence
C 25	5	100.0	10	6	AR088074	Sequence
C 26	5	100.0	10	6	AR092704	Sequence
27	5	100.0	10	6	AR096109	Sequence
C 28	5	100.0	10	6	AR100871	Sequence
C 29	5	100.0	10	6	AR104232	Sequence
C 30	5	100.0	10	6	AR104233	Sequence
C 31	5	100.0	10	6	AR106688	Sequence
C 32	5	100.0	10	6	AR107848	Sequence
C 33	5	100.0	10	6	AR143496	Sequence
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c 412	5	100.0	11	6	AX470476	Sequence	AX470476	Sequence	5	100.0	11	6	AX626126	Sequence
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c 418	5	100.0	11	6	AX470852	Sequence	AX470852	Sequence	5	100.0	11	6	AX626571	Sequence
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423	5	100.0	11	6	AX471020	Sequence	AX471020	Sequence	5	100.0	11	6	AX627085	Sequence
c 424	5	100.0	11	6	AX471352	Sequence	AX471352	Sequence	5	100.0	11	6	AX627151	Sequence
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ALIGNMENTS

RESULT 1

LOCUS

AS2270

Sequence 60 from Patent EP0705842.

10 bp

DNA

linear

PAT 12-DEC-1997

DEFINITION

AS2270

Sequence 60 from Patent EP0705842.

ACCESSION

AS2270

GI:2852042

VERSION

AS2270.1

KEYWORDS

unidentified

SOURCE

unidentified

ORGANISM

unclassified.

REFERENCE

1

AUTHORS

Bartnik, E.D. and Margerie, D.D.

TITLE

Regulated genes by stimulation of chondrocytes with 1L-beta

JOURNAL

Patent: EP 0705842-A 60 10-APR-1996;

COMMENT

HOECHST AG (DE)

Other publication 2A 9508381 960424

Other publication JP 8191893 960730

Other publication CA 2159957 960407

Other publication AU 3308695 960418.

FEATURES

Location/Qualifiers

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QY      1 GGGTG 5
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DB      6 GGGTG 10

RESULT 2
A52271
LOCUS      A52271      10 bp      DNA      linear      PAT 12-DEC-1997
DEFINITION      Sequence 61 from Patent EP0705842.
ACCESSION      A52271
VERSION      A52271.1 GI:2852041
KEYWORDS      .
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1
AUTHORS      Bartnik,E.D. and Margerie,D.D.
TITLE      Regulated genes by stimulation of chondrocytes with 1L-1beta
JOURNAL      Patent: EP 0705842-A 61 10-APR-1996;
COMMENT      HOECHST AG (DE)
Other publication ZA 9508381 960424
Other publication JP 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
      |||||
DB      6 GGGTG 10

RESULT 3
A98816
LOCUS      A98816      10 bp      DNA      linear      PAT 26-JAN-2000
DEFINITION      Sequence 16 from Patent WO9909817.
ACCESSION      A98816
VERSION      A98816.1 GI:6781837
KEYWORDS      .
SOURCE      unidentified
ORGANISM      unidentified
REFERENCE      1 (bases 1 to 10)
AUTHORS      Finnegan,D.J. and Sang,H.
TITLE      USE OF MARINER TRANSPOSAN IN THE PRODUCTION OF TRANSGENIC ANIMALS
JOURNAL      Patent: WO 9909817-A 16 04-MAR-1999;
FINNEGAN DAVID JOHN (GB); SANG HELEN (GB)
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Query Match      100.0%; Score 5; DB 6; Length 10;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      4 GGGTG 8

RESULT 4
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LOCUS      AR013952      10 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION      Sequence 7 from patent US 5773226.
ACCESSION      AR013952
VERSION      AR013952.1 GI:3971406
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Millan,J.L.
TITLE      Recombinant calf intestinal alkaline phosphatase
JOURNAL      Patent: US 5773226-A 7 30-JUN-1998;
FEATURES      Location/Qualifiers
source      1..10
/mol_type="unassigned DNA"

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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
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DB      10 GGGTG 6

RESULT 5
AR016043/c
LOCUS      AR016043      10 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION      Sequence 11 from patent US 5776679.
ACCESSION      AR016043
VERSION      AR016043.1 GI:3972320
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Villeponteau,B., Ferg,J., Funk,W. and Andrews,W.H.
TITLE      Assays for the DNA component of human telomerase
JOURNAL      Patent: US 5776679-A 11 07-JUL-1998;
FEATURES      Location/Qualifiers
source      1..10
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ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
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DB      7 GGGTG 3

RESULT 6
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LOCUS      AR016245      10 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION      Sequence 13 from patent US 5776683.
ACCESSION      AR016245
VERSION      AR016245.1 GI:3972522
KEYWORDS      .
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
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AUTHORS Smith,H.S. and Chen,L.-C.
TITLE Methods for identifying genes amplified in cancer cells
JOURNAL Patent: US 5776683-A 13 07-JUL-1998;
FEATURES Location/Qualifiers
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Qy 1 GGGTG 5
Db 8 GGGTG 4

RESULT 7
LOCUS AR017948 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 13 from patent US 5780273.
ACCESSION AR017948
VERSION AR017948.1 GI:3973551
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 10)
          Burg,J.Lawrence.
TITLE Insertion elements and amplifiable nucleic acids
JOURNAL Patent: US 5780273-A 13 14-JUL-1998;
FEATURES Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGTG 5
Db 2 GGGTG 6

RESULT 8
LOCUS AR020527/c 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 3 from patent US 5789174.
ACCESSION AR020527
VERSION AR020527.1 GI:3975142
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 10)
          Mouton,C., Guillot,E. and Menard,C.
TITLE Detection of periodontal pathogens including bacteroides forsythus,
          porphyromonas gingivalis, prevotella intermedia and prevotella
          nigrescens
JOURNAL Patent: US 5789174-A 3 04-AUG-1998;
FEATURES Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGTG 5
Db 2 GGGTG 6

AUTHORS Smith,H.S. and Chen,L.-C.
TITLE Methods for identifying genes amplified in cancer cells
JOURNAL Patent: US 5776683-A 13 07-JUL-1998;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGTG 5
Db 8 GGGTG 4

RESULT 9
LOCUS AR030206 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 17 from patent US 5861246.
ACCESSION AR030206
VERSION AR030206.1 GI:5943420
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 10)
          Weisman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding
          proteins
JOURNAL Patent: US 5861246-A 17 19-JAN-1999;
FEATURES Location/Qualifiers
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGTG 5
Db 2 GGGTG 6

RESULT 10
LOCUS AR030234 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 45 from patent US 5861246.
ACCESSION AR030234
VERSION AR030234.1 GI:5943448
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS 1 (bases 1 to 10)
          Weisman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE Multiple selection process for binding sites of DNA-binding
          proteins
JOURNAL Patent: US 5861246-A 45 19-JAN-1999;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGGTG 5
Db 3 GGGTG 7

RESULT 11
LOCUS AR035526 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 52 from patent US 5871910.
ACCESSION AR035526
VERSION AR035526.1 GI:5952194
KEYWORDS
SOURCE
ORGANISM Unknown.
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ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Arthur M., Dukt-Malen, S., Molinas, C. and Courvalin, P.  
TITLE Probes for the detection of nucleotide sequences implicated in the expression of resistance to glycopeptides, in particular in gram-positive bacteria  
JOURNAL Patent: US 5871910-A 52 16-FEB-1999;  
FEATURES Location/Qualifiers  
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QY 1 GGGTG 5  
Db 6 GGGTG 10  
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AR050986  
LOCUS AR050986 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 55 from patent US 5830644.  
ACCESSION AR050986  
VERSION AR050986.1 GI:5974350  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS West, M.D., Shay, J. and Wright, W.E.  
TITLE Method for screening for agents which increase telomerase activity in a cell  
JOURNAL Patent: US 5830644-A 55 03-NOV-1998;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 2 GGGTG 6  
RESULT 13  
AR059204/c  
LOCUS AR059204 10 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 11 from patent US 5837857.  
ACCESSION AR059204  
VERSION AR059204.1 GI:5984781  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau, B., Feng, J., Funk, W. and Andrews, W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 5837857-A 11 17-NOV-1998;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 7 GGGTG 3  
RESULT 14  
AR069288/c  
LOCUS AR069288 10 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 27 from patent US 5891631.  
ACCESSION AR069288  
VERSION AR069288.1 GI:7220176  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Goldstein, J.L., Brown, M.S., Briggs, M.R. and Wang, X.  
TITLE Methods relating tosterol regulatory element binding proteins  
JOURNAL Patent: US 5891631-A 27 06-APR-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 7 GGGTG 3  
RESULT 15  
AR069301  
LOCUS AR069301 10 bp DNA linear PAT 18-FEB-2000  
DEFINITION Sequence 43 from patent US 5891631.  
ACCESSION AR069301  
VERSION AR069301.1 GI:7220189  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Goldstein, J.L., Brown, M.S., Briggs, M.R. and Wang, X.  
TITLE Methods relating tosterol regulatory element binding proteins  
JOURNAL Patent: US 5891631-A 43 06-APR-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGGTG 5  
Db 6 GGGTG 10  
RESULT 16  
AR074300  
LOCUS AR074300 10 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 108 from patent US 5952490.  
ACCESSION AR074300  
VERSION AR074300.1 GI:10001055

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y., Brown-Driver,V.L., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and Imbach,J.Louis.  
TITLE Oligonucleotides having a conserved G4 core sequence  
JOURNAL Patent: US 5952490-A 108 14-SEP-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGGTG 5

RESULT 17  
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LOCUS AR074448 10 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 19 from patent US 5955075.  
ACCESSION AR074448  
VERSION AR074448.1 GI:10001203  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Method of inhibiting tumor growth using antibodies to MN protein  
JOURNAL Patent: US 5955075-A 19 21-SEP-1999;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
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Db 10 GGGTG 6

RESULT 18  
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LOCUS AR074449 10 bp DNA linear PAT 28-AUG-2000  
DEFINITION Sequence 20 from patent US 5955075.  
ACCESSION AR074449  
VERSION AR074449.1 GI:10001204  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE Method of inhibiting tumor growth using antibodies to MN protein  
JOURNAL Patent: US 5955075-A 20 21-SEP-1999;  
FEATURES Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
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Db 6 GGGTG 2

RESULT 19  
AR075515/c  
LOCUS AR075515 10 bp DNA linear PAT 30-AUG-2000  
DEFINITION Sequence 12 from patent US 5958680.  
ACCESSION AR075515  
VERSION AR075515.1 GI:10002263  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.  
TITLE Mammalian telomerase  
JOURNAL Patent: US 5958680-A 12 28-SEP-1999;  
FEATURES Location/Qualifiers  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
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Db 7 GGGTG 3

RESULT 20  
AR081128/c  
LOCUS AR081128 10 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 19 from patent US 5972353.  
ACCESSION AR081128  
VERSION AR081128.1 GI:10007856  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides  
JOURNAL Patent: US 5972353-A 19 26-OCT-1999;  
FEATURES Location/Qualifiers  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 10 GGGTG 6

RESULT 21  
AR081129/c  
LOCUS AR081129 10 bp DNA linear PAT 31-AUG-2000  
DEFINITION Sequence 20 from patent US 5972353.  
ACCESSION AR081129

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VERSION      AR081129.1  GI:10007857
KEYWORDS
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE       MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL      Patent: US 5972353-A 20 26-OCT-1999;
FEATURES     Location/Qualifiers
              1..10
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              /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGTG 5
    |||||
Db   6 GGGTG 2

RESULT 22
AR085325/c
LOCUS      AR085325
DEFINITION Sequence 19 from patent US 5981711.
ACCESSION  AR085325
VERSION    AR085325.1  GI:10012094
KEYWORDS   Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN-specific antibodies and hybridomas
JOURNAL    Patent: US 5981711-A 19 09-NOV-1999;
FEATURES   Location/Qualifiers
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              /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGTG 5
    |||||
Db   6 GGGTG 2

RESULT 23
AR085326/c
LOCUS      AR085326
DEFINITION Sequence 20 from patent US 5981711.
ACCESSION  AR085326
VERSION    AR085326.1  GI:10012095
KEYWORDS   Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      MN-specific antibodies and hybridomas
JOURNAL    Patent: US 5981711-A 20 09-NOV-1999;
FEATURES   Location/Qualifiers
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              /mol_type="unassigned DNA"
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGTG 5
    |||||
Db   10 GGGTG 6

RESULT 24
AR088073/c
LOCUS      AR088073
DEFINITION Sequence 19 from patent US 5989838.
ACCESSION  AR088073
VERSION    AR088073.1  GI:10014836
KEYWORDS   Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL    Patent: US 5989838-A 19 23-NOV-1999;
FEATURES   Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGTG 5
    |||||
Db   10 GGGTG 6

RESULT 25
AR088074/c
LOCUS      AR088074
DEFINITION Sequence 20 from patent US 5989838.
ACCESSION  AR088074
VERSION    AR088074.1  GI:10014837
KEYWORDS   Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL    Patent: US 5989838-A 20 23-NOV-1999;
FEATURES   Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGTG 5
    |||||
Db   10 GGGTG 6

RESULT 26
AR092704
LOCUS      AR092704
DEFINITION Sequence 16 from patent US 5998193.
ACCESSION  AR092704
VERSION    AR092704.1  GI:10019456

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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGTG 5
    |||||
Db   6 GGGTG 2

RESULT 24
AR088073/c
LOCUS      AR088073
DEFINITION Sequence 19 from patent US 5989838.
ACCESSION  AR088073
VERSION    AR088073.1  GI:10014836
KEYWORDS   Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL    Patent: US 5989838-A 19 23-NOV-1999;
FEATURES   Location/Qualifiers
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              /organism="unknown"
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ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGTG 5
    |||||
Db   10 GGGTG 6

RESULT 25
AR088074/c
LOCUS      AR088074
DEFINITION Sequence 20 from patent US 5989838.
ACCESSION  AR088074
VERSION    AR088074.1  GI:10014837
KEYWORDS   Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE      Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL    Patent: US 5989838-A 20 23-NOV-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 GGGTG 5
    |||||
Db   6 GGGTG 2

RESULT 26
AR092704
LOCUS      AR092704
DEFINITION Sequence 16 from patent US 5998193.
ACCESSION  AR092704
VERSION    AR092704.1  GI:10019456

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KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keese, P., Stepper, M. and Perriman, R.  
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA embedded ribozymes and compositions thereof  
JOURNAL Patent: US 5998193-A 16 07-DEC-1999;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 4 GGGTG 8  
RESULT 27  
AR096109  
LOCUS AR096109 10 bp DNA linear PAT 08-SEP-2000  
DEFINITION Sequence 4 from patent US 6005089.  
ACCESSION AR096109  
VERSION AR096109.1 GI:10024613  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Lanza, F., Phillips, D.R. and Cazenave, J.-P.  
TITLE Platelet glycoprotein V gene and uses  
JOURNAL Patent: US 6005089-A 4 21-DEC-1999;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 2 GGGTG 6  
RESULT 28  
AR100871  
LOCUS AR100871 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 4 from patent US 6083688.  
ACCESSION AR100871  
VERSION AR100871.1 GI:12811669  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Lanza, F., Phillips, D.R. and Cazenave, J.-P.  
TITLE Platelet glycoprotein V gene and uses  
JOURNAL Patent: US 6083688-A 4 04-JUL-2000;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 2 GGGTG 6  
RESULT 29  
AR104232/c  
LOCUS AR104232 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 19 from patent US 6093548.  
ACCESSION AR104232  
VERSION AR104232.1 GI:12816940  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada, J., Pastorekova, S. and Pastorek, J.  
TITLE Detection and quantitation of MN-specific antibodies  
JOURNAL Patent: US 6093548-A 19 25-JUL-2000;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 10 GGGTG 6  
RESULT 30  
AR104233/c  
LOCUS AR104233 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 20 from patent US 6093548.  
ACCESSION AR104233  
VERSION AR104233.1 GI:12816941  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada, J., Pastorekova, S. and Pastorek, J.  
TITLE Detection and quantitation of MN-specific antibodies  
JOURNAL Patent: US 6093548-A 20 25-JUL-2000;  
FEATURES Location/Qualifiers  
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/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 6 GGGTG 2  
RESULT 31  
AR106688  
LOCUS AR106688 10 bp DNA linear PAT 14-FEB-2001  
DEFINITION Sequence 16 from patent US 6107078.  
ACCESSION AR106688  
VERSION AR106688.1 GI:12821218

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KEYWORDS
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Keese,P., Stapper,M. and Perriman,R.
TITLE       Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
            embedded ribozymes and compositions thereof
JOURNAL     Patent: US 6107078-A 16 22-AUG-2000;
FEATURES    Location/Qualifiers
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            /mol_type="unassigned DNA"

ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 4 GGGTG 8

RESULT 32
LOCUS      ARI07848              10 bp      DNA              linear      PAT 14-FEB-2001
DEFINITION Sequence 94 from patent US 6110667.
ACCESSION  ARI07848
VERSION     ARI07848.1 GI:12823335
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Lopez-Nieto,C.Eduardo. and Nigam,S.Kumar.
TITLE       Processes, apparatus and compositions for characterizing nucleotide
            sequences based on K-tuple analysis
JOURNAL     Patent: US 6110667-A 94 29-AUG-2000;
FEATURES    Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 4 GGGTG 8

RESULT 33
LOCUS      ARI43496/c           10 bp      DNA              linear      PAT 08-AUG-2001
DEFINITION Sequence 19 from patent US 6204370.
ACCESSION  ARI43496
VERSION     ARI43496.1 GI:15104782
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE       MN gene and protein
JOURNAL     Patent: US 6204370-A 19 20-MAR-2001;
FEATURES    Location/Qualifiers
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            /organism="unknown"
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ORIGIN

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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 10 GGGTG 6

RESULT 34
LOCUS      ARI43497/c           10 bp      DNA              linear      PAT 08-AUG-2001
DEFINITION Sequence 20 from patent US 6204370.
ACCESSION  ARI43497
VERSION     ARI43497.1 GI:15104783
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE       MN gene and protein
JOURNAL     Patent: US 6204370-A 20 20-MAR-2001;
FEATURES    Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 6 GGGTG 2

RESULT 35
LOCUS      ARI61913/c           10 bp      DNA              linear      PAT 17-OCT-2001
DEFINITION Sequence 11 from patent US 6258535.
ACCESSION  ARI61913
VERSION     ARI61913.1 GI:16228931
KEYWORDS   .
SOURCE     .
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS     Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE       Mammalian telomerase
JOURNAL     Patent: US 6258535-A 11 10-JUL-2001;
FEATURES    Location/Qualifiers
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            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 7 GGGTG 3

RESULT 36
LOCUS      ARI61930              10 bp      DNA              linear      PAT 17-OCT-2001
DEFINITION Sequence 3 from patent US 6258537.
ACCESSION  ARI61930

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VERSION AR161930.1 GI:16228961  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Keinath,A.P., Somai,B.M. and Dean,R.A.  
TITLE Method of diagnosing gummy stem blight in plants using a polymerase chain reaction assay  
JOURNAL Patent: US 6258537-A 3 10-JUL-2001;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 1 GGGTG 5  
RESULT 37  
AR168826  
LOCUS AR168826 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 52 from patent US 6288042.  
ACCESSION AR168826  
VERSION AR168826.1 GI:17904948  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.  
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides  
JOURNAL Patent: US 6288042-A 52 11-SEP-2001;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 3 GGGTG 7  
RESULT 38  
AR171402/c  
LOCUS AR171402 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 20 from patent US 6297041.  
ACCESSION AR171402  
VERSION AR171402.1 GI:17910352  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6297041-A 20 02-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
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Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 6 GGGTG 2  
RESULT 39  
AR171573/c  
LOCUS AR171573 10 bp DNA linear PAT 17-DEC-2001  
DEFINITION Sequence 20 from patent US 6297051.  
ACCESSION AR171573  
VERSION AR171573.1 GI:17910523  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6297051-A 20 02-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..10  
/organism="unknown"  
/mol\_type="unassigned DNA"  
ORIGIN  
Query Match 100.0%; Score 5; DB 6; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.4e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 6 GGGTG 2  
RESULT 40  
BD175925/c  
LOCUS BD175925 10 bp DNA linear PAT 18-MAR-2003  
DEFINITION Paramyxovirus vectors used for transduction of foreign genes.  
ACCESSION BD175925  
VERSION BD175925.1 GI:29131633  
KEYWORDS JP 2002272465-A/1.  
SOURCE synthetic construct  
ORGANISM artificial sequences.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Tokusumi,T., Iida,A. and Hasegawa,M.  
TITLE Paramyxovirus vectors used for transduction of foreign genes  
JOURNAL Patent: JP 2002272465-A 1 24-SEP-2002;  
COMMENT Dनावेक RESEARCH INC  
OS Artificial Sequence  
PN JP 2002272465-A/1  
PD 24-SEP-2002 JP 2001145935  
PF 16-MAY-2001 JP 2002272465-A/1  
PR 27-OCT-2000 CA 2322057  
PI TSUYOSHI TOKUSUMI,AKIHIRO IIDA,MAMORU HASEGAWA PC  
C12N15/09//A61K35/76,A61K48/00,A61P29/00,A61P31/16,A61P35/00, PC  
C12N15/00  
CC Description of Artificial Sequence: artificially synthesized  
CC sequence  
FT Key Location/Qualifiers  
FT source 1..10  
/organism='Artificial Sequence'.  
FEATURES Location/Qualifiers  
source 1..10  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
ORIGIN

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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
DB 9 GGGTG 5

RESULT 41
BD176154/c
LOCUS BD176154 10 bp DNA linear PAT 18-MAR-2003
DEFINITION Mammalian telomerase.
ACCESSION BD176154
VERSION BD176154.1 GI:29121858
KEYWORDS JP 2002272489-A/13.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Villeponteau,B., Feng,J., Funk,W. and Andrews,W.H.
TITLE Mammalian telomerase
JOURNAL Patent: JP 2002272489-A 13 24-SEP-2002;
COMMENT OS Unidentified
PN JP 2002272489-A/13
PD 24-SEP-2002
PF 06-MAR-2002 JP 2002061125
PR 07-JUL-1994 US 08/272102,27-OCT-1994 US 08/330123 PR
07-JUN-1995 US 08/472802,07-JUN-1995 US 08/482115 FI BRYANT
VILLEPONTEAU,JUNLI FENG,WALTER FUNK,WILLIAM H ANDREWS PC
C12N15/09,C12N9/99,C12Q1/68,G01N33/53,G01N33/566,C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
CC Mammalian telomerase
FH Key Location/Qualifiers
FT source 1..10
/organism='Unidentified'.

FEATURES
source
1..10
/organism='Unidentified'
/mol_type='genomic DNA'
/db_xref='taxon:32644'

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
DB 6 GGGTG 10

RESULT 43
BD238590
LOCUS BD238590 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238590
VERSION BD238590.1 GI:33048360
KEYWORDS JP 2002534056-A/8.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 8 15-OCT-2002;
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/8
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61P35/00,A61P37/04,C12N1/15, PC

Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.4e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
DB 7 GGGTG 3

RESULT 42
BD181867
LOCUS BD181867 10 bp DNA linear PAT 15-MAY-2003
DEFINITION Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis.
ACCESSION BD181867
VERSION BD181867.1 GI:30792785
KEYWORDS JP 2002320494-A/23.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Arthur,M., Duktamalen,S., Molinas,C. and Courvalin,P.
TITLE Polypeptides implicated in the expression of resistance to
glycopeptides, in particular in gram-positive bacteria, nucleotide
sequence cod ing for these polypeptides and use for diagnosis
JOURNAL Patent: JP 2002320494-A 23 05-NOV-2002;

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VERSION JP 2002534056-A/13.  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 13 15-OCT-2002;  
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COMMENT OS Homo sapiens (human)  
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DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238645.1 GI:33048415  
VERSION JP 2002534056-A/63.  
KEYWORDS Homo sapiens (human)  
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REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 63 15-OCT-2002;  
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PN JP 2002534056-A/63  
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DEFINITION Preparation and use of superior vaccines.  
ACCESSION BD238645.1 GI:33048415  
VERSION JP 2002534056-A/63.  
KEYWORDS Homo sapiens (human)  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE 1 (bases 1 to 10)  
AUTHORS Roberts,B.L. and Shankara,S.  
TITLE Preparation and use of superior vaccines  
JOURNAL Patent: JP 2002534056-A 63 15-OCT-2002;  
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COMMENT OS Homo sapiens (human)  
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ACCESSION  BD238727
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REFERENCE  1 (bases 1 to 10)
AUTHORS    Roberts, B.L. and Shankara, S.
TITLE      Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 145 15-OCT-2002;
GENZYME CORP
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            REFERENCE  1 (bases 1 to 10)
            AUTHORS    Roberts, B.L. and Shankara, S.
            TITLE      Preparation and use of superior vaccines
            JOURNAL    Patent: JP 2002534056-A 188 15-OCT-2002;
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            ACCESSION  BD238804
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            AUTHORS    Roberts, B.L. and Shankara, S.
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TITLE      Preparation and use of superior vaccines
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            AUTHORS    Roberts, B.L. and Shankara, S.
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DEFINITION Preparation and use of superior vaccines.
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AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
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GENZYME CORP
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PI BRUCE L ROBERTS,SRINIVAS SHANKARA

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1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 239 15-OCT-2002;
GENZYME CORP
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Db 2 GGGTG 6

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GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:35:05 ; Search time 254.4 Seconds  
(without alignment)  
103.173 Million cell updates/sec

Title: GCGTG

Perfect score: 5

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Scoring table: IDENTITY\_NUC

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Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 3979404

Minimum DB seq length: 10

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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c 256	5	100.0	10	3	AAZ06057	AAZ06057	CFTR gene
c 257	5	100.0	10	3	AAZ48449	AAZ48449	Primer sp
c 258	5	100.0	10	3	AAZ79804	AAZ79804	Human cys
259	5	100.0	10	3	AAZ79741	AAZ79741	Human col
c 260	5	100.0	10	3	AAZ79848	AAZ79848	Human den
c 261	5	100.0	10	3	AAZ16550	AAZ16550	Initiator
c 262	5	100.0	10	3	AAZ36727	AAZ36727	PCR prime
c 263	5	100.0	10	3	AAZ20359	AAZ20359	Human eos
264	5	100.0	10	3	AAZ20296	AAZ20296	Human GM-
c 265	5	100.0	10	3	AAZ20263	AAZ20263	Human RAN
c 266	5	100.0	10	3	AAZ20346	AAZ20346	Human ind
c 267	5	100.0	10	3	AAZ52469	AAZ52469	Human MN
c 268	5	100.0	10	3	AAZ61026	AAZ61026	Protein b
c 269	5	100.0	10	3	AAZ58804	AAZ58804	Human bet
c 270	5	100.0	10	3	AAZ58812	AAZ58812	Human bet
c 271	5	100.0	10	3	AAZ58806	AAZ58806	Human bet
c 272	5	100.0	10	3	AAZ58808	AAZ58808	Human bet
c 273	5	100.0	10	3	AAZ58802	AAZ58802	Human bet
c 274	5	100.0	10	3	AAZ58810	AAZ58810	Human bet
c 275	5	100.0	10	3	AAZ58792	AAZ58792	Human bet
c 276	5	100.0	10	4	AAH18974	AAH18974	UCP3 poly
c 277	5	100.0	10	4	AAH41417	AAH41417	Escherich
c 278	5	100.0	10	4	AAH73613	AAH73613	DNA seque
c 279	5	100.0	10	4	AAH04427	AAH04427	Primer #3
c 280	5	100.0	10	4	AAI67389	AAI67389	Human FKB
c 281	5	100.0	10	4	AAI67387	AAI67387	Human FKB
c 282	5	100.0	10	4	AAI67391	AAI67391	Human FKB
c 283	5	100.0	10	4	AAI67377	AAI67377	Human FKB
c 284	5	100.0	10	4	AAI67386	AAI67386	Human FKB
c 285	5	100.0	10	4	AAZ92848	AAZ92848	Transcrip
c 286	5	100.0	10	4	AAZ13004	AAZ13004	Human CCR
c 287	5	100.0	10	4	AAZ86115	AAZ86115	Sendai vi
c 288	5	100.0	10	4	AAZ04440	AAZ04440	Human DAX
c 289	5	100.0	10	4	AAH63932	AAH63932	Human ubi
c 290	5	100.0	10	4	AAH64065	AAH64065	Human ubi
c 291	5	100.0	10	4	AAH63622	AAH63622	Human ubi
c 292	5	100.0	10	4	AAH63774	AAH63774	Human ubi
c 293	5	100.0	10	4	AAH64129	AAH64129	Human ubi
c 294	5	100.0	10	4	AAH64176	AAH64176	Human ubi
c 295	5	100.0	10	4	AAH63274	AAH63274	Human col
c 296	5	100.0	10	4	AAH63433	AAH63433	Human ubi
c 297	5	100.0	10	4	AAH63600	AAH63600	Human ubi
c 298	5	100.0	10	4	AAH63629	AAH63629	Human ubi
c 299	5	100.0	10	4	AAH64312	AAH64312	Human ubi
c 300	5	100.0	10	4	AAH64704	AAH64704	Human hig
c 301	5	100.0	10	4	AAH63575	AAH63575	Human ubi
c 302	5	100.0	10	4	AAH64228	AAH64228	Human ubi
c 303	5	100.0	10	4	AAH64602	AAH64602	Human ubi
c 304	5	100.0	10	4	AAH63520	AAH63520	Human ubi
c 305	5	100.0	10	4	AAH63653	AAH63653	Human ubi
c 306	5	100.0	10	4	AAH64396	AAH64396	Human ubi
c 307	5	100.0	10	4	AAH64515	AAH64515	Human ubi
c 308	5	100.0	10	4	AAH64290	AAH64290	Human ubi
c 309	5	100.0	10	4	AAH64628	AAH64628	Human col
c 310	5	100.0	10	4	AAH64710	AAH64710	Human hig
c 311	5	100.0	10	4	AAH63353	AAH63353	Human mel
c 312	5	100.0	10	4	AAH63662	AAH63662	Human ubi
c 313	5	100.0	10	4	AAH63716	AAH63716	Human ubi
c 314	5	100.0	10	4	AAH64128	AAH64128	Human ubi
c 315	5	100.0	10	4	AAH63229	AAH63229	Human col
c 316	5	100.0	10	4	AAH63625	AAH63625	Human ubi
c 317	5	100.0	10	4	AAH63434	AAH63434	Human ubi
c 318	5	100.0	10	4	AAH63931	AAH63931	Human ubi
c 319	5	100.0	10	4	AAH64600	AAH64600	Human ubi
c 320	5	100.0	10	4	AAH64601	AAH64601	Human ubi
c 321	5	100.0	10	4	AAH64514	AAH64514	Human ubi
c 322	5	100.0	10	4	AAH63437	AAH63437	Human ubi
c 323	5	100.0	10	4	AAH64009	AAH64009	Human ubi
c 324	5	100.0	10	4	AAH64313	AAH64313	Human ubi
c 325	5	100.0	10	4	AAH63418	AAH63418	Human can
c 326	5	100.0	10	4	AAH63462	AAH63462	Human ubi
c 327	5	100.0	10	4	AAH63576	AAH63576	Human ubi
c 328	5	100.0	10	4	AAH63738	AAH63738	Human ubi
c 329	5	100.0	10	4	AAH63976	AAH63976	Human ubi
c 330	5	100.0	10	4	AAH64340	AAH64340	Human ubi
c 331	5	100.0	10	4	AAH64344	AAH64344	Human ubi
c 332	5	100.0	10	4	AAH64472	AAH64472	Human ubi
c 333	5	100.0	10	4	AAH64641	AAH64641	Human col
c 334	5	100.0	10	4	AAH63165	AAH63165	Human col
c 335	5	100.0	10	4	AAH63430	AAH63430	Human ubi
c 336	5	100.0	10	4	AAZ57306	AAZ57306	Human CHR
c 337	5	100.0	10	4	AAZ93021	AAZ93021	C. cibari
c 338	5	100.0	10	4	AAZ70100	AAZ70100	Human TNF
c 339	5	100.0	10	4	AAZ20553	AAZ20553	Human MTR
c 340	5	100.0	10	4	AAZ20561	AAZ20561	Human MTR
c 341	5	100.0	10	4	AAZ20569	AAZ20569	Human MTR
c 342	5	100.0	10	4	AAZ28609	AAZ28609	Human int
c 343	5	100.0	10	4	AAZ28606	AAZ28606	Human int
c 344	5	100.0	10	4	AAZ77598	AAZ77598	Modified
c 345	5	100.0	10	4	AAZ23653	AAZ23653	S sequenc
c 346	5	100.0	10	4	AAI65896	AAI65896	Nucleotid
c 347	5	100.0	10	4	AAZ91834	AAZ91834	C. cibari
c 348	5	100.0	10	4	AAH32756	AAH32756	LPS activ
c 349	5	100.0	10	4	AAH32801	AAH32801	LPS activ
c 350	5	100.0	10	4	AAH32658	AAH32658	LPS activ
c 351	5	100.0	10	4	AAH32693	AAH32693	LPS activ
c 352	5	100.0	10	4	ABA81650	ABA81650	Human pho
c 353	5	100.0	10	5	ABA41710	ABA41710	Anti-PEP
c 354	5	100.0	10	5	ABA06171	ABA06171	Human nor
c 355	5	100.0	10	5	ABA06215	ABA06215	Human nor
c 356	5	100.0	10	5	ABA06140	ABA06140	Human nor
c 357	5	100.0	10	5	ABA06054	ABA06054	Human nor
c 358	5	100.0	10	5	ABA06110	ABA06110	Human nor
c 359	5	100.0	10	5	AAZ70421	AAZ70421	Human DRD
c 360	5	100.0	10	5	AAZ70437	AAZ70437	Human DRD
c 361	5	100.0	10	5	AAZ70409	AAZ70409	Human DRD
c 362	5	100.0	10	5	AAZ70449	AAZ70449	Human DRD
c 363	5	100.0	10	5	AAZ69600	AAZ69600	Human IL4
c 364	5	100.0	10	5	AAZ69606	AAZ69606	Human IL4
c 365	5	100.0	10	5	AAZ69604	AAZ69604	Human IL4
c 366	5	100.0	10	5	AAZ69607	AAZ69607	Human IL4
c 367	5	100.0	10	5	AAZ74020	AAZ74020	Human SIC
c 368	5	100.0	10	5	AAZ74008	AAZ74008	Human SIC
c 369	5	100.0	10	5	AAZ74011	AAZ74011	Human SIC
c 370	5	100.0	10	5	AAZ74009	AAZ74009	Human SIC
c 371	5	100.0	10	5	AAZ7447	AAZ7447	Yeast NOR
c 372	5	100.0	10	5	AAZ40013	AAZ40013	Yeast NOR
c 373	5	100.0	10	5	AAZ40578	AAZ40578	Yeast NOR
c 374	5	100.0	10	5	AAZ40601	AAZ40601	Yeast NOR
c 375	5	100.0	10	5	AAZ43272	AAZ43272	Yeast NOR
c 376	5	100.0	10	5	AAZ43807	AAZ43807	Yeast NOR
c 377	5	100.0	10	5	AAZ36146	AAZ36146	Yeast NOR
c 378	5	100.0	10	5	AAZ36882	AAZ36882	Yeast NOR
c 379	5	100.0	10	5	AAZ42299	AAZ42299	Yeast NOR
c 380	5	100.0	10	5	AAZ34305	AAZ34305	Yeast NOR
c 381	5	100.0	10	5	AAZ35619	AAZ35619	Yeast NOR
c 382	5	100.0	10	5	AAZ37388	AAZ37388	Yeast NOR
c 383	5	100.0	10	5	AAZ42700	AAZ42700	Yeast NOR
c 384	5	100.0	10	5	AAZ43725	AAZ43725	Yeast NOR
c 385	5	100.0	10	5	AAZ43208	AAZ43208	Yeast NOR
c 386	5	100.0	10	5	AAZ36611	AAZ36611	Yeast NOR

C 387 5 100.0 10 5 AAF38678 Aaf38678 Yeast NOR  
C 388 5 100.0 10 5 AAF39525 Aaf39525 Yeast NOR  
C 389 5 100.0 10 5 AAF39794 Aaf39794 Yeast NOR  
C 390 5 100.0 10 5 AAF41877 Aaf41877 Yeast NOR  
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C 422 5 100.0 10 5 AAF34421 Aaf34421 Yeast NOR  
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C 434 5 100.0 10 5 AAF33635 Aaf33635 Yeast NOR  
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C 438 5 100.0 10 5 AAF37063 Aaf37063 Yeast NOR  
C 439 5 100.0 10 5 AAF37745 Aaf37745 Yeast NOR  
C 440 5 100.0 10 5 AAF38236 Aaf38236 Yeast NOR  
C 441 5 100.0 10 5 AAF41499 Aaf41499 Yeast NOR  
C 442 5 100.0 10 5 AAF42059 Aaf42059 Yeast NOR  
C 443 5 100.0 10 5 AAF35014 Aaf35014 Yeast NOR  
C 444 5 100.0 10 5 AAF36705 Aaf36705 Yeast NOR  
C 445 5 100.0 10 5 AAF37893 Aaf37893 Yeast NOR  
C 446 5 100.0 10 5 AAF38031 Aaf38031 Yeast NOR  
C 447 5 100.0 10 5 AAF38496 Aaf38496 Yeast NOR  
C 448 5 100.0 10 5 AAF40349 Aaf40349 Yeast NOR  
C 449 5 100.0 10 5 AAF40576 Aaf40576 Yeast NOR  
C 450 5 100.0 10 5 AAF42263 Aaf42263 Yeast NOR  
C 451 5 100.0 10 5 AAF43277 Aaf43277 Yeast NOR  
C 452 5 100.0 10 6 AAS19599 Aas19599 Primer-ex  
C 453 5 100.0 10 6 AAS19657 Aas19657 Primer-ex  
C 454 5 100.0 10 6 AAS19649 Aas19649 Primer-ex  
C 455 5 100.0 10 6 AAS19665 Aas19665 Primer-ex  
C 456 5 100.0 10 6 AAS64901 Aas64901 Primer-ex  
C 457 5 100.0 10 6 AAD26711 Aad26711 Human GPR  
C 458 5 100.0 10 6 AAD26716 Aad26716 Human GPR  
C 459 5 100.0 10 6 ABK24237 Abk24237 Retinalde

Abk46595 EDG4 gene  
Abk51085 Human CCR  
Aas9288 Human F12  
Ab188326 Human CHR  
Ab188335 Human CHR  
Ab152185 Human PER  
Aal39611 SSTR4 gen  
Aal38369 Oligonuc  
Abk81958 Human CYP  
Aas98913 Colony st  
Aas98911 Colony st  
Ab102297 Human MMP  
Ad25890 Primer #1  
Ab142694 Human mat  
Ab142849 Human mat  
Ab142683 Human mat  
Abk70547 Human G p  
Adn84300 RP primer  
Abes1974 Human FMO  
Abes1962 Human FMO  
Abes53693 Mint RAPD  
Abn81489 Human HTA  
Abn81496 Human HTA  
Abk81400 SCYA21 ge  
Aal47265 Sendai vi  
Abk96075 Human LIP  
Abk96047 Human LIP  
Abk96083 Human LIP  
Aas96201 Human Ace  
Aas96199 Human Ace  
Aas96210 Human Ace  
Aas96188 Human Ace  
Abag97031 ZFP36 ext  
Abag97043 ZFP36 ext  
Ad22919 Human MC4  
Ad26188 Human end  
Ab139904 Sendai vi  
Abk96383 Human SA  
Aal48059 Human CSF  
Aas95402 Human ICA  
Adn12444 Synthetic

## ALIGNMENTS

RESULT 1  
AAN82154  
ID AAN82154 standard; DNA; 10 BP.  
XX  
AC AAN82154;  
XX  
DT 25-MAR-2003 (revised)  
DT 12-DEC-1990 (first entry)  
XX  
Sequence #12 recognised by probe for 16S RNA gene.  
KW Mollicutes.  
XX  
OS Mycoplasma.  
XX  
FN EP250662-A.  
XX  
PD 07-JAN-1988.  
XX  
PF 25-JUN-1986; 86EP-00304919.  
XX  
PR 25-JUN-1986; 86EP-00304919.  
XX  
PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Gobel U, Stanbridge EU;  
XX



DR WPI; 1988-000726/01.  
 XX  
 PT Detection of prokaryotic organisms - esp. mycoplasma by hybridisation  
 PT with an oligonucleotide probe complementary to nucleotide sequence in  
 PT the prokaryote.  
 XX  
 PS Claim 16; Page 6; 9pp; English.  
 XX  
 CC A probe which is complementary to this sequence can be used to detect any  
 CC prokaryotic organism. See also AAN82143-71. (Updated on 25-MAR-2003 to  
 CC correct PA field.)  
 XX  
 SQ Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 1; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 DB 3 GGGTG 7

RESULT 2  
 AAQ79368  
 ID AAQ79368 standard; DNA; 10 BP.  
 AC AAQ79368;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-JUN-1995 (first entry)  
 XX  
 DE Regulatory element AP2/Rev located at posn. 708 of the extended 3'  
 DE flanking region of human erythropoietin.  
 XX  
 KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9423570-A1.  
 XX  
 PD 27-OCT-1994.  
 XX  
 PF 15-APR-1994; 94WO-US004141.  
 XX  
 PR 15-APR-1993; 93US-00046295.  
 PR 23-JUN-1993; 93US-00082850.  
 XX  
 PA (UWNY ) UNIV NEW YORK STATE.  
 XX  
 PI Lee-Huang S;  
 XX  
 PD WPI; 1994-341353/42.  
 XX  
 PF New regulatory regions of human erythropoietin gene - used for studying  
 PT and treating diseases and for prodn. of transgenic animal models (Eng).  
 XX  
 PS Disclosure; Table II, page 14; 81pp; English.  
 XX  
 CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
 CC hEpsLH. This nucleic acid sequence includes a coding sequence, a 5'  
 CC flanking region contg. multiple regulatory elements and a 3' flanking  
 CC region contg. multiple regulatory elements. AAQ79355 consists of the last  
 CC 1777 bases of AAQ79753. It corresp. to the non-coding 3' flanking region  
 CC of AAQ79753 and includes all the regulatory elements contained therein.  
 CC It extends from the 5'-most PstI site 3' of the end of the coding  
 CC sequence to a BamHI site. It comprises 1777 bp exhibiting many stem-loop  
 CC structures. It also contains TATA boxes in forward and reverse  
 CC orientation, and at least about 184 potential transcriptional regulatory  
 CC elements. AAQ79365-Q79369 list several of these elements and their  
 CC positions. The nucleotide posns. are measured from first nucleotide at  
 CC the extended 3' end of hEpsLH as shown in AAQ79355. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX  
 SQ Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 DB 1 GGGTG 5

RESULT 3  
 AAQ79367  
 ID AAQ79367 standard; DNA; 10 BP.  
 XX  
 AC AAQ79367;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-JUN-1995 (first entry)  
 XX  
 DE Regulatory element AP2/Rev located at posn. 707 of the extended 3'  
 DE flanking region of human erythropoietin.  
 XX  
 KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
 XX  
 OS Synthetic.  
 OS  
 PN WO9423570-A1.  
 XX  
 PD 27-OCT-1994.  
 XX  
 PF 15-APR-1994; 94WO-US004141.  
 XX  
 PR 15-APR-1993; 93US-00046295.  
 PR 23-JUN-1993; 93US-00082850.  
 XX  
 PA (UWNY ) UNIV NEW YORK STATE.  
 XX  
 PI Lee-Huang S;  
 XX  
 PD WPI; 1994-341353/42.  
 XX  
 PF New regulatory regions of human erythropoietin gene - used for studying  
 PT and treating diseases and for prodn. of transgenic animal models (Eng).  
 XX  
 PS Disclosure; Table II, page 14; 81pp; English.  
 XX  
 CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
 CC hEpsLH. This nucleic acid sequence includes a coding sequence, a 5'  
 CC flanking region contg. multiple regulatory elements and a 3' flanking  
 CC region contg. multiple regulatory elements. AAQ79355 consists of the last  
 CC 1777 bases of AAQ79753. It corresp. to the non-coding 3' flanking region  
 CC of AAQ79753 and includes all the regulatory elements contained therein.  
 CC It extends from the 5'-most PstI site 3' of the end of the coding  
 CC sequence to a BamHI site. It comprises 1777 bp exhibiting many stem-loop  
 CC structures. It also contains TATA boxes in forward and reverse  
 CC orientation, and at least about 184 potential transcriptional regulatory  
 CC elements. AAQ79365-Q79369 list several of these elements and their  
 CC positions. The nucleotide posns. are measured from first nucleotide at  
 CC the extended 3' end of hEpsLH as shown in AAQ79355. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 SQ Sequence 10 BP; 0 A; 0 C; 9 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 DB 2 GGGTG 6

```

RESULT 4
AAQ79359/c
ID AAQ79359 standard; DNA; 10 BP.
XX
AC AAQ79359;
XX
DT 25-MAR-2003 (revised)
DT 05-JUN-1995 (first entry)
XX
XX Sequence of AP2 regulatory sequence located at posn. 2621 in hspSLH.
DE
XX Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.
KW
XX Synthetic.
OS
XX WO9423570-A1.
XX
XX 27-OCT-1994.
XX
XX 15-APR-1994; 94WO-US004141.
XX
XX 15-APR-1993; 93US-00046295.
XX
XX 23-JUN-1993; 93US-00082850.
XX
XX (UYNV ) UNIV NEW YORK STATE.
XX
XX Lee-Huang S;
XX
XX WPI; 1994-341353/42.
XX
XX New regulatory regions of human erythropoietin gene - used for studying
XX and treating diseases and for prodn. of transgenic animal models (Eng).
XX
XX Disclosure; Table I, p. 12; 81pp; English.
XX
XX AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone
XX hEPLH. This nucleic acid sequence includes EPO coding sequence, a 5'
XX flanking region contg. multiple regulatory elements and a 3' flanking
XX region contg. multiple regulatory elements. AAQ79354 shows the extended
XX 5' flanking region and includes all the 5' regulatory elements. This
XX region, consisting of the first 3892 of AAQ79353, was not found in the
XX 3.6 kb EPO genomic clone from fetal liver reported by others. The
XX flanking region comprises 3892 bp and contains CAAT and TATA boxes and at
XX lease 321 potential transcriptional regulatory elements. AAQ79356-Q79362
XX show several of these elements and their positions. The nucleotide
XX position of these elements is measured from the BamHI site at the 5' end
XX of AAQ79353. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 1 A; 8 C; 0 G; 1 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 10 GGGTG 6

RESULT 5
AAQ61967
ID AAQ61967 standard; DNA; 10 BP.
XX
AC AAQ61967;
XX
DT 25-MAR-2003 (revised)
DT 04-NOV-1994 (first entry)
XX
XX Phospholipase A2 inhibiting oligomer, ISIS no 4962.
DE
XX Inhibition; replication; herpes simplex virus; HSV; HIV; aging;
KW human cytomegalovirus; influenza virus; inflammation; telomere length;
KW

```

```

KW neurological disorders; phospholipase A2 activity; hyperproliferation;
KW malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..10
FT /*tag= a
FT /note= "Phosphorothioate intersugar linkages"
XX
XX WO9408053-A1.
XX
XX 14-APR-1994.
XX
XX 29-SEP-1993; 93WO-US009297.
XX
XX 29-SEP-1992; 92US-00954185.
XX
XX (ISIS-) ISIS PHARM INC.
XX
XX Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
XX Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
XX WPI; 1994-135613/16.
XX
XX New modified oligo-nucleotide contg guanine quartet - inhibits activity
XX of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
XX of chromosomes.
XX
XX Disclosure; Page 29; 144pp; English.
XX
XX The sequences given in AAQ61956-67 are oligonucleotides which represent
XX the core sequences of G4 containing oligos which may be used for
XX inhibiting phospholipase A2 enzyme activity. Oligonucleotides such as
XX these may also be used for inhibiting activity of HSV, HIV, human
XX cytomegalovirus or influenza virus, or for treating inflammatory and
XX neurological disorders caused by phospholipase A2 activity in cases of
XX hyperproliferation, malignancy, cardiovascular disease and snake bite.
XX They may also be used for inhibiting division of malignant cells by
XX modulating telomere length, which may also retard aging. (Updated on 25-
XX MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 1 GGGTG 5

RESULT 6
AAQ63553
ID AAQ63553 standard; DNA; 10 BP.
XX
XX AAQ63553;
XX
XX 25-MAR-2003 (revised)
XX 21-DEC-1994 (first entry)
XX
XX C22 5' spacer element.
XX
XX Insertion element; junk DNA; spacer element; functional DNA sequence;
KW primer binding site; reaction product; binding specificity; primer;
KW recombinant molecule; structural stress; hybridisation assay; ss.
XX
XX Synthetic.
XX
XX WO9409159-A2.
XX
XX 28-APR-1994.
XX

```



PI Coppola GR, Beutel BA, Bertelsen AH;  
 DR WPI; 1995-051993/07.  
 XX Oligo-nucleotide(s) which bind to interferon-gamma - used for modulating,  
 PT inhibiting or enhancing the activity or function of interferon-gamma.  
 XX  
 PS Claim 4; Page 32; 43pp; English.  
 XX  
 CC Oligonucleotides which bind to interferon-gamma are useful for  
 CC modulating, inhibiting or enhancing the activity or function of the IFN.  
 CC Particularly, they are useful for treatment of septic shock, rheumatoid  
 CC arthritis and HIV infection. Preferred oligonucleotides are given in  
 CC AA081894-081909 and AA081913-081932; esp. the oligo- nucleotides comprise  
 CC at least one of the sequences AAGUUG, UGANGCUC, GCACNC, AA081903 or  
 CC AAQ81904. (Updated on 25-MAR-2003 to correct FN field.)  
 XX  
 SQ Sequence 10 BP; 1 A; 6 C; 2 G; 0 T; 1 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 Db 7 GGGTG 3  
 RESULT 9  
 AAX32613  
 ID AAX32613 standard; DNA; 10 BP.  
 AC AAX32613;  
 XX  
 DT 23-JUN-1999 (first entry)  
 DE Anticancer duplex forming oligonucleotide SEQ ID #13.  
 XX  
 KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
 KW multiple drug resistance; MDR; ss.  
 OS Synthetic.  
 XX  
 PN WO9523162-A1.  
 XX  
 PD 31-AUG-1995.  
 XX  
 PF 27-FEB-1995; 95WO-US002419.  
 XX  
 PR 28-FEB-1994; 94US-00202927.  
 XX  
 PA (MICR-) MICROPROBE CORP.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 XX WPI; 1995-311501/40.  
 DR  
 XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 PS Disclosure; Page 49; 107pp; English.  
 XX  
 CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance

XX  
 SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 Db 6 GGGTG 10  
 RESULT 10  
 AAX32607  
 ID AAX32607 standard; DNA; 10 BP.  
 XX  
 AC AAX32607;  
 XX  
 DT 23-JUN-1999 (first entry)  
 DE Anticancer duplex forming oligonucleotide SEQ ID #7.  
 XX  
 KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
 KW multiple drug resistance; MDR; ss.  
 OS Synthetic.  
 XX  
 PN WO9523162-A1.  
 XX  
 PD 31-AUG-1995.  
 XX  
 PF 27-FEB-1995; 95WO-US002419.  
 XX  
 PR 28-FEB-1994; 94US-00202927.  
 XX  
 PA (MICR-) MICROPROBE CORP.  
 PA (UYVA ) UNIV YALE.  
 XX  
 PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 XX WPI; 1995-311501/40.  
 DR  
 XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 PS Disclosure; Page 47; 107pp; English.  
 XX  
 CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX  
 SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 Db 4 GGGTG 8  
 RESULT 11  
 AAX32622  
 ID AAX32622 standard; DNA; 10 BP.  
 XX



CC New oligonucleotides are disclosed which are 8-18 nucleotides in length and which have a steroid structure attached to the 3'-end through a linker attached to the A-ring of the steroid skeleton. In particular, the present sequence has a cholesterol moiety attached by its A-ring to the 3'-phosphate through a carbonyl group attached to the ring nitrogen of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The oligonucleotides form stable duplexes at physiological temperature and have selective cytotoxic activity against certain tumour cell lines, including some with multiple drug resistance

SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 14  
AAX32612  
ID AAX32612 standard; DNA; 10 BP.  
AC AAX32612;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #12.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX  
DR WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including intramolecular duplex with hairpin loop region, having selective cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 49; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length and which have a steroid structure attached to the 3'-end through a linker attached to the A-ring of the steroid skeleton. In particular, the present sequence has a cholesterol moiety attached by its A-ring to the 3'-phosphate through a carbonyl group attached to the ring nitrogen of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The oligonucleotides form stable duplexes at physiological temperature and have selective cytotoxic activity against certain tumour cell lines, including some with multiple drug resistance

SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 15  
AAX32620  
ID AAX32620 standard; DNA; 10 BP.  
AC AAX32620;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #20.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX  
DR WPI; 1995-311501/40.  
XX  
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including intramolecular duplex with hairpin loop region, having selective cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 52; 107pp; English.  
XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length and which have a steroid structure attached to the 3'-end through a linker attached to the A-ring of the steroid skeleton. In particular, the present sequence has a cholesterol moiety attached by its A-ring to the 3'-phosphate through a carbonyl group attached to the ring nitrogen of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The oligonucleotides form stable duplexes at physiological temperature and have selective cytotoxic activity against certain tumour cell lines, including some with multiple drug resistance

SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 16  
AAX32624  
ID AAX32624 standard; DNA; 10 BP.  
AC AAX32624;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #24.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;

KW multiple drug resistance; MDR; ss.  
 XX Synthetic.  
 OS  
 XX WO9523162-A1.  
 PN  
 XX 31-AUG-1995.  
 PD  
 XX 27-FEB-1995; 95WO-US002419.  
 PF  
 XX 28-FEB-1994; 94US-00202927.  
 PR  
 XX (MICR-) MICROPROBE CORP.  
 PA  
 PA (UYVA ) UNIV YALE.  
 XX  
 XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 PI WPI; 1995-311501/40.  
 DR  
 XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 PS Disclosure; Page 53; 107pp; English.  
 XX  
 CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX  
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 DB 6 GGGTG 10  
 RESULT 17  
 AAX32623  
 ID AAX32623 standard; DNA; 10 BP.  
 AC  
 XX AAX32623;  
 XX  
 XX 23-JUN-1999 (first entry)  
 DT Anticancer duplex forming oligonucleotide SEQ ID #23.  
 DE Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
 KW multiple drug resistance; MDR; ss.  
 XX Synthetic.  
 OS  
 XX WO9523162-A1.  
 PN  
 XX 31-AUG-1995.  
 PD  
 XX 27-FEB-1995; 95WO-US002419.  
 PF  
 XX 28-FEB-1994; 94US-00202927.  
 PR  
 XX (MICR-) MICROPROBE CORP.  
 PA  
 PA (UYVA ) UNIV YALE.  
 XX  
 XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 PI

XX WPI; 1995-311501/40.  
 DR  
 XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 XX  
 PS Disclosure; Page 53; 107pp; English.  
 XX  
 CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX  
 SQ Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 DB 6 GGGTG 10  
 RESULT 18  
 AAX32605  
 ID AAX32605 standard; DNA; 10 BP.  
 XX  
 XX AAX32605;  
 AC  
 XX 23-JUN-1999 (first entry)  
 DT Anticancer duplex forming oligonucleotide SEQ ID #5.  
 DE Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
 KW multiple drug resistance; MDR; ss.  
 XX Synthetic.  
 OS  
 XX WO9523162-A1.  
 PN  
 XX 31-AUG-1995.  
 PD  
 XX 27-FEB-1995; 95WO-US002419.  
 PF  
 XX 28-FEB-1994; 94US-00202927.  
 PR  
 XX (MICR-) MICROPROBE CORP.  
 PA  
 PA (UYVA ) UNIV YALE.  
 XX  
 XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 PI WPI; 1995-311501/40.  
 DR  
 XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 XX  
 PS Disclosure; Page 46; 107pp; English.  
 XX  
 CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC including some with multiple drug resistance

CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 2 A; 3 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 19  
AAAX32626  
ID AAAX32626 standard; DNA; 10 BP.  
XX  
AC AAAX32626;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #26.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.

XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA) UNIV YALE.

XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX  
DR WPI; 1995-311501/40.  
XX  
PT New stable oligo.nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 54; 107pp; English.

XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 20  
AAAX32626/c

ID AAAX32626 standard; DNA; 10 BP.  
XX  
AC AAAX32626;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #26.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.  
XX  
PF 27-FEB-1995; 95WO-US002419.  
XX  
PR 28-FEB-1994; 94US-00202927.  
XX  
PA (MICR-) MICROPROBE CORP.  
PA (UYVA) UNIV YALE.  
XX  
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
XX  
DR WPI; 1995-311501/40.  
XX  
PT New stable oligo.nucleotide duplex with 3'-steroid gp - including  
PT intramolecular duplex with hairpin loop region, having selective  
PT cytotoxicity against some tumour cells.  
XX  
PS Disclosure; Page 54; 107pp; English.

XX  
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length  
CC and which have a steroid structure attached to the 3'-end through a  
CC linker attached to the A-ring of the steroid skeleton. In particular, the  
CC present sequence has a cholesterol moiety attached by its A-ring to to  
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
CC oligonucleotides form stable duplexes at physiological temperature and  
CC have selective cytotoxic activity against certain tumour cell lines,  
CC including some with multiple drug resistance  
XX  
SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGTG 5  
Db 5 GGGTG 1

RESULT 21  
AAAX32621  
ID AAAX32621 standard; DNA; 10 BP.  
XX  
AC AAAX32621;  
XX  
DT 23-JUN-1999 (first entry)  
XX  
DE Anticancer duplex forming oligonucleotide SEQ ID #21.  
XX  
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
KW multiple drug resistance; MDR; ss.  
XX  
OS Synthetic.  
XX  
PN WO9523162-A1.  
XX  
PD 31-AUG-1995.



XX 27-FEB-1995; 95WO-US002419.  
 XX 28-FEB-1994; 94US-00202927.  
 XX (MICR-) MICROPROBE CORP.  
 XX (UYVA ) UNIV YALE.  
 XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 XX WPI; 1995-311501/40.  
 XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 XX Disclosure; Page 52; 107pp; English.  
 XX New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGTG 5  
 Db |||||  
 6 GGGTG 10  
 RESULT 22  
 AAX32627  
 ID AAX32627 standard; DNA; 10 BP.  
 XX AC AAX32627;  
 XX 23-JUN-1999 (first entry)  
 XX Anticancer duplex forming oligonucleotide SEQ ID #27.  
 XX Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
 XX multiple drug resistance; MDR; ss.  
 XX Synthetic.  
 XX WO9523162-A1.  
 XX 31-AUG-1995.  
 XX 27-FEB-1995; 95WO-US002419.  
 XX 28-FEB-1994; 94US-00202927.  
 XX (MICR-) MICROPROBE CORP.  
 XX (UYVA ) UNIV YALE.  
 XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 XX WPI; 1995-311501/40.  
 XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 XX Disclosure; Page 52; 107pp; English.  
 XX New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGTG 5  
 Db |||||  
 6 GGGTG 10

PS Disclosure; Page 54; 107pp; English.  
 XX New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGTG 5  
 Db |||||  
 6 GGGTG 10  
 RESULT 23  
 AAX32630  
 ID AAX32630 standard; DNA; 10 BP.  
 XX AC AAX32630;  
 XX 23-JUN-1999 (first entry)  
 XX Anticancer duplex forming oligonucleotide SEQ ID #30.  
 XX Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
 XX multiple drug resistance; MDR; ss.  
 XX Synthetic.  
 XX WO9523162-A1.  
 XX 31-AUG-1995.  
 XX 27-FEB-1995; 95WO-US002419.  
 XX 28-FEB-1994; 94US-00202927.  
 XX (MICR-) MICROPROBE CORP.  
 XX (UYVA ) UNIV YALE.  
 XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 XX WPI; 1995-311501/40.  
 XX New stable oligo:nucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 XX Disclosure; Page 56; 107pp; English.  
 XX New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;

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Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
Qy      1 GGGTG 5
Db      6 GGGTG 10

RESULT 24
AAX32628
ID AAX32628 standard; DNA; 10 BP.
XX
AC AAX32628;
XX
DT 23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #28.
XX
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.
XX
PR 28-FEB-1994; 94US-00202927.
XX
PA (MICR-) MICROPROBE CORP.
XX
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
PI WPI; 1995-311501/40.
XX
DR
XX
PF 27-FEB-1995; 95WO-US002419.
XX
PR 28-FEB-1994; 94US-00202927.
XX
PA (MICR-) MICROPROBE CORP.
XX
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
PI WPI; 1995-311501/40.
XX
DR
XX
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT intramolecular duplex with hairpin loop region, having selective
PT cytotoxicity against some tumour cells.
XX
PS Disclosure; Page 55; 107pp; English.
XX
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC and which have a steroid structure attached to the 3'-end through a
CC linker attached to the A-ring of the steroid skeleton. In particular, the
CC present sequence has a cholesterol moiety attached by its A-ring to to
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC oligonucleotides form stable duplexes at physiological temperature and
CC have selective cytotoxic activity against certain tumour cell lines,
CC including some with multiple drug resistance
XX
SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity      100.0%; Pred. No. 1.4e+06;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
Qy      1 GGGTG 5
Db      6 GGGTG 10

RESULT 25
AAX32643/c
ID AAX32643 standard; DNA; 10 BP.
XX
AC AAX32643;
XX
DT 23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #43.

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XX Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.
XX
PR 28-FEB-1994; 94US-00202927.
XX
PA (MICR-) MICROPROBE CORP.
XX
PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
PI WPI; 1995-311501/40.
XX
DR
XX
PT New stable oligo:nucleotide duplex with 3'-steroid gp - including
PT intramolecular duplex with hairpin loop region, having selective
PT cytotoxicity against some tumour cells.
XX
PS Disclosure; Page 60; 107pp; English.
XX
CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
CC and which have a steroid structure attached to the 3'-end through a
CC linker attached to the A-ring of the steroid skeleton. In particular, the
CC present sequence has a cholesterol moiety attached by its A-ring to to
CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
CC oligonucleotides form stable duplexes at physiological temperature and
CC have selective cytotoxic activity against certain tumour cell lines,
CC including some with multiple drug resistance
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;
Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity      100.0%; Pred. No. 1.4e+06;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
Qy      1 GGGTG 5
Db      5 GGGTG 1

RESULT 26
AAX32629
ID AAX32629 standard; DNA; 10 BP.
XX
AC AAX32629;
XX
DT 23-JUN-1999 (first entry)
XX
DE Anticancer duplex forming oligonucleotide SEQ ID #29.
XX
KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
KW multiple drug resistance; MDR; ss.
XX
OS Synthetic.
XX
PN WO9523162-A1.
XX
PD 31-AUG-1995.
XX
PF 27-FEB-1995; 95WO-US002419.
XX
PR 28-FEB-1994; 94US-00202927.
XX
PA (MICR-) MICROPROBE CORP.
PA (UYVA ) UNIV YALE.

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XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 XX WPI; 1995-311501/40.  
 XX New stable oligonucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 XX Disclosure; Page 55; 107pp; English.  
 XX New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX Sequence 10 BP; 3 A; 2 C; 4 G; 1 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 DB 6 GGGTG 10  
 RESULT 27  
 AAX32631  
 ID AAX32631 standard; DNA; 10 BP.  
 XX AC AAX32631;  
 XX 23-JUN-1999 (first entry)  
 DE Anticancer duplex forming oligonucleotide SEQ ID #31.  
 XX Steroid; anticancer; antitumour; cytotoxic; duplex; linker;  
 KW multiple drug resistance; MDR; ss.  
 XX Synthetic.  
 XX WO9523162-A1.  
 XX 31-AUG-1995.  
 XX 27-FEB-1995; 95WO-US002419.  
 XX 28-FEB-1994; 94US-00202927.  
 XX (MICR-) MICROPROBE CORP.  
 XX (UYVA) UNIV YALE.  
 XX Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;  
 XX WPI; 1995-311501/40.  
 XX New stable oligonucleotide duplex with 3'-steroid gp - including  
 PT intramolecular duplex with hairpin loop region, having selective  
 PT cytotoxicity against some tumour cells.  
 XX Disclosure; Page 56; 107pp; English.  
 XX New oligonucleotides are disclosed which are 8-18 nucleotides in length  
 CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance

CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 DB 6 GGGTG 10  
 RESULT 28  
 AAQ96407  
 ID AAQ96407 standard; DNA; 10 BP.  
 XX AC AAQ96407;  
 XX 16-OCT-2003 (revised)  
 DT 19-MAR-1996 (first entry)  
 XX HIV-1 NL4-3 nef gene nucleotide deletion 2.  
 DE HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 KW Human immunodeficiency virus 1.  
 XX WO9521912-A1.  
 XX 17-AUG-1995.  
 XX 14-FEB-1995; 95WO-AU000063.  
 XX 14-FEB-1994; 94AU-00003864.  
 PR 21-FEB-1994; 94AU-00004002.  
 PR 23-DEC-1994; 94AU-0000284.  
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 PA (AURE-) AUSTRALIAN RED CROSS SOC.  
 XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 WPI; 1995-293115/38.  
 XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.  
 XX Claim 13; Page 188; 301pp; English.  
 XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX Sequence 10 BP; 2 A; 1 C; 5 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 DB 2 GGGTG 6



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XX DR WPI; 1995-293115/38.
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 194; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 2 A; 4 C; 2 G; 2 T; 0 U; 0 Other;
      Query Match      100.0%; Score 5; DB 2; Length 10;
      Best Local Similarity 100.0%; Pred. No. 1.4e+06;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 6 GGGTG 2

RESULT 22
AAQ96486
ID AAQ96486 standard; DNA; 10 BP.
XX AC AAQ96486;
XX DT 16-OCT-2003 (revised)
XX DT 20-MAR-1996 (first entry)
XX XX HIV-1 NL4-3 nef gene nucleotide deletion 81.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 199; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic

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CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX standardise OS field)
XX SQ Sequence 10 BP; 2 A; 0 C; 6 G; 2 T; 0 U; 0 Other;
      Query Match      100.0%; Score 5; DB 2; Length 10;
      Best Local Similarity 100.0%; Pred. No. 1.4e+06;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 6 GGGTG 10

RESULT 33
AAQ96896/c
ID AAQ96896 standard; DNA; 10 BP.
XX AC AAQ96896;
XX DT 16-OCT-2003 (revised)
XX DT 26-MAR-1996 (first entry)
XX XX HIV-1 NL4-3 nef gene nucleotide deletion 491.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX XX (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 194; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
      Query Match      100.0%; Score 5; DB 2; Length 10;
      Best Local Similarity 100.0%; Pred. No. 1.4e+06;
      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 10 GGGTG 6

RESULT 34

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PT	LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
XX	Claim 13; Page 194; 30ipp; English.
XX	Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more dezanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more dezanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The resulting avirulent HIV strains are still capable of inducing an immune response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)
XX	Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;
SQ	Query Match 100.0%; Score 5; DB 2; Length 10; Best Local Similarity 100.0%; Pred. No. 1.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GGGTG 5 
DB	7 GGGTG 3 
RESULT 42	
AAQ96898/c	
ID	AAQ96898 standard; DNA; 10 BP.
XX	AAQ96898;
XX	16-OCT-2003 (revised)
DT	26-MAR-1996 (first entry)
DT	HIV-1 NL4-3 nef gene nucleotide deletion 493.
DE	HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX	Human immunodeficiency virus 1.
OS	WO9521912-A1.
PN	17-AUG-1995.
XX	14-FEB-1995; 95WO-AU000063.
XX	14-FEB-1994; 94AU-00003864.
PR	21-FEB-1994; 94AU-00004002.
PR	23-DEC-1994; 94AU-00000284.
XX	(MACF-) MACFARLANE BURNET CENT MEDICAL.
PA	(AURE-) AUSTRALIAN RED CROSS SOC.
XX	Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D; WPI; 1995-293115/38.
XX	New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or LTR region - can be used in a vaccine to inhibit/reduce productive infection in an individual by a pathogenic strain.
PT	Claim 13; Page 194; 30ipp; English.
XX	Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or more dezanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more dezanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The resulting avirulent HIV strains are still capable of inducing an immune response in humans, and enable the generation of therapeutic, diagnostic and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to standardise OS field)
XX	Sequence 10 BP; 2 A; 4 C; 1 G; 3 T; 0 U; 0 Other;

KW disease diagnosis; ss.  
 OS Synthetic.  
 XX WO9531574-A1.  
 FN 23-NOV-1995.  
 XX 12-MAY-1995; 95WO-US006032.  
 PF 16-MAY-1994; 94US-00242887.  
 PR (BGHM ) BRIGHAM & WOMENS HOSPITAL.  
 XX Lopeznieta CE, Nigam SK;  
 PI WPI; 1996-010958/01.  
 XX Characterisation of nucleotide sequences using primer pairs - by PCR  
 PT amplification and indexing of amplification prods. w.r.t. primers used  
 PT for genome mapping and disease diagnosis.  
 XX Claim 46; Page 55; 72pp; English.  
 PS The 5'-primers AAT29262-382, and the complementary 3'-primers derived  
 CC from them, which target mammalian G-protein coupled receptor coding  
 CC sequences, together comprise a PCR primer kit. The kit is used in a new  
 CC method for the characterisation of nucleic acid sequences obt'd. from  
 CC mammalian biological samples, which comprises PCR amplification and  
 CC indexing of the prods. w.r.t the primer pair that hybridised to its  
 CC delineating subsequences. The method may be used in the identification,  
 CC cloning and analysis of genes, e.g. in genome mapping, and disease  
 CC diagnosis. (Updated on 25-MAR-2003 to correct PI field.)  
 XX Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 Db |||||  
 4 GGGTG 8  
 RESULT 45  
 AAT18613  
 ID AAT18613 standard; DNA; 10 BP.  
 XX AAT18613;  
 AC 06-NOV-1996 (first entry)  
 DT Arbitrary 5' oligodecamer DDRT-PCR primer OPA 8.  
 XX Differential display of mRNA; reverse transcription; DDRT-PCR; human;  
 DE chondrocyte; gene specific; primer; probe; isolation; interleukin-lbета;  
 XX IL-lbета; diagnosis; connective tissue disease; osteoarthritis;  
 KW rheumatoid arthritis; polymerase chain reaction; ss.  
 XX Synthetic.  
 OS EP705842-A2.  
 XX 10-APR-1996.  
 PD 02-OCT-1995; 95EP-00115510.  
 XX 06-OCT-1994; 94EP-00115751.  
 PF (FARH ) HOECHST AG.  
 XX Bartnik E, Margerie D;  
 PI WPI; 1996-181045/19.  
 DR Diagnosis and treatment of IL-1 mediated connective tissue diseases -  
 XX using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or  
 PT antibodies to them.  
 XX Example; Page 15; 31pp; English.  
 The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which  
 were used along with 4 degenerate 3' oligo dT primers for the  
 differential display of human chondrocyte mRNA by reverse transcription  
 and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA  
 clones, which were then searched against DNA databases for homology to  
 known human genes. The cDNA mols. can be used for the prodn. of gene  
 specific primers and probes to isolate genes induced by treating (esp.  
 human) chondrocytes with interleukin-lbета (IL-lbета), and for the  
 diagnosis of IL-lbета related connective tissue diseases, in partic.  
 CC osteoarthritis or rheumatoid arthritis  
 XX Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 Db |||||  
 6 GGGTG 10  
 RESULT 46  
 AAT18612  
 ID AAT18612 standard; DNA; 10 BP.  
 XX AAT18612;  
 AC 06-NOV-1996 (first entry)  
 DT Arbitrary 5' oligodecamer DDRT-PCR primer OPA 7.  
 XX Differential display of mRNA; reverse transcription; DDRT-PCR; human;  
 KW chondrocyte; gene specific; primer; probe; isolation; interleukin-lbета;  
 KW IL-lbета; diagnosis; connective tissue disease; osteoarthritis;  
 KW rheumatoid arthritis; polymerase chain reaction; ss.  
 XX Synthetic.  
 OS EP705842-A2.  
 XX 10-APR-1996.  
 PD 02-OCT-1995; 95EP-00115510.  
 XX 06-OCT-1994; 94EP-00115751.  
 PR (FARH ) HOECHST AG.  
 XX Bartnik E, Margerie D;  
 PI WPI; 1996-181045/19.  
 DR Diagnosis and treatment of IL-1 mediated connective tissue diseases -  
 XX using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or  
 PT antibodies to them.  
 XX Example; Page 15; 31pp; English.  
 The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which  
 were used along with 4 degenerate 3' oligo dT primers for the  
 differential display of human chondrocyte mRNA by reverse transcription  
 and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA  
 clones, which were then searched against DNA databases for homology to

XX WPI; 1996-181045/19.  
 DR Diagnosis and treatment of IL-1 mediated connective tissue diseases -  
 XX using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or  
 PT antibodies to them.  
 XX Example; Page 15; 31pp; English.  
 XX The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which  
 CC were used along with 4 degenerate 3' oligo dT primers for the  
 CC differential display of human chondrocyte mRNA by reverse transcription  
 CC and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA  
 CC clones, which were then searched against DNA databases for homology to  
 CC known human genes. The cDNA mols. can be used for the prodn. of gene  
 CC specific primers and probes to isolate genes induced by treating (esp.  
 CC human) chondrocytes with interleukin-lbета (IL-lbета), and for the  
 CC diagnosis of IL-lbета related connective tissue diseases, in partic.  
 CC osteoarthritis or rheumatoid arthritis  
 XX Sequence 10 BP; 1 A; 1 C; 6 G; 2 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 Db |||||  
 6 GGGTG 10  
 RESULT 46  
 AAT18612  
 ID AAT18612 standard; DNA; 10 BP.  
 XX AAT18612;  
 AC 06-NOV-1996 (first entry)  
 DT Arbitrary 5' oligodecamer DDRT-PCR primer OPA 7.  
 XX Differential display of mRNA; reverse transcription; DDRT-PCR; human;  
 KW chondrocyte; gene specific; primer; probe; isolation; interleukin-lbета;  
 KW IL-lbета; diagnosis; connective tissue disease; osteoarthritis;  
 KW rheumatoid arthritis; polymerase chain reaction; ss.  
 XX Synthetic.  
 OS EP705842-A2.  
 XX 10-APR-1996.  
 PD 02-OCT-1995; 95EP-00115510.  
 XX 06-OCT-1994; 94EP-00115751.  
 PR (FARH ) HOECHST AG.  
 XX Bartnik E, Margerie D;  
 PI WPI; 1996-181045/19.  
 DR Diagnosis and treatment of IL-1 mediated connective tissue diseases -  
 XX using osteopontin, calnexin, TSG-6 gene prod., genes encoding them or  
 PT antibodies to them.  
 XX Example; Page 15; 31pp; English.  
 XX The present sequence is 1 of 25 arbitrary 5' oligodecamer primers, which  
 CC were used along with 4 degenerate 3' oligo dT primers for the  
 CC differential display of human chondrocyte mRNA by reverse transcription  
 CC and PCR (DDRT-PCR). Sequence analysis revealed the sequences of 52 cDNA  
 CC clones, which were then searched against DNA databases for homology to

CC known human genes. The cDNA mols. can be used for the prodn. of gene  
 CC specific primers and probes to isolate genes induced by treating (esp.  
 CC human) chondrocytes with interleukin-1beta (IL-1beta), and for the  
 CC diagnosis of IL-1beta related connective tissue diseases, in partic.  
 CC osteoarthritis or rheumatoid arthritis  
 XX  
 XX Sequence 10 BP; 3 A; 1 C; 5 G; 1 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGTG 5  
 Db 6 GGGTG 10  
 RESULT 47  
 AAQ99300/C  
 ID AAQ99300 standard; cDNA; 10 BP.  
 XX  
 AC AAQ99300;  
 XX  
 XX 06-SEP-1996 (first entry)  
 DT  
 DE Multi-drug resistant-1 gene antisense oligonucleotide 1114.  
 XX  
 XX Antisense oligonucleotide; nucleotides 1712-1721 and 3642-3656;  
 KW multi-drug resistant-1; MDR-1; nucleotide binding sites; plasma membrane;  
 KW glycoprotein; P170; inhibition; expression; treatment; cancer cells;  
 KW induction; prevention; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9602556-A2.  
 XX  
 PD 01-FEB-1996.  
 XX  
 XX 18-JUL-1995; 95WO-US009011.  
 PF  
 XX 18-JUL-1994; 94US-00276567.  
 PR  
 XX (HYBR-) HYBRIDON INC.  
 PA  
 XX Smyth AP;  
 PT  
 XX WPI; 1996-105848/11.  
 DR  
 XX New oligo:nucleotide(s) complementary to the MDR-1 gene - used for  
 PT preventing induction of multi:drug resistance or for treating multi:drug  
 PT resistant cancer cells.  
 XX  
 PS Disclosure; Page 14; 43pp; English.  
 XX  
 CC The present oligonucleotide is antisense to nucleotides 1712-1721 and  
 CC 3642-3656 of the multi-drug resistant-1 (MDR-1) gene, which encode the  
 CC nucleotide binding sites of the plasma membrane glycoprotein, P170. The  
 CC oligonucleotide inhibits the expression of P170, and can therefore be  
 CC used to treat MDR cancer cells, and prevent the induction of MDR in  
 CC cancer cells and the expression of P170 in cells  
 XX  
 SQ Sequence 10 BP; 1 A; 6 C; 0 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGTG 5  
 Db 5 GGGTG 1  
 RESULT 48  
 AAQ98860  
 ID AAQ98860 standard; DNA; 10 BP.  
 XX  
 AC AAQ98860;  
 XX  
 DT 20-MAR-1998 (first entry)  
 XX  
 DE Core-binding site clone 6-7-1.  
 XX  
 KW Protein-binding site isolation; transcription factor modification;  
 KW DNA-binding protein; inhibitor identification; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9727330-A1.  
 XX  
 PD 31-JUL-1997.  
 XX  
 XX 24-JAN-1997; 97WO-US001230.  
 PF  
 XX 24-JAN-1996; 96US-00590571.  
 PR  
 XX (UYVA ) UNIV YALE.  
 PA  
 XX Weissman SM, Kulkarni P, Nallur GN;  
 PI  
 XX WPI; 1997-393714/36.  
 DR  
 XX Identifying protein-binding sites for DNA-binding proteins - using  
 PT duplexes having 5' and 3' sequences for annealing to amplification  
 PT primers with an internal potential protein-binding site sequence.  
 XX  
 PS Example 3; Page 22; 52pp; English.  
 XX  
 CC This sequence represents a core-binding site identified using the method  
 CC of the invention. This sequence was identified using the 32P-labelled  
 CC oligonucleotide duplex shown in AAT76581 and the primers shown in  
 CC AAT76582-T76583 in the method of the invention. The method is for  
 CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
 CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
 CC having 5' and 3' sequences capable of annealing to primers for  
 CC amplification and an internal sequence having a potential protein-binding  
 CC site, a non-specific inhibitor and a sample containing DNA-binding  
 CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
 CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
 CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
 CC binding proteins. The methods can be used to identify protein-binding  
 CC sites which can be used to identify corresponding DNA-binding proteins in  
 CC an expression library. They can also be used to develop products to  
 CC inhibit the function of a given DNA-binding protein or for the  
 CC modification of transcription factors  
 XX  
 SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGTG 5  
 Db 3 GGGTG 7  
 RESULT 49  
 AAT98837  
 ID AAT98837 standard; DNA; 10 BP.  
 XX  
 AC AAT98837;  
 XX  
 DT 20-MAR-1998 (first entry)  
 XX  
 XX Binding site BSN7 identified using the method of the invention.  
 XX

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KW Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
XX WO9727330-A1.
XX
XX 31-JUL-1997.
XX
XX 24-JAN-1997; 97WO-US001230.
XX
XX 24-JAN-1996; 96US-00590571.
XX
XX (UYVA ) UNIV YALE.
XX
XX Weissman SM, Kulkarni P, Nallur GN;
XX
XX WPI; 1997-393714/36.
XX
XX Identifying protein-binding sites for DNA-binding proteins - using
XX duplexes having 5' and 3' sequences for annealing to amplification
XX primers with an internal potential protein-binding site sequence.
XX
XX Example 3; Page 19; 52pp; English.
XX
XX This sequence represents a binding site identified using the method of
XX the invention. This sequence was identified using the 32p-labelled
XX oligonucleotide duplex shown in AAT76581 and the primers shown in
XX AAT76582-T76583 in the method of the invention. The method is for
XX simultaneously isolating protein-binding sites for DNA-binding proteins.
XX The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
XX having 5' and 3' sequences capable of annealing to primers for
XX amplification and an internal sequence having a potential protein-binding
XX site, a non-specific inhibitor and a sample containing DNA-binding
XX proteins; (b) separating unbound ON duplexes from ON duplexes complexed
XX with the DNA-binding proteins; (c) amplifying complexed duplexes to form
XX amplified duplexes; thereby isolating protein-binding sites for the DNA-
XX binding proteins. The methods can be used to identify protein-binding
XX sites which can be used to identify corresponding DNA-binding proteins in
XX an expression library. They can also be used to develop products to
XX inhibit the function of a given DNA-binding protein or for the
XX modification of transcription factors
XX
XX Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGTG 5
XX |||||
XX 2 GGGTG 6
XX
XX RESULT 50
XX AAT51668
XX ID AAT51668 standard; DNA; 10 BP.
XX
XX AC AAT51668;
XX
XX 12-NOV-1997 (first entry)
XX
XX Viral integrase inhibiting oligonucleotide.
XX
XX Human immunodeficiency virus; HIV; Epstein Barr virus; EBV;
XX herpes simplex virus; HSV; human papilloma virus; HPV; adenovirus;
XX respiratory syncytial virus; RSV; cytomegalovirus; CMV; hepatitis B;
XX integrase inhibition; guanosine tetrad; ss.
XX
XX Synthetic.
XX
XX WO9703997-A1.
XX

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PD 06-FEB-1997.
XX
XX 17-JUL-1996; 96WO-US011786.
XX
XX 19-JUL-1995; 95US-0001505P.
XX 23-OCT-1995; 95US-00535168.
XX 19-MAR-1996; 96US-0013688P.
XX 25-MAR-1996; 96US-0014007P.
XX 17-APR-1996; 96US-0015714P.
XX 23-APR-1996; 96US-0016271P.
XX
XX (ARON-) ARONEX PHARM INC.
XX
XX Rando RF, Fennewald S, Zengdegi JG, Ojwang JO, Hogan ME;
XX Pommier Y, Mazumder A;
XX
XX WPI; 1997-132569/12.
XX
XX Oligo:nucleotide(s) capable of forming guanosine tetrads - inhibit viral
XX enzyme responsible for integrating viral nucleic acid into the host
XX genome.
XX
XX Claim 3; Page 168; 245pp; English.
XX
XX AAT51619-T51698 are oligonucleotides used to inhibit the production of
XX viruses within a host cell. The oligonucleotides may form guanosine
XX tetrads (structures formed of eight hydrogen bonds by coordination of the
XX four oxygen atoms of guanine with alkali cations believed to bind to the
XX centre of a quadruplex, and by strong stacking interactions) and are used
XX to prevent the integration of viral nucleic acid into a host genome. The
XX oligonucleotides inhibit functioning of the integrase enzyme and hence
XX prevent viral infection. Viral infections that may be treated include
XX human immunodeficiency virus (HIV), Epstein Barr virus (EBV), herpes
XX simplex virus (HSV), human papilloma virus (HPV), adenovirus, respiratory
XX syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis B virus (HBV),
XX especially HIV-1 infection
XX
XX Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGTG 5
XX |||||
XX 3 GGGTG 7
XX
XX Search completed: January 7, 2005, 07:12:09
XX Job time : 258.4 secs

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98	5	100.0	19	8	AZ808178	2M0071A15	C 171	5	100.0	21	2	AW248836	2B21108.3
99	5	100.0	19	8	AZ809394	2M0073E19	172	5	100.0	21	4	BM398994	5009-0-51
C 100	5	100.0	19	8	AZ818421	2M0088M19	C 173	5	100.0	21	6	CD533377	31H19 Ar
101	5	100.0	19	8	AZ819494	2M0091I10	174	5	100.0	21	7	CO779017	BL005B GO
102	5	100.0	19	8	AZ822954	2M0096I10	175	5	100.0	21	8	AZ313243	1M0029H16
103	5	100.0	19	8	AZ827092	2M0103M18	176	5	100.0	21	8	AZ341831	1M0074D02
104	5	100.0	19	8	AZ842166	2M0140G06	C 177	5	100.0	21	8	AZ341842	1M0080O11
105	5	100.0	19	8	AZ954606	2M0220B32	C 178	5	100.0	21	8	AZ345472	1M0074F05
106	5	100.0	19	8	AZ967656	2M0238M09	179	5	100.0	21	8	AZ369855	1M0120G07
C 107	5	100.0	19	8	AZ969805	2M0242O12	180	5	100.0	21	8	AZ377507	1M0131G21
C 108	5	100.0	19	9	AJ600584	Arabidops	181	5	100.0	21	8	AZ398828	1M0165A23
C 109	5	100.0	20	3	CNS08X08	Single re	182	5	100.0	21	8	AZ410517	1M0183M02
C 110	5	100.0	20	4	BG896991	HOA59-1-G	183	5	100.0	21	8	AZ419497	1M0196J04
C 111	5	100.0	20	4	BG927393	HNC1-1-F7	C 184	5	100.0	21	8	AZ424095	1M0203E03
112	5	100.0	20	4	BM399070	5009-0-52	185	5	100.0	21	8	AZ429736	1M0213A23
C 113	5	100.0	20	6	CD533611	32L6 Arab	186	5	100.0	21	8	AZ443821	1M0238I07
C 114	5	100.0	20	6	CF393092	32DGS--02	C 187	5	100.0	21	8	AZ445481	1M0241P15
C 115	5	100.0	20	6	CF315027	HD--03-M1	188	5	100.0	21	8	AZ451384	1M0250D13
C 116	5	100.0	20	8	AZ303771	1M0003E03	189	5	100.0	21	8	AZ468862	1M0282O04
117	5	100.0	20	8	AZ307088	1M0008M23	C 190	5	100.0	21	8	AZ495585	1M0331H02
118	5	100.0	20	8	AZ308143	1M0010A21	C 191	5	100.0	21	8	AZ503574	1M0343H19
C 119	5	100.0	20	8	AZ330662	1M0056F15	192	5	100.0	21	8	AZ504494	1M0344O17
C 120	5	100.0	20	8	AZ336487	1M0066J13	C 193	5	100.0	21	8	AZ512534	1M0358B07
C 121	5	100.0	20	8	AZ345583	1M0080L18	C 194	5	100.0	21	8	AZ580960	1M0369P04
C 122	5	100.0	20	8	AZ359918	1M0103A01	C 195	5	100.0	21	8	AZ581103	1M0369E22
C 123	5	100.0	20	8	AZ368205	1M0118L07	196	5	100.0	21	8	AZ596349	1M0409K03
C 124	5	100.0	20	8	AZ369118	1M0119I06	197	5	100.0	21	8	AZ596843	1M0410C23
C 125	5	100.0	20	8	AZ379036	1M0134L02	198	5	100.0	21	8	AZ598137	1M0412F16
C 126	5	100.0	20	8	AZ386570	1M0145C08	199	5	100.0	21	8	AZ610251	1M0435M21
127	5	100.0	20	8	AZ405596	1M0174B06	200	5	100.0	21	8	AZ645749	1M0511C20
128	5	100.0	20	8	AZ408559	1M0179K14	C 201	5	100.0	21	8	AZ648575	1M0517G07
129	5	100.0	20	8	AZ423710	1M0202J21	C 202	5	100.0	21	8	AZ654730	1M0529P05
130	5	100.0	20	8	AZ430735	1M0215A22	C 203	5	100.0	21	8	AZ656028	1M0531O17
131	5	100.0	20	8	AZ447706	1M0245C06	C 204	5	100.0	21	8	AZ657224	1M0533I18
C 132	5	100.0	20	8	AZ468486	1M0281G04	C 205	5	100.0	21	8	AZ660221	1M0538M09
133	5	100.0	20	8	AZ478502	1M0298B09	206	5	100.0	21	8	AZ758704	1M0550A20
134	5	100.0	20	8	AZ487730	1M0317P04	207	5	100.0	21	8	AZ760907	1M0554P21
C 135	5	100.0	20	8	AZ490328	1M0323A18	C 208	5	100.0	21	8	AZ774703	2M0004G14
C 136	5	100.0	20	8	AZ514611	1M0361M20	C 209	5	100.0	21	8	AZ7783943	2M0026P05
C 137	5	100.0	20	8	AZ590476	1M0400P06	C 210	5	100.0	21	8	AZ785173	2M0028G19
C 138	5	100.0	20	8	AZ592635	1M0403M11	C 211	5	100.0	21	8	AZ785825	2M0030G05
139	5	100.0	20	8	AZ601843	1M0420M13	212	5	100.0	21	8	AZ788269	2M0035D18
140	5	100.0	20	8	AZ609449	1M0434D20	C 213	5	100.0	21	8	AZ788597	2M0035B19
141	5	100.0	20	8	AZ627859	1M0476E04	C 214	5	100.0	21	8	AZ792515	2M0045H04
C 142	5	100.0	20	8	AZ628029	1M0476F17	C 215	5	100.0	21	8	AZ812415	2M0079N04
C 143	5	100.0	20	8	AZ642891	1M0506D12	C 216	5	100.0	21	8	AZ816100	2M0084M11
144	5	100.0	20	8	AZ652975	1M0526L20	C 217	5	100.0	21	8	AZ819244	2M0089F14
C 145	5	100.0	20	8	AZ653361	1M0527D04	C 218	5	100.0	21	8	AZ819492	2M0091I108
C 146	5	100.0	20	8	AZ663302	1M0542D22	C 219	5	100.0	21	8	AZ830720	2M0110D12
147	5	100.0	20	8	AZ766582	1M0564G16	220	5	100.0	21	8	AZ834643	2M0117N24
C 148	5	100.0	20	8	AZ769146	1M0569C05	221	5	100.0	21	8	AZ864022	2M0173G22
C 149	5	100.0	20	8	AZ769811	1M0570B23	222	5	100.0	21	8	AZ875300	2M0189D22
C 150	5	100.0	20	8	AZ774978	2M0004C23	223	5	100.0	21	8	AZ878432	2M0254G15
151	5	100.0	20	8	AZ780905	2M0018M12	224	5	100.0	21	8	AZ995847	2M0281N16
152	5	100.0	20	8	AZ782314	2M0022D03	C 225	5	100.0	21	8	AZ997000	2M0283D24
153	5	100.0	20	8	AZ784073	2M0026B06	226	5	100.0	21	9	AJ590147	Arabidops
154	5	100.0	20	8	AZ792281	2M0043F09	C 227	5	100.0	21	9	CL669293	PR1015a_B
C 155	5	100.0	20	8	AZ793982	2M0047I05	228	5	100.0	21	9	AG190803	Pan trogl
C 156	5	100.0	20	8	AZ796123	2M0051O04	229	5	100.0	21	9	AG201733	Pan trogl
157	5	100.0	20	8	AZ797468	2M0053P09	C 230	5	100.0	21	9	AG202462	Pan trogl
158	5	100.0	20	8	AZ808291	2M0071D09	C 231	5	100.0	21	9	AG203513	Pan trogl
159	5	100.0	20	8	AZ828544	2M0105O04	232	5	100.0	22	1	AA908627	og86e01.8
C 160	5	100.0	20	8	AZ833695	2M0115N20	233	5	100.0	22	1	AA931331	oo66c03.8
161	5	100.0	20	8	AZ836147	2M0130O14	234	5	100.0	22	1	AA936651	o187b12.8
162	5	100.0	20	8	AZ846316	2M0146N24	235	5	100.0	22	1	AA938474	oo56h02.8
163	5	100.0	20	8	AZ846437	2M0146E10	236	5	100.0	22	1	AA973612	oo47f01.8
164	5	100.0	20	8	AZ853944	2M0157B21	C 237	5	100.0	22	1	AA978171	ny316f08.8
165	5	100.0	20	8	AZ948873	2M0212P02	238	5	100.0	22	1	AA982956	ua23q03.r
C 166	5	100.0	20	8	AZ995803	2M0281G14	239	5	100.0	22	1	A1000026	ot03q12.x
167	5	100.0	20	9	AJ587163	Arabidops	C 240	5	100.0	22	1	A1056251	oy90k01.x
168	5	100.0	20	9	AG188183	Pan trogl	C 241	5	100.0	22	1	A1183338	qq41a12.x
169	5	100.0	20	9	AG197313	Pan trogl	242	5	100.0	22	1	A1186405	qd20605.x
C 170	5	100.0	21	1	AU257028	AU257028	C 243	5	100.0	22	1	A1318264	tb03b12.x

C 244	5	100.0	22	1	A1354432	A1354432	qul7d02.x	317	5	100.0	22	8	A2966411	A2966411	2M0236B22
C 245	5	100.0	22	1	A1357851	A1357851	qv73g11.x	C 318	5	100.0	22	8	A2973872	A2973872	2M0248E13
C 246	5	100.0	22	1	A1371446	A1371446	qy06b02.x	319	5	100.0	22	8	A2976229	A2976229	2M0251N06
C 247	5	100.0	22	1	A1433927	A1433927	ti5a002.x	C 320	5	100.0	22	8	A2991498	A2991498	2M0275C14
C 248	5	100.0	22	1	A1521380	A1521380	ti05g01.x	321	5	100.0	22	8	A2994320	A2994320	2M0279D17
C 249	5	100.0	22	1	A1566619	A1566619	tr95c08.x	322	5	100.0	22	9	AJ590074	AJ590074	Arabidops
C 250	5	100.0	22	1	A1601113	A1601113	ar89d02.x	323	5	100.0	22	9	TA140A04P	TA140A04P	AL466405
C 251	5	100.0	22	1	A1633039	A1633039	tz33g06.x	324	5	100.0	22	9	TA19D05Q	TA19D05Q	AL452318
C 252	5	100.0	22	1	A1673793	A1673793	to73c10.x	325	5	100.0	22	9	TA205F05Q	TA205F05Q	AL476402
C 253	5	100.0	22	1	A1677768	A1677768	wc80b01.x	C 326	5	100.0	22	9	TA219F10Q	TA219F10Q	AL478653
C 254	5	100.0	22	1	A1678266	A1678266	tp94d10.x	327	5	100.0	22	9	TA245E10P	TA245E10P	AL483585
C 255	5	100.0	22	1	A1707945	A1707945	as34g10.x	328	5	100.0	22	9	TA247D05Q	TA247D05Q	AL482020
C 256	5	100.0	22	1	A1721471	A1721471	fc28b01.x	329	5	100.0	22	9	TA327G01Q	TA327G01Q	AL493368
C 257	5	100.0	22	1	A1738599	A1738599	w139g02.x	330	5	100.0	22	9	TA7H01P	TA7H01P	AL452382
C 258	5	100.0	22	1	AJ649192	AJ649192	AJ649192	331	5	100.0	22	9	CL439535	CL439535	PS19468-N
C 259	5	100.0	22	1	AJ649983	AJ649983	AJ649983	C 332	5	100.0	22	9	CL670376	CL670376	PR10161D
C 260	5	100.0	22	1	AJ795224	AJ795224	AJ795224	C 333	5	100.0	22	9	CL684513	CL684513	PR10139D
C 261	5	100.0	22	8	AQ051296	AQ051296	rbxb0001C	C 334	5	100.0	22	9	CL693157	CL693157	PR10160A
C 262	5	100.0	22	8	A2303893	A2303893	IM0003011	C 335	5	100.0	22	9	AG199763	AG199763	Pan trogl
C 263	5	100.0	22	8	A2307488	A2307488	IM0009B13	336	5	100.0	22	9	AG200537	AG200537	Pan trogl
C 264	5	100.0	22	8	A2307952	A2307952	IM0010L24	C 337	5	100.0	22	9	AG201938	AG201938	Pan trogl
C 265	5	100.0	22	8	A2314354	A2314354	IM0031E07	338	5	100.0	22	9	AJ658745	AJ658745	AJ658745
C 266	5	100.0	22	8	A2318425	A2318425	IM0037M14	339	5	100.0	23	1	AJ691390	AJ691390	AJ691390
C 267	5	100.0	22	8	A2327083	A2327083	IM0050D17	340	5	100.0	23	4	BG924552	BG924552	HNC27-1-H
C 268	5	100.0	22	8	A2330040	A2330040	IM0055I06	C 341	5	100.0	23	4	BG927413	BG927413	HNC1-1-G1
C 269	5	100.0	22	8	A2334102	A2334102	IM0068B16	C 342	5	100.0	23	6	BQ591005	BQ591005	E012598-0
C 270	5	100.0	22	8	A2349291	A2349291	IM0086B16	C 343	5	100.0	23	6	CA851455	CA851455	D13H10_O1
C 271	5	100.0	22	8	A2351959	A2351959	IM0090C16	C 344	5	100.0	23	7	CO408356	CO408356	VRK503_V1
C 272	5	100.0	22	8	A2391617	A2391617	IM0153B19	C 345	5	100.0	23	8	A2303974	A2303974	IM0003E01
C 273	5	100.0	22	8	A2419130	A2419130	IM0195D03	C 346	5	100.0	23	8	AZ308643	AZ308643	IM0011013
C 274	5	100.0	22	8	A2422530	A2422530	IM0201E14	347	5	100.0	23	8	AZ309363	AZ309363	IM0013G22
C 275	5	100.0	22	8	A2425344	A2425344	IM0205G19	C 348	5	100.0	23	8	AZ309945	AZ309945	IM0017K22
C 276	5	100.0	22	8	A2434635	A2434635	IM0238O08	C 349	5	100.0	23	8	AZ310681	AZ310681	IM0025F13
C 277	5	100.0	22	8	A2452101	A2452101	IM0251I15	350	5	100.0	23	8	AZ316806	AZ316806	IM0035E13
C 278	5	100.0	22	8	A2454940	A2454940	IM0257B10	351	5	100.0	23	8	AZ329120	AZ329120	IM0053A14
C 279	5	100.0	22	8	A2462655	A2462655	IM0269F12	C 352	5	100.0	23	8	AZ330727	AZ330727	IM0056B07
C 280	5	100.0	22	8	A2479083	A2479083	IM0299F03	C 353	5	100.0	23	8	AZ333226	AZ333226	IM0062P12
C 281	5	100.0	22	8	A2479594	A2479594	IM0300B22	354	5	100.0	23	8	AZ334719	AZ334719	IM0064P07
C 282	5	100.0	22	8	A2484950	A2484950	IM0311K16	355	5	100.0	23	8	AZ339656	AZ339656	IM0071A14
C 283	5	100.0	22	8	A2490723	A2490723	IM0323F19	C 356	5	100.0	23	8	AZ345482	AZ345482	IM0080B01
C 284	5	100.0	22	8	A2491269	A2491269	IM0324B18	C 357	5	100.0	23	8	AZ356191	AZ356191	IM0097L07
C 285	5	100.0	22	8	A2582417	A2582417	IM0374N13	358	5	100.0	23	8	AZ372664	AZ372664	IM0124E09
C 286	5	100.0	22	8	A2592243	A2592243	IM0403F05	359	5	100.0	23	8	AZ374746	AZ374746	IM0127D15
C 287	5	100.0	22	8	A2602345	A2602345	IM0421K05	C 360	5	100.0	23	8	AZ387178	AZ387178	IM0146K19
C 288	5	100.0	22	8	A2610334	A2610334	IM0435L04	361	5	100.0	23	8	AZ389539	AZ389539	IM0150D14
C 289	5	100.0	22	8	A2624301	A2624301	IM0462J19	362	5	100.0	23	8	AZ404383	AZ404383	IM0172I19
C 290	5	100.0	22	8	A2627938	A2627938	IM0469A24	363	5	100.0	23	8	AZ410218	AZ410218	IM0182F23
C 291	5	100.0	22	8	A2641435	A2641435	IM0503P21	364	5	100.0	23	8	AZ418429	AZ418429	IM0194F02
C 292	5	100.0	22	8	A2643849	A2643849	IM0507H05	C 365	5	100.0	23	8	AZ425674	AZ425674	IM0205F19
C 293	5	100.0	22	8	A2650525	A2650525	IM0520F13	C 366	5	100.0	23	8	AZ445479	AZ445479	IM0241O15
C 294	5	100.0	22	8	A2651001	A2651001	IM0521O23	367	5	100.0	23	8	AZ445661	AZ445661	IM0241O15
C 295	5	100.0	22	8	A2663539	A2663539	IM0543A15	368	5	100.0	23	8	AZ446113	AZ446113	IM0242B21
C 296	5	100.0	22	8	A2762378	A2762378	IM0557I22	C 369	5	100.0	23	8	AZ448352	AZ448352	IM0246A06
C 297	5	100.0	22	8	A2762424	A2762424	IM0557K08	370	5	100.0	23	8	AZ475927	AZ475927	IM0294B21
C 298	5	100.0	22	8	A2766712	A2766712	IM0564A03	371	5	100.0	23	8	AZ477223	AZ477223	IM0296F02
C 299	5	100.0	22	8	A2769521	A2769521	IM0570O18	C 372	5	100.0	23	8	AZ478826	AZ478826	IM0309F09
C 300	5	100.0	22	8	A2773608	A2773608	IM0001H10	C 373	5	100.0	23	8	AZ498180	AZ498180	IM0335A24
C 301	5	100.0	22	8	A2777352	A2777352	IM0011N11	374	5	100.0	23	8	AZ585259	AZ585259	IM0390Q14
C 302	5	100.0	22	8	A2778032	A2778032	IM0013A11	375	5	100.0	23	8	AZ586739	AZ586739	IM0390Q14
C 303	5	100.0	22	8	A2779122	A2779122	IM0015M03	376	5	100.0	23	8	AZ586739	AZ586739	IM0390Q14
C 304	5	100.0	22	8	A2785081	A2785081	IM0028I08	C 377	5	100.0	23	8	AZ588741	AZ588741	IM0397I16
C 305	5	100.0	22	8	A2792883	A2792883	IM0045J09	C 378	5	100.0	23	8	AZ592207	AZ592207	IM0402N20
C 306	5	100.0	22	8	A2802111	A2802111	IM0061G04	C 379	5	100.0	23	8	AZ595375	AZ595375	IM0407P19
C 307	5	100.0	22	8	A2805739	A2805739	IM0067K14	380	5	100.0	23	8	AZ595643	AZ595643	IM0408H23
C 308	5	100.0	22	8	A2807992	A2807992	IM0071C14	381	5	100.0	23	8	AZ599021	AZ599021	IM0414F08
C 309	5	100.0	22	8	A2819251	A2819251	IM0089G18	382	5	100.0	23	8	AZ602207	AZ602207	IM0420B23
C 310	5	100.0	22	8	A2828663	A2828663	IM0105I14	383	5	100.0	23	8	AZ602337	AZ602337	IM0421J03
C 311	5	100.0	22	8	A2837879	A2837879	IM0133A22	384	5	100.0	23	8	AZ613963	AZ613963	IM0442K06
C 312	5	100.0	22	8	A2854947	A2854947	IM0158I18	385	5	100.0	23	8	AZ623979	AZ623979	IM0462E14
C 313	5	100.0	22	8	A2863707	A2863707	IM0171N19	386	5	100.0	23	8	AZ626143	AZ626143	IM0466B15
C 314	5	100.0	22	8	A2868780	A2868780	IM0180E12	387	5	100.0	23	8	AZ628572	AZ628572	IM0480D16
C 315	5	100.0	22	8	A2937666	A2937666	IM0195L23	C 388	5	100.0	23	8	AZ635716	AZ635716	IM0493H18
C 316	5	100.0	22	8	A2953028	A2953028	IM0218O03	389	5	100.0	23	8	AZ654389	AZ654389	IM0258H06







```

TITLE
JOURNAL
COMMENT
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
Contact: Alkharouf, N.W.
Soybean Genomics and Improvement Laboratory (SGIL)
US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5720
Fax: 301 504 5728
Email: alkharouf@ars.usda.gov.

FEATURES
source
1. .12
/organism="Glycine max"
/mol_type="mRNA"
/cultivar="Peking"
/db_xref="taxon:3847"
/clones="D15H12"
/tissue_type="Roots"
/dev stage="Seedlings"
/clone_lib="cDNA Peking library 2, 4 day SCN3"
/note="Vector: pluescript SK; cDNA clones from mRNA
extracted from Peking roots 2 and 4 days post invasion."

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
|||||
Db 9 GGGTG 5

RESULT 5
AJ600145
LOCUS
DEFINITION
Arabidopsis thaliana T-DNA flanking sequence, right border, clone
501A06, genomic survey sequence.
12 bp DNA linear GSS 15-JAN-2004

ACCESSION
AJ600145
VERSION
AJ600145.1 GI:37949773
KEYWORDS
GSS; right border; T-DNA flanking sequence.
SOURCE
Arabidopsis thaliana
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE
1
AUTHORS
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL
EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE
22363535
PUBMED
12446565
REFERENCE
2 (bases 1 to 12)
AUTHORS
Balzerque,S.
TITLE
Direct Submission
JOURNAL
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (e) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap-versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers

FEATURES

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1. .12
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassiljewskija"
/db_xref="taxon:3702"
/clone="S01A06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1. .12
/note="T-DNA flanking sequence
right border"

ORIGIN
Query Match 100.0%; Score 5; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
|||||
Db 7 GGGTG 11

RESULT 6
AJ647906/c
LOCUS
DEFINITION
AJ647906 CSEQRAN19 Sus scrofa cDNA clone C0003263_A12, mRNA
13 bp mRNA linear EST 07-JUL-2004
sequence.
ACCESSION
AJ647906
VERSION
AJ647906.1 GI:49324751
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
1 (bases 1 to 13)
AUTHORS
Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE
Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
Unpublished (2004)
JOURNAL
Contact: Anderson SI
COMMENT
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBluescriptII(KS) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pooled ovaries. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.ark-genomics.org.

FEATURES
Location/Qualifiers
1. .13
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clones="C0003263_A12"
/tissue_type="ovary"
/clone_lib="CSEQRAN19"
/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing; Normalised library
constructed from pooled ovaries"

ORIGIN
Query Match 100.0%; Score 5; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
|||||
Db 11 GGGTG 7

RESULT 7
AJ65556/c

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LOCUS      AJ655566                      14 bp      mRNA      linear      EST 28-JUN-2004
DEFINITION AJ655566 KN277 Sus scrofa cDNA clone C0005190_p15, mRNA sequence.
ACCESSION  AJ655566
VERSION    AJ655566.1  GI:49339598
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE  1 (bases 1 to 14)
AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE     Development of cDNA and EST resources for studying reproduction and
          embryo development in pigs and cattle
JOURNAL   Unpublished (2004)
COMMENT   Contact: Anderson SI
          Genomics and Bioinformatics
          Roslin Institute
          Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
          Single pass sequencing. Bases called and trimmed with phred
          v0.020425.c. Vector identified by cross match with the -minscore 20
          and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcORI
          R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
          from pooled early embryos, from 8- cell stage to blastocysts,
          Clones available from UK Centre for Functional Genomics in Farm
          Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,
          www.arkgenomics.org.
FEATURES   source
            1..14
            /organism="Sus scrofa"
            /mol_type="mRNA"
            /db_xref="taxon:9823"
            /clone="C0005190_p15"
            /tissue type="embryo"
            /clone_lib="KN277"
            /note="Vector: pBlueScriptII(SK+); Site 1: EcORI; Site 2:
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            constructed from pooled early embryos, from 8-cell stage
            to blastocysts."
ORIGIN
    Query Match      100.0%; Score 5; DB 1; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
        |||||
Db      9 GGGTG 5

RESULT 8
BQ605961/c
LOCUS      BQ605961                      14 bp      mRNA      linear      EST 25-JUN-2002
DEFINITION BRX_1556 wheat EST endosperm library Triticum aestivum cDNA 5',
          mRNA sequence.
ACCESSION  BQ605961
VERSION    BQ605961.1  GI:21555112
KEYWORDS   EST.
SOURCE     Triticum aestivum (bread wheat)
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Triticum.
            1 (bases 1 to 14)
            Clarke,B., Lambrecht,M. and Rhee,S.Y.
            Arabidopsis genomic information for interpreting wheat EST
            sequences
            Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
JOURNAL   22478026
MEDLINE   12590341
PUBMED
COMMENT   Contact: Lambrecht M
          The Arabidopsis Information Resource
          Carnegie Institution of Washington, Dept. of Plant Biology
          260 Panama Street, Stanford, CA 94305, USA

```

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Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rhee@acoma.stanford.edu.
Location/Qualifiers
1..14
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wyuna"
/db_xref="taxon:4565"
/tissue type="endosperm"
/dev stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/clone_lib="wheat EST endosperm library"
FEATURES   source
            1..14
            /organism="Triticum aestivum"
            /mol_type="mRNA"
            /db_xref="taxon:4565"
            /tissue type="endosperm"
            /dev stage="developing endosperm tissue 8, 10 and 12 DPA
            (days post anthesis)"
            /clone_lib="wheat EST endosperm library"
ORIGIN
    Query Match      100.0%; Score 5; DB 5; Length 14;
    Best Local Similarity 100.0%; Pred. No. 1e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
        |||||
Db      8 GGGTG 4

RESULT 9
L76129
LOCUS      L76129                      15 bp      mRNA      linear      EST 21-FEB-1996
DEFINITION SCWRAP0223 G2/KS adult worm mini-library Schistosoma mansoni cDNA
          clone SMRAP0223, mRNA sequence.
ACCESSION  L76129
VERSION    L76129.1  GI:1196867
KEYWORDS   EST.
SOURCE     Schistosoma mansoni
ORGANISM   Schistosoma mansoni
            Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
            Strigoida; Schistosomatoidea; Schistosomatidae; Schistosoma.
            1 (bases 1 to 15)
            Neto,E.D., Harrop,R., Correa-Oliveira,R, Wilson,R.A., Pena,S.D. and
            Simpson,A.J.G.
            Minilibraries constructed from cDNA generated by arbitrarily primed
            RT-PCR: an alternative to normalized libraries for the generation
            of ESTs from nanogram quantities of mRNA
            Gene 186 (1), 135-142 (1997)
JOURNAL   9047356
MEDLINE   97199380
PUBMED
COMMENT   Contact: Neto,E.D., Harrop,R., Correa-Oliveira,R., Wilson,R.A.,
          Pena,S.D. and Simpson,A.J.
          Location/Qualifiers
          1..15
          /organism="Schistosoma mansoni"
          /mol_type="mRNA"
          /db_xref="taxon:6183"
          /clone_lib="G2/KS adult worm mini-library"
          /note="A mini-library was made by cloning products derived
          from RNA-arbitrarily primed PCR (RAP PCR) profiles into
          the pUC 18 vector. Reverse transcription of adult worm
          mRNA was primed with G2and subsequent PCR amplification
          was performed in the presence of primer KS"
ORIGIN
    Query Match      100.0%; Score 5; DB 7; Length 15;
    Best Local Similarity 100.0%; Pred. No. 1e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
        |||||
Db      3 GGGTG 7

RESULT 10
R41075
LOCUS      R41075                      15 bp      mRNA      linear      EST 16-MAY-1995

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DEFINITION Hk082-f Adult heart, Clontech Homo sapiens cDNA clone k082-f, mRNA
sequence.
ACCESSION R41075
VERSION R41075.1 GI:798691
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 15)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Waye,M.M.Y., Chung,H.K.Y., Lam,W.Y., Law,P.T.W., Lo,A.S.Y.,
Lui,V.W.Y., Luk,S.C.W., Tsui,S.K.W., Tung,C.K.C., Yam,N.Y.H.,
Liew,C.C. and Lee,C.Y.
TITLE Gene expression of adult human heart as revealed by random
sequencing of cDNA library
JOURNAL Miami Winter Biotechnol. Symp. Proc. 6, 90 (1995)
COMMENT Contact: Wayne Mary M.Y.
Department of Biochemistry
The Chinese University of Hong Kong
Rm 302C, Basic Medical Science Building, The Chinese University of
Hong Kong, Shatin, N.T., Hong Kong.
Tel: 8526096874
Fax: 8526035123
Email: b133723@vax.csc.cuhk.hk
Seq primer: GGTGGCGACGACTCTCTGGAGCC.
FEATURES             source
1..15
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="k082-f"
/lab_host="E. coli Y1090"
/clone_lib="Adult heart, Clontech"
/notes="Vector: Lambda gt11; Site_1: EcoRI; Site_2: EcoRI"
ORIGIN
Query Match      100.0%; Score 5; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 1 GGGTG 5

RESULT 11
AA937364
LOCUS oJ08f10.81 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595 3'
DEFINITION similar to SW:ACRO.FABIT P48038 ACROSIN PRECURSOR ;contains MSR1.b2
MSR1 repetitive element ;, mRNA sequence.
ACCESSION AA937364
VERSION AA937364.1 GI:3095475
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
unknown library type
Trace considered overall poor quality
Insert Length: 1265 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"

AA937364
LOCUS oJ08f10.81 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595 3'
DEFINITION similar to SW:ACRO.FABIT P48038 ACROSIN PRECURSOR ;contains MSR1.b2
MSR1 repetitive element ;, mRNA sequence.
ACCESSION AA937364
VERSION AA937364.1 GI:3095475
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
unknown library type
Trace considered overall poor quality
Insert Length: 1265 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"

```

```

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1491595"
/tissue_type="metastatic melanoma to bowel"
/lab_host="DH10B"
/clone_lib="NCI CGAP Mel3"
/notes="Organ: bowel (skin primary); Vector: pCMV-SPORT4;
Site 1: SalI; Site 2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 0.9 kb. Life
Technologies catalog #: 10981-017"
ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 6 GGGTG 10

RESULT 12
AI248882/c
LOCUS qu73e07.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1977732 3'
DEFINITION similar to SW:CA13_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN. ;,
mRNA sequence.
ACCESSION AI248882
VERSION AI248882.1 GI:3844279
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute / National Institute of Neurological
Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTCAP), Tumor Gene Index
Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
unknown library type
Trace considered overall poor quality
Insert Length: 1913 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1977732"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn35"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life Technologies
catalog #: 11544-012"
ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 10 GGGTG 6

```

```

RESULT 13
AI569544/c
LOCUS
DEFINITION
AI569544      16 bp      mRNA      linear      EST 12-MAY-1999
tx28d10.x1 NCI CGAP Ut-4 Homo sapiens cDNA clone IMAGE:2180371 3'
similar to TR:Q18447 Q18444 COSMID C34D4. ;contains MSRI.b2 MSRI
repetitive element ;, mRNA sequence.
AI569544
AI569544.1 GI:4532918
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 16)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@e-mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert length: 1683 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 1
POLYA=No.

FEATURES             Location/Qualifiers
     ..16
     /organism="Homo sapiens"
     /mol_type="mRNA"
     /db_xref="taxon:9606"
     /clone="IMAGE:2180371"
     /tissue_type="serous papillary carcinoma, high grade, 2
     pooled tumors"
     /lab_host="DH10B"
     /clone_lib="NCI CGAP Ut-4"
     /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
     Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
     Average insert size 1.48 Kb. Life Technologies catalog #:
     11542-016"

ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 16 GGGTG 12

RESULT 14
AI684114/c
LOCUS
DEFINITION
AI684114      16 bp      mRNA      linear      EST 16-DEC-1999
tx79402.x1 NCI CGAP Ut-1 Homo sapiens cDNA clone IMAGE:2275779 3'
similar to TR:Q09084 Q09084 EXTENSIN CLASS II PRECURSOR ;, mRNA
sequence.
AI684114
AI684114.1 GI:4895408
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 16)

```

Possible reversed clone: similarity on wrong strand

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

#### FEATURES

source  
Location/Qualifiers  
1. .16  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2335755"  
/sex="male"  
/dev\_stages="adult, age 25"  
/lab\_host="DH10B (phage resistant)"  
/clone\_lib="Barstead colon HPLRB7"  
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACGAATCTGAAGTGGAGCGGCCCTTTTTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors [5' AATTCAGTAAAT 3' and 5' ATTACTAGT 3'], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed by Bob Barstead."

#### ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5

Db 13 GGGTG 9

#### RESULT 16

LOCUS

DEFINITION A1741762 16 bp mRNA linear EST 19-DEC-1999  
IMAGE:2365859 3', similar to TR:004154 004154 SALIVARY PROLINE-RICH  
PROTEIN RP15 PRECURSOR.; contains PTF5.b3 MSRI MSRI repetitive  
element.; mRNA sequence.

ACCESSION A1741762

VERSION A1741762.1 GI:5110050

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 16)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (infoimage.lnl.gov) for further information.

Trace considered overall poor quality

Insert Length: 630 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

1. .16

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:2365859"

/lab\_host="DH10B"

/clone\_lib="Soares NSF P8 9W OT PA P S1"  
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI;

Equal amounts of plasmid DNA from five normalized

libraries were mixed, and ss circles were made in vitro.

Following HAP purification, this DNA was used as tracer in

a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and clones: Soares NBHSP pool 1:

30384-310919, 323208-325895 Soares Nb2HP pool 1:

145032-147335, 147720-148103, 148872-149255, 15002 -

150407, 151176-152327 Soares Nb2HF8-9W pool 1:

758280-760583, 772104-774407 Soares NBHPA pool 1:

304776-306311, 320136-322823, 326280-326663 Soares NBHOT

pool 1: 723720-726407, 739080-740999 Subtraction by Bento

Soares and M. Fatima Bonaldo."

#### ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;

Best Local Similarity 100.0%; Pred. No. 1e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5

Db 5 GGGTG 1

#### RESULT 17

CNS08PR1/c

LOCUS

DEFINITION Single read from an extremity of a full-length cDNA clone made from  
Anopheles gambiae total adult females. 3-PRIME end of clone  
FK0AAA34DD10 of strain 6-9 of Anopheles gambiae (African malaria  
mosquito).

ACCESSION BX022793

VERSION BX022793.1 GI:27572013

KEYWORDS HTC.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM

Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoides;

REFERENCE 1 (bases 1 to 16)

Genoscope.

Direct Submission

Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Location/Qualifiers

1. .16

/organism="Anopheles gambiae"

/mol\_type="mRNA"

/strain="6-9"

/db\_xref="taxon:7165"

/clone="FK0AAA34DD10"

/plasmid="pME18S-FL"

/note="end : 3-PRIME"

#### ORIGIN

Query Match 100.0%; Score 5; DB 3; Length 16;

Best Local Similarity 100.0%; Pred. No. 1e+07;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5

Db 5 GGGTG 1

#### RESULT 18

LOCUS

DEFINITION BM399085 16 bp mRNA linear EST 17-JAN-2002  
5009-0-52-G11.t.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION BM399085

VERSION BM399085.1 GI:18199138

KEYWORDS EST.

SOURCE Tetrahymena thermophila

ORGANISM Tetrahymena thermophila

```

Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymena; Tetrahymena.
1 (bases 1 to 16)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
JOURNAL
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
    source
        1..16
            /organism="Tetrahymena thermophila"
            /mol_type="mRNA"
            /strain="CU428.1"
            /db_xref="taxon:5911"
            /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
            /note="Vector: Bluescript2 SK+; Details on library
            preparation can be found in Chilcoat and Turkewitz (2001)
            Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 11 GGGTG 15

RESULT 19
LOCUS CF317464
DEFINITION HD--07-C19.b1 OshDAC1-overexpressing transgenic rice plasmid cDNA
library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
HD--07-C19, mRNA sequence.
ACCESSION CF317464.1 GI:33689225
VERSION EST.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 16)
Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
JOURNAL
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Kyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES
    source
        1..16
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="HD--07-C19"
            /tissue_type="callus"
            /dev_stage="proliferated callus on 2N6 media for 2 weeks"
            /lab_host="E.coli DH10B"
            /clone_lib="OshDAC1-overexpressing transgenic rice plasmid

```

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cDNA library (HD)"
/note="vector: pCR4-TOPO; Site_1: EcoRI; Callus was
treated with ABA(20um) for 1hr. Oligo-capped mRNA was
reverse transcribed and then used for PCR. mRNA was
derived from rice Histone Deacetylase overexpression
line."
ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 15 GGGTG 11

RESULT 20
LOCUS AJ596548
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
435H06, genomic survey sequence.
ACCESSION AJ596548.1 GI:37946176
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
JOURNAL
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 16)
AUTHORS Balzerque,S.
TITLE Direct Submision
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
    source
        1..16
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /cultivar="Wassiliewskaja"
            /db_xref="taxon:3702"
            /clone="435H06"
            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
        1..16
            /note="T-DNA flanking sequence
            left border"
ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5

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Db      10 GGGTG 14
|||||
RESULT 21
AJ666397/c
LOCUS   17 bp  mRNA  linear  EST 28-JUN-2004
DEFINITION  AJ666397 CSEQRAN09 Sus scrofa cDNA clone C000033_K10, mRNA
sequence.
ACCESSION  AJ666397
VERSION    AJ666397.1 GI:49350848
KEYWORDS   EST.
SOURCE     Sus scrofa (pig)
ORGANISM   Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE     Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL   Unpublished (2004)
COMMENT   Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the _minscore 20
and -minmatch 12 options. Vector:pBluescriptII(KS+). R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK EH25 9PS, www.arkgenomics.org.
FEATURES             source
    source
        1..17
            /organism="Sus scrofa"
            /mol_type="mRNA"
            /db_xref="taxon:9823"
            /clone="C000033_K10"
            /tissue_type="placenta"
            /clone_lib="CSEQRAN09"
            /note="Vector: pBluescriptII(KS+); Site.1: EcoRI; Site.2:
            NotI; Single pass sequencing. Normalised library
            constructed from pooled tissue from day 30 placentas."

ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 GGGTG 5
    |||||
Db   7 GGGTG 3

RESULT 22
BQ589968/c
LOCUS   17 bp  mRNA  linear  EST 06-DEC-2002
DEFINITION  BQ589968 S013719-024-019-B24-T7 MP1Z-ADIS-024-storage root Beta vulgaris
cDNA clone 024-019-B24 3-PRIME, mRNA sequence.
ACCESSION  BQ589968
VERSION    BQ589968.1 GI:26119551
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE  1 (bases 1 to 17)
AUTHORS   Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes

JOURNAL MEDLINE
PUBMED 12472698
COMMENT  Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 19 row: B column: 24
Seq primer: T7; GTAATAGACTCACTATAGGCG.
Location/Qualifiers
    1..17
        /organism="Beta vulgaris"
        /mol_type="mRNA"
        /cultivar="KWS2320 (double haploid, monogerm breeding
        line)"
        /db_xref="taxon:161934"
        /clone="024-019-B24"
        /tissue_type="storage root"
        /lab_host="EMDH10B"
        /clone_lib="MP1Z-ADIS-024-storage root"
        /note="Vector: pCMVSPORT6; Site.1: SalI; Site.2: NotI;
        cDNA library from sugar beet, library provided by KWS
        Kleinwanzlebener Saat-zucht AG Einbeck, Germany, contact:
        b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
        orientation:
        SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
        Sequencing granted in the context of the GABI-Beet
        project, local PI: Dr. Katharina Schneider, coordinator:
        Prof. Christian Jung; Sequence submission managed by
        RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match      100.0%; Score 5; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 GGGTG 5
    |||||
Db   7 GGGTG 3

RESULT 23
AJ594891/c
LOCUS   17 bp  DNA  linear  GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
407D12, genomic survey sequence.
ACCESSION  AJ594891
VERSION    AJ594891.1 GI:37944515
KEYWORDS   GSS; left border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE  1
AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE  22363535
PUBMED  12446565
REFERENCE  2 (bases 1 to 17)
AUTHORS   Balzergue,S.
TITLE     Direct Submission
JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremeux, 91057 Evry cedex, FRANCE
COMMENT   PCR was performed on DNA from transformants of Arabidopsis thaliana

```



plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr/>).

FEATURES  
source  
1. .17  
/organism="Arabidopsis thaliana"  
/mol\_type="genomic DNA"  
/cultivar="wasillewskija"  
/db\_xref="taxon:3702"  
/clone="407D12"  
/clone\_lib="Arabidopsis thaliana T-DNA insertion lines"  
misc\_feature  
1. .17  
/note="T-DNA flanking sequence  
left border"

## ORIGIN

Query Match 100.0%; Score 5; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 14 GGGTG 10

RESULT 24  
BM395046  
LOCUS  
DEFINITION  
50072-2-7-C05.f.2 Chilcoat/Turkewitz cDNA (large fraction)  
Tetrahymena thermophila cDNA, mRNA sequence.

ACCESSION  
BM395046  
VERSION  
BM395046.1 GI:18195099  
KEYWORDS  
EST.  
SOURCE  
Tetrahymena thermophila  
ORGANISM  
Tetrahymena thermophila  
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;  
Hymenostomatida; Tetrahymenina; Tetrahymena.  
REFERENCE  
1 (bases 1 to 18)  
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,  
Frankel, J. and Klobutcher, L.  
EST from Tetrahymena thermophila, strain CU428.1, growing cells  
Unpublished (2002)  
TITLE  
Contact: Turkewitz AP  
Molecular Genetics and Cell Biology  
University of Chicago  
920 E. 58th Street, Chicago, IL 60637, USA  
Tel: 773 702 4374  
Fax: 773 702 3172  
Email: apturkew@midway.uchicago.edu  
Seq primer: T3.  
Location/Qualifiers

FEATURES  
source  
1. .18  
/organism="Tetrahymena thermophila"  
/mol\_type="mRNA"  
/strain="CU428.1"  
/db\_xref="taxon:5911"  
/clone\_lib="Chilcoat/Turkewitz cDNA (large fraction)"  
/note="Vector: Bluescript2 SK+; Details on library  
preparation can be found in Chilcoat and Turkewitz (2001)  
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

## ORIGIN

Query Match 100.0%; Score 5; DB 4; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 9 GGGTG 13

RESULT 25  
BO594466

LOCUS  
DEFINITION  
E012442-024-024-I18-SP6 MP12-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-024-I18 5-PRIME, mRNA sequence.

ACCESSION  
BO594466  
VERSION  
BO594466.1 GI:26124049  
KEYWORDS  
EST.  
SOURCE  
Beta vulgaris  
ORGANISM  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

REFERENCE  
1 (bases 1 to 18)  
Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,  
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.  
and Radelof, U.

## TITLE

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

## JOURNAL

MEDLINE  
22362189  
PUBMED  
12472698

## COMMENT

Contact: Weisshaar B  
ADIS DNA core facility at MP12  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 18 Std Error: 0.00  
Plate: 24 row: 1 column: 18  
Seq primer: SP6; CATACGATTAGTGACACTATAG.  
Location/Qualifiers

FEATURES  
source  
1. .18  
/organism="Beta vulgaris"  
/mol\_type="mRNA"  
/cultivar="KWS2320 (double haploid, monogerm breeding  
line)"  
/db\_xref="GABI:192392"  
/db\_xref="taxon:161934"  
/clone="024-024-I18"  
/tissue\_type="developing root"  
/lab\_host="EMDH108"  
/clone\_lib="MP12-ADIS-024-developing root"  
/note="Vector: pCWSFOR6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: <http://gabi.rzpd.de>"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 10 GGGTG 14

RESULT 26  
CA850820

LOCUS  
DEFINITION  
D06H05\_H05\_15.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max

CA850820 18 bp mRNA linear EST 01-AUG-2003

```

cDNA clone D06H05 5', mRNA sequence.
ACCESSION CA850820
VERSION CA850820.1 GI:33387613
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 18)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
JOURNAL Soybean Genomics and Improvement Laboratory (SGIL)
COMMENT US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="Glycine max"
                /mol_type="mRNA"
                /cultivar="Peking"
                /db_xref="taxon:3847"
                /clone="D06H05"
                /tissue_type="Roots"
                /dev_stage="Seedlings"
                /clone_lib="cDNA Peking library 2, 4 day SCN3"
                /notes="Vector: pBluescript SK-; cDNA clones from mRNA
                extracted from Peking roots 2 and 4 days post invasion."

ORIGIN
    Query Match 100.0%; Score 5; DB 6; Length 18;
    Best Local Similarity 100.0%; Pred. No. 1e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 7 GGGTG 11

RESULT 27
CA853355/c
LOCUS B07C12.seq cDNA Peking library 12hr SCN3 Glycine max cDNA clone
DEFINITION B07C12.5', mRNA sequence.
ACCESSION CA853355
VERSION CA853355.1 GI:33390148
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 18)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
JOURNAL Soybean Genomics and Improvement Laboratory (SGIL)
COMMENT US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

cDNA clone D06H05 5', mRNA sequence.
ACCESSION CA850820
VERSION CA850820.1 GI:33387613
KEYWORDS EST.
SOURCE Glycine max (soybean)
ORGANISM Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 18)
Alkharouf, N.W., Khan, R. and Matthews, B.F.
Analysis of expressed sequence tags from roots of resistant soybean
infected by the soybean cyst nematode
Unpublished (2002)
JOURNAL Soybean Genomics and Improvement Laboratory (SGIL)
COMMENT US Department of Agriculture (USDA), ARS, PSI
Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
USA
Tel: 301 504 5750
Fax: 301 504 5728
Email: alkharon@ba.ars.usda.gov.

FEATURES
    source
        Location/Qualifiers
            1..18
                /organism="Glycine max"
                /mol_type="mRNA"
                /cultivar="Peking"
                /db_xref="taxon:3847"
                /clone="D06H05"
                /tissue_type="Roots"
                /dev_stage="Seedlings"
                /clone_lib="cDNA Peking library 12hr SCN3"
                /notes="Vector: pBluescript SK-; cDNA clones from mRNA
                extracted from roots of soybean cv. Peking 12 hrs after
                infection by SCN race 3. These are cloned in pBluescript
                SK- phagemid."

ORIGIN
    Query Match 100.0%; Score 5; DB 6; Length 18;
    Best Local Similarity 100.0%; Pred. No. 1e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 12 GGGTG 8

RESULT 28
AA878747/c
LOCUS AA878747
DEFINITION AA878747.19 bp mRNA linear EST 25-MAR-1998
OF85501.61 NCI CGAP L15 Homo sapiens cDNA clone IMAGE:1437097 3'
similar to TR:Q26739 Q26739 CYTOCHROME C OXIDASE III ;contains
element MSRI repetitive element i, mRNA sequence.
ACCESSION AA878747
VERSION AA878747.1 GI:2987712
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
unknown library type
Trace considered overall poor quality
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.

FEATURES
    source
        Location/Qualifiers
            1..19
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:1437097"
                /tissue_type="hepatic adenoma"
                /lab_host="DH10B"
                /clone_lib="NCI CGAP L15"
                /notes="Organ: liver; Vector: pCMV-SPORT4; Site_1: SalI;
                Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 0.8 kb."

ORIGIN
    Query Match 100.0%; Score 5; DB 1; Length 19;
    Best Local Similarity 100.0%; Pred. No. 1e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 9 GGGTG 5

RESULT 29

```



/lab host="DH10B (ampicillin resistant)"  
 /clone lib="Soares sequester fibroblasts NbHSF"  
 /note="Vector: pT7T3D (Pharmacia) with a modified  
 polylinker V TYPE: phagemid; Site 1: Not I; Site 2: Eco  
 RI; 1st strand cDNA was primed with a Not I - oligo(dT)  
 primer [5'  
 TGTACCAATCTGAGTGGGAGCGCGCATTTTTTTTTTTTTTTT 3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
 |||||  
 Db 9 GGGTG 13

## RESULT 32

A1187072/c

## LOCUS

## DEFINITION

q38a01.s1 Soares fetal\_lung NbHL19W Homo sapiens cDNA clone  
 IMAGE:1741224 3' similar to TR:Q07912 Q07912 TYROSINE-PROTEIN  
 KINASE ACK ; contains TARI.t1 MSRI repetitive element ;, mRNA  
 sequence.

## ACCESSION

A1187072

## VERSION

EST.

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 19)

## AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Trace considered overall poor quality  
 Insert Length: 2024 Std Error: 0.00  
 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 1.  
 Location/Qualifiers

## FEATURES

source

1..19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1741224"

/dev\_stage="19 weeks"

/lab host="DH10B (ampicillin resistant)"

/clone lib="Soares fetal lung NbHL19W"

/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer  
 [5'-TGTACCAATCTGAGTGGGAGCGCGCATTTTTTTTTTTTTTTT-3']  
 double-stranded cDNA was size selected, ligated to Eco RI  
 adapters (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of a modified pT7T3 vector  
 (Pharmacia). Library went through one round of  
 normalization to a Cot = 5. Library constructed by Bento  
 Soares and M.Fatima Bonaldo. This library was constructed  
 from the same fetus as the fetal heart library, Soares  
 fetal heart NbHL19W."

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
 |||||  
 Db 15 GGGTG 11

## RESULT 33

A1364573/c

## LOCUS

## DEFINITION

qw37903.x1 NCI CGAP Ut-4 Homo sapiens cDNA clone IMAGE:1993300 3'  
 similar to TR:Q39835 Q39835 EXTENSIN., mRNA sequence.

## ACCESSION

A1364573

## VERSION

EST.

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 19)

## AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

## TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index

## JOURNAL

Unpublished (1997)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1632 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

Location/Qualifiers

## FEATURES

source

1..19

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:1993300"

/tissue\_type="serous papillary carcinoma, high grade, 2  
 pooled tumors"

/lab host="DH10B"

/clone lib="NCI CGAP Ut-4"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.48 kb. Life Technologies catalog #:  
 11542-016"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
 |||||  
 Db 10 GGGTG 6

## RESULT 34

A1431460/c

## LOCUS

## DEFINITION

th40c01.x1 NCI CGAP Lym12 Homo sapiens cDNA clone IMAGE:2120736 3'  
 similar to TR:Q04117 Q04117 SALIVARY PROLINE-RICH PROTEIN RP4  
 PRECURSOR.; contains element MSRI repetitive element ;, mRNA

19 bp mRNA linear EST 13-APR-1999

```

sequence.
ACCESSION AI431460
VERSION AI431460.1 GI:4303341
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 653 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2120736"
/tissue_type="lymphoma, follicular mixed small and large
cell"
/lab host="DH10B"
/clone_lib="NCI CGAP Lym12"
/notes="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
SalI; Site_2: NotI; Cloned unidirectionally. Primer:
Oligo dt. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"

ORIGIN
Query Match 100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. le+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
|||||
Db 16 GGGTG 12

RESULT 35
AI584018/c
LOCUS AI584018 19 bp mRNA linear EST 14-DEC-1999
DEFINITION ts12el0.x1 NCI CGAP Panl Homo sapiens cDNA clone IMAGE:228394 3'
similar to SW:RPRL_HUMAN P10162 SALIVARY PROLINE-RICH PROTEIN PO ;,
mRNA sequence.
ACCESSION AI584018
VERSION AI584018.1 GI:4569915
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Life Technologies catalog #: 11548-013
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1803 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2278260"
/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"

FEATURES
source

```

```

found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1996 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1
POLYA=No.
Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2228394"
/tissue_type="adenocarcinoma"
/lab host="DH10B"
/clone_lib="NCI CGAP Panl"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"

ORIGIN
Query Match 100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. le+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
|||||
Db 9 GGGTG 5

RESULT 36
AI758301/c
LOCUS AI758301 19 bp mRNA linear EST 16-DEC-1999
DEFINITION cy06a07.x1 NCI CGAP Ut3 Homo sapiens cDNA clone IMAGE:2278260 3'
similar to SW:S949_HUMAN Q15427 SPLICEOSOME ASSOCIATED PROTEIN 49
;contains MSRI.b2 MSRI repetitive element ;, mRNA sequence.
ACCESSION AI758301
VERSION AI758301.1 GI:5152024
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmer-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1803 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1. .19
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2278260"
/tissue_type="poorly-differentiated endometrial
adenocarcinoma, 2 pooled tumors"

FEATURES
source

```

```

/lab host="DH10B"
/clone lib="NCI CGAP Ut3"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"

ORIGIN

Query Match      100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 6 GGGTG 2

RESULT 37
AI804310
LOCUS
DEFINITION
tc69g08.x1 Soares NHMPu S1 Homo sapiens cDNA clone IMAGE:2069918
3', similar to SW-AC3_HUMAN Q08043 ALPHA-ACTININ 3, SKELETAL MUSCLE
ISOFORM ; contains element PTR5 repetitive element ;, mRNA sequence.
ACCESSION
AI804310
VERSION
AI804310.1 GI:5369782
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 786 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
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    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:2069918"
    /tissue type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab host="DH10B"
/clone lib="Soares NHMPu S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBW, pregnant uterus
NBHPU, and fetal heart NBHL19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 48488-489479."

ORIGIN

Query Match      100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 1 GGGTG 5

/lab host="DH10B"
/clone lib="NCI CGAP Ut3"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"

ORIGIN

Query Match      100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 6 GGGTG 2

RESULT 37
AI804310
LOCUS
DEFINITION
tc69g08.x1 Soares NHMPu S1 Homo sapiens cDNA clone IMAGE:2069918
3', similar to SW-AC3_HUMAN Q08043 ALPHA-ACTININ 3, SKELETAL MUSCLE
ISOFORM ; contains element PTR5 repetitive element ;, mRNA sequence.
ACCESSION
AI804310
VERSION
AI804310.1 GI:5369782
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 786 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
    source
    1..19
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:2069918"
    /tissue type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab host="DH10B"
/clone lib="Soares NHMPu S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBW, pregnant uterus
NBHPU, and fetal heart NBHL19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 48488-489479."

ORIGIN

Query Match      100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 1 GGGTG 5

/lab host="DH10B"
/clone lib="NCI CGAP Ut3"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.45 kb. Life Technologies catalog #:
11541-018"

ORIGIN

Query Match      100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 6 GGGTG 2

RESULT 37
AI804310
LOCUS
DEFINITION
tc69g08.x1 Soares NHMPu S1 Homo sapiens cDNA clone IMAGE:2069918
3', similar to SW-AC3_HUMAN Q08043 ALPHA-ACTININ 3, SKELETAL MUSCLE
ISOFORM ; contains element PTR5 repetitive element ;, mRNA sequence.
ACCESSION
AI804310
VERSION
AI804310.1 GI:5369782
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 724 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
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    1..19
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:2359240"
    /lab host="DH10B"
    /clone lib="Soares NFL T GBC S1"
    /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W testis NHT, and B-cell
NCI-CGAP-CCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
```

```

RESULT 38
AI807936/c
LOCUS
DEFINITION
wf52e09.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
IMAGE:2359240 3' similar to TR:Q39600 Q39600 EXTENSIN. ; contains
element MSR1 repetitive element ;, mRNA sequence.
ACCESSION
AI807936
VERSION
AI807936.1 GI:5394502
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 724 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
FEATURES
    source
    1..19
    /organism="Homo sapiens"
    /mol_type="mRNA"
    /db_xref="taxon:9606"
    /clone="IMAGE:2359240"
    /lab host="DH10B"
    /clone lib="Soares NFL T GBC S1"
    /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W testis NHT, and B-cell
NCI-CGAP-CCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "
```

```

ORIGIN

Query Match      100.0%; Score 5; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 16 GGGTG 12

RESULT 39
AJ660078/c
LOCUS
DEFINITION
AJ660078 KN277 Sus scrofa cDNA clone C005218_I04, mRNA sequence.
ACCESSION
AJ660078
VERSION
AJ660078.1 GI:49344223
KEYWORDS
EST.
SOURCE
Sus scrofa (pig)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 19)
Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
Development of cDNA and EST resources for studying reproduction and
```

embryo development in pigs and cattle  
 Unpublished (2004)  
 Contact: Anderson SI  
 Genomics and Bioinformatics  
 Roslin Institute  
 Roslin, Midlothian, EH25 9PS, UNITED KINGDOM  
 Single pass sequencing. Bases called and trimmed with phred  
 v0.020425.c. Vector identified by cross\_match with the -minscore 20  
 and -mismatch 12 options. Vector: pBlueScriptII(SK+) R. Site1: EcoRI  
 R. Site2: NotI 5' Seq Primer M13F Normalised library constructed  
 from pooled early embryos, from 8- cell stage to blastocysts.  
 Clones available from UK Centre for Functional Genomics in Farm  
 Animals, Roslin Institute, Roslin, Midlothian, UK, EH25 9PS,  
 www.arkgenomics.org.

**FEATURES**  
 Location/Qualifiers  
 1..19  
 /organism="Sus scrofa"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9823"  
 /clone="C005218.104"  
 /tissue\_type="embryo"  
 /clone\_lib="KN277"  
 /note="Vector: pBlueScriptII(SK+); Site 1: EcoRI; Site 2:  
 NotI: Single pass sequencing. Normalised library  
 constructed from pooled early embryos, from 8-cell stage  
 to blastocysts."

**ORIGIN**  
 Query Match 100.0%; Score 5; DB 1; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 |||||  
 Db 12 GGGTG 8

**RESULT 40**  
 BG925619/c  
 LOCUS  
 DEFINITION HNC5-1-E5.R HNC (Human Normal Cartilage) Homo sapiens CDNA, mRNA  
 sequence.  
 ACCESSION BG925619.1 GI:14320142  
 VERSION  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 19)  
 Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J.,  
 Sathe, G., Mui, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and  
 Lark, M.W.  
 Identification and initial characterization of 5000 expressed  
 sequenced tags (ESTs) each from adult human normal and  
 osteoarthritic cartilage cDNA libraries  
 Osteoarthr. Cartil. 9 (7), 641-653 (2001)  
 21482651  
 11597177  
 Contact: Sanjay Kumar  
 UW2109  
 GlaxoSmithKline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay\_kumar-l@gsk.com  
 Seq primer: 77.

**FEATURES**  
 Location/Qualifiers  
 1..19  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /tissue\_type="cartilage"

**JOURNAL**  
 COMMENT

**ORIGIN**  
 Query Match 100.0%; Score 5; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 |||||  
 Db 14 GGGTG 10

**RESULT 41**  
 CF298891  
 LOCUS  
 DEFINITION 7LEAF--02-J10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--02-J10, mRNA  
 sequence.  
 ACCESSION CF298891.1 GI:33670652  
 VERSION  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 19)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhah@gbio.com, bnhah@bio.myongji.ac.kr.

**FEATURES**  
 Location/Qualifiers  
 1..19  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="7LEAF--02-J10"  
 /tissue\_type="leaf"  
 /dev\_stages="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

**ORIGIN**  
 Query Match 100.0%; Score 5; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 |||||  
 Db 8 GGGTG 12

**RESULT 42**  
 CF334260/c  
 LOCUS  
 DEFINITION JMT--03-H18.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
 JMT--03-H18, mRNA sequence.  
 CF334260

/lab\_host="E.coli DH10 B"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI;  
 Directional"

**ORIGIN**  
 Query Match 100.0%; Score 5; DB 4; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 |||||  
 Db 14 GGGTG 10

**RESULT 41**  
 CF298891  
 LOCUS  
 DEFINITION 7LEAF--02-J10.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza  
 sativa (japonica cultivar-group) cDNA clone 7LEAF--02-J10, mRNA  
 sequence.  
 ACCESSION CF298891.1 GI:33670652  
 VERSION  
 KEYWORDS EST.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 19)  
 Kim, J.S., Jun, K.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C.,  
 Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
 Large-scale Sequencing Analysis of Rice ESTs  
 Unpublished (2003)  
 Contact: Nahm B.H.  
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division  
 of Bioscience and Bioinformatics, Myongji University  
 Yongin, Gyeonggi, Korea  
 Tel: 82 31 330 6193  
 Fax: 82 31 321 6355  
 Email: bnhah@gbio.com, bnhah@bio.myongji.ac.kr.

**FEATURES**  
 Location/Qualifiers  
 1..19  
 /organism="Oryza sativa (japonica cultivar-group)"  
 /mol\_type="mRNA"  
 /cultivar="Nackdong"  
 /db\_xref="taxon:39947"  
 /clone="7LEAF--02-J10"  
 /tissue\_type="leaf"  
 /dev\_stages="7 days after germination"  
 /lab\_host="E.coli DH10B"  
 /clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped  
 with oligoribonucleotides and then used as templates for  
 RT-PCR."

**ORIGIN**  
 Query Match 100.0%; Score 5; DB 6; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGTG 5  
 |||||  
 Db 8 GGGTG 12

**RESULT 42**  
 CF334260/c  
 LOCUS  
 DEFINITION JMT--03-H18.g1 AtJMT-overexpressing transgenic rice plasmid cDNA  
 library (JMT) Oryza sativa (japonica cultivar-group) cDNA clone  
 JMT--03-H18, mRNA sequence.  
 CF334260

```

VERSION CF334260.1 GI:33816853
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)

REFERENCE 1 (bases 1 to 19)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
    source
        1..19
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nackdong"
            /db_xref="taxon:39947"
            /clone="JMT-03-H18"
            /tissue_type="leaf"
            /dev_stages="14 days after germination"
            /lab_host="E.coli DH10B"
            /clone_lib="AJMT-overexpressing transgenic rice plasmid
            /note="Vector: PCR4-TOPO; Site 1: EcoRI; Oligo-capped mRNA
            was reverse transcribed and then used for PCR. mRNA was
            prepared from Arabidopsis Jasmonate Carboxyl
            methyltransferase overexpression line."

ORIGIN
    Query Match 100.0%; Score 5; DB 6; Length 19;
    Best Local Similarity 100.0%; Pred. No. 1e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 17 GGGTG 13

RESULT 43
CF542982
LOCUS S014680w-024-030-P12-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA
DEFINITION Clone 024-030-P12 5-PRIME, mRNA sequence.
ACCESSION CF542982
VERSION CF542982.1 GI:34891422
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris

REFERENCE 1 (bases 1 to 19)
AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 2362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

Email: weishaar@piz-koeln.mpg.de
Insert Length: 19 Std Error: 0.00
Plate: 30 row: P column: 12
Seq primer: SP6.

FEATURES
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            /organism="Beta vulgaris"
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            /cultivar="KWS2320 (double haploid, monogerm breeding
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            /db_xref="GABI:936786"
            /db_xref="taxon:161934"
            /clone="024-030-P12"
            /tissue_type="leaf"
            /lab_host="EMDH10B"
            /clone_lib="MP1Z-ADIS-024-leaf"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatgut AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-SALI-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
    Query Match 100.0%; Score 5; DB 7; Length 19;
    Best Local Similarity 100.0%; Pred. No. 1e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
    |||||
Db 11 GGGTG 15

RESULT 44
CO792214/c
LOCUS NT014C A10 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'
DEFINITION similar to hypothetical protein, mRNA sequence.
ACCESSION CO792214
VERSION CO792214.1 GI:51008185
KEYWORDS EST.
SOURCE Ambystoma mexicanum (axolotl)
ORGANISM Ambystoma mexicanum

REFERENCE 1 (bases 1 to 19)
AUTHORS Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
Penke,K., Epperlein,H.H., Schacker,H.K., Wiebe,G. and Tanaka,E.M.
TITLE An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
expressed sequence tags from embryonic and regenerating blastema
cDNA libraries
JOURNAL Genome Biol. (2004) In press
COMMENT Contact: Elly M. Tanaka
Tanaka Lab
Max Planck Institute of Molecular Cell Biology and Genetics,
Dresden
Pfeifenhauserstrasse 108, 01307 Dresden, Germany
Tel: 0049 351 210 2620
Fax: 0049 351 210 1489
Email: tanaka@mpi-cbg.de
Plate: NT014C row: 10 column: A
Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.

FEATURES
    source
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            /organism="Ambystoma mexicanum"
            /mol_type="mRNA"
            /db_xref="taxon:8296"
            /tissue_type="Neural Tube, Notochord, Somites"

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/cell\_type="Includes Neural tube, notochord, somites"  
/dev\_stage="Stage 18-22"  
/clone\_lib="St18-22 Neural tube (NT)"  
/notes="Vector: pCMVSPORT6; Site 1: NotI; Site 2: SalI;  
Unnormalized cDNA plasmid library prepared by Invitrogen.  
Size fractionated mRNA was polydT primed and cloned into  
NotI-SalI site of pCMVSPORT6. Bacterial host is  
ENDH10B-TONA. Average insert size is 1.5 kb.  
TAG\_LIB=NT"

# ORIGIN

Query Match 100.0%; Score 5; DB 7; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 17 GGGTG 13

RESULT 45  
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LOCUS  
DEFINITION  
1M0031B20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0031B20 F, genomic survey sequence.

ACCESSION  
AZ314511  
VERSION  
AZ314511.1 GI:10360474  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0031 row: B column: 20

Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends

High quality sequence stop: 19.

# FEATURES

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/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0031B20"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pWD42 [gi|4732114|gb|AF129072.1], a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adaptor mouse DNA was annealed to  
adaptor vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

# ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
|||||  
Db 1 GGGTG 5

RESULT 46  
AZ324865  
LOCUS  
DEFINITION  
1M0047G10F Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
clone UUGC1M0047G10 F, genomic survey sequence.

ACCESSION  
AZ324865  
VERSION  
AZ324865.1 GI:10381216  
KEYWORDS  
GSS.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus

REFERENCE  
AUTHORS  
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von  
Niederhausern,A. and Wright,D.,Weiss,R.

TITLE  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts

JOURNAL  
COMMENT  
Contact: Robert B. Weiss  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177

Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0047 row: G column: 10

Seq primer: CGTTGTAACGACGCCAGT  
Class: plasmid ends

High quality sequence stop: 19.

# FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC1M0047G10"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC1M library"  
/notes="Vector: PWD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
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ligated to the blunt ends in high molar excess. The  
adaptor DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 4 GGGTG 8

## RESULT 47

AZ330741/c 19 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION IM0056G11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0056G11 F, genomic survey sequence.

ACCESSION AZ330741

VERSION AZ330741.1 GI:10392745

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

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84112 USA

Tel: 801 585 5606

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Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0056 row: G column: 11

Seq primer: CGTTGTAACGACGCGCAGT

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0056G11"

/sex="Male"

/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

was hydrodynamically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

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10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 7 GGGTG 3

## RESULT 48

AZ341989/c 19 bp DNA linear GSS 29-SEP-2000  
LOCUS  
DEFINITION IM0074H13R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0074H13 R, genomic survey sequence.

ACCESSION AZ341989

VERSION AZ341989.1 GI:10418787

KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 19)

## REFERENCE

## AUTHORS

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,R., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.

Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112 USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0074 row: H column: 13

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

## FEATURES

source

1..19

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUGC1M0074H13"

/sex="Male"

/lab\_hosts="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_lib="Mouse 10kb plasmid UUGC1M library"

/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA

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0.005 inch orifice at constant velocity. The sheared DNA

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## ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
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 Db 11 GGGTG 7

RESULT 49  
 AZ343228  
 LOCUS 19 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1M0076M05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0076M05 R, genomic survey sequence.

ACCESSION AZ343228  
 VERSION AZ343228.1 GI:10421448  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.

## TITLE

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## JOURNAL

Unpublished (2000)

## COMMENT

Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0076 row: M column: 05

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

## source

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 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:10090"  
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 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
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 (http://www.jax.org/resources/documents/dnares/). The DNA  
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 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 [gi|4732114|gb|AF129072.1], a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1e+07; Indels 0; Gaps 0;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
 |||||  
 Db 1 GGGTG 5

RESULT 50  
 AZ344069/c

## LOCUS

19 bp DNA linear GSS 29-SEP-2000  
 DEFINITION 1M0077G21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 clone UUGC1M0077G21 R, genomic survey sequence.

ACCESSION AZ344069  
 VERSION AZ344069.1 GI:10422948  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

AUTHORS 1 (bases 1 to 19)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D.,Weiss,R.

## TITLE

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## JOURNAL

Unpublished (2000)

## COMMENT

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 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0077 row: G column: 21

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends

High quality sequence stop: 19.

## FEATURES

## source

1..19  
 /location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0077G21"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
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 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adapted DNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 100.0%; Score 5; DB 8; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1e+07;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||  
Db 6 GGGTG 2

Search completed: January 7, 2005, 11:01:39  
Job time : 2234.4 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 05:37:38 ; Search time 58 Seconds  
(Without alignments)  
61.275 Million cell updates/sec

Title: GGCTG

Perfect score: 5

Sequence: 1 gggtg 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 896372

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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1: /cgn2\_6/ptodata/1/ina/5A COMB.seq:  
2: /cgn2\_6/ptodata/1/ina/5B COMB.seq:  
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4: /cgn2\_6/ptodata/1/ina/6B COMB.seq:  
5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq:  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 2	5	100.0	10	1	US-09-263-790-29
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C 4	5	100.0	10	1	US-09-721-777-9
C 5	5	100.0	10	1	US-09-721-777-12
C 6	5	100.0	10	1	US-09-793-880-7
C 7	5	100.0	10	1	US-09-482-645A-7
C 8	5	100.0	10	1	US-08-061-697-27
C 9	5	100.0	10	1	US-08-131-365B-27
C 10	5	100.0	10	1	US-08-131-365B-43
C 11	5	100.0	10	1	US-08-330-123A-11
C 12	5	100.0	10	1	US-08-210-222-34
C 13	5	100.0	10	1	US-08-197-463-4
C 14	5	100.0	10	1	US-08-153-051B-55
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34	5	100.0	10	1	US-08-060-952C-54	Sequence 54, Appl
35	5	100.0	10	1	US-08-368-071-7	Sequence 7, Appl
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41	5	100.0	10	1	US-08-590-804-13	Sequence 13, Appl
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45	5	100.0	10	2	US-08-590-571-17	Sequence 17, Appl
46	5	100.0	10	2	US-08-590-571-45	Sequence 45, Appl
47	5	100.0	10	2	US-08-286-819A-52	Sequence 52, Appl
48	5	100.0	10	2	US-08-485-778-42	Sequence 42, Appl
49	5	100.0	10	2	US-08-668-123-27	Sequence 27, Appl
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303	5	100.0	13	2	US-08-390-888A-9	Sequence 9, Appl	376	5	100.0	14	1	US-08-499-523-75	Sequence 75, Appl
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305	5	100.0	13	2	US-08-390-888A-13	Sequence 13, Appl	378	5	100.0	14	2	US-08-151-477A-57	Sequence 57, Appl
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307	5	100.0	13	3	US-09-069-434-15	Sequence 15, Appl	380	5	100.0	14	2	US-08-485-689-71	Sequence 71, Appl
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309	5	100.0	13	3	US-09-102-977-11	Sequence 11, Appl	382	5	100.0	14	2	US-08-765-176-5	Sequence 5, Appl
310	5	100.0	13	3	US-09-102-977-16	Sequence 16, Appl	383	5	100.0	14	2	US-08-478-608B-71	Sequence 71, Appl
311	5	100.0	13	3	US-08-505-307-14	Sequence 14, Appl	384	5	100.0	14	2	US-08-866-958-39	Sequence 39, Appl
312	5	100.0	13	3	US-08-987-574-49	Sequence 49, Appl	c 385	5	100.0	14	2	US-08-866-958-86	Sequence 86, Appl
313	5	100.0	13	3	US-08-729-601A-63	Sequence 63, Appl	c 386	5	100.0	14	2	US-08-722-187-74	Sequence 74, Appl
314	5	100.0	13	3	US-08-535-168-49	Sequence 49, Appl	387	5	100.0	14	2	US-08-934-877A-22	Sequence 22, Appl
315	5	100.0	13	3	US-08-964-817-20	Sequence 20, Appl	c 388	5	100.0	14	2	US-08-485-133-44	Sequence 44, Appl
316	5	100.0	13	3	US-09-117-217-15	Sequence 15, Appl	389	5	100.0	14	3	US-08-819-867-78	Sequence 78, Appl
317	5	100.0	13	3	US-09-017-974-49	Sequence 49, Appl	390	5	100.0	14	3	US-08-318-794-5	Sequence 5, Appl
318	5	100.0	13	3	US-09-307-924-2	Sequence 2, Appl	391	5	100.0	14	3	US-08-646-789A-42	Sequence 42, Appl
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394 5 100.0 14 3 US-08-981-462-62 Sequence 62, Appl  
395 5 100.0 14 3 US-08-985-162-1782 Sequence 1782, Ap  
396 5 100.0 14 3 US-08-985-162-1824 Sequence 1824, Ap  
397 5 100.0 14 3 US-08-797-722-2 Sequence 2, Appl  
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457 5 100.0 14 4 US-09-601-326-166 Sequence 166, App  
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460 5 100.0 14 4 US-09-601-326-175 Sequence 175, App  
461 5 100.0 14 4 US-09-069-847-1 Sequence 1, Appl  
462 5 100.0 14 4 US-09-856-662-107 Sequence 107, App  
463 5 100.0 14 5 PCT-US95-02419-1 Sequence 1, Appl  
464 5 100.0 14 5 PCT-US95-04063-200 Sequence 20, App  
465 5 100.0 14 5 PCT-US95-04712-74 Sequence 74, Appl

466 5 100.0 14 5 PCT-US95-12880-2 Sequence 2, Appl  
c 467 5 100.0 14 5 PCT-US95-16904-1 Sequence 1, Appl  
468 5 100.0 14 5 PCT-US96-11786-51 Sequence 51, Appl  
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c 471 5 100.0 15 1 US-07-684-989B-119 Sequence 119, App  
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c 476 5 100.0 15 1 US-07-744-282C-123 Sequence 123, App  
c 477 5 100.0 15 1 US-07-744-282C-125 Sequence 125, App  
c 478 5 100.0 15 1 US-08-050-073-264 Sequence 264, App  
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480 5 100.0 15 1 US-08-182-968A-14 Sequence 14, Appl  
481 5 100.0 15 1 US-08-182-968A-15 Sequence 15, Appl  
482 5 100.0 15 1 US-08-182-968A-23 Sequence 23, Appl  
c 483 5 100.0 15 1 US-08-182-968A-38 Sequence 38, Appl  
484 5 100.0 15 1 US-08-182-968A-219 Sequence 219, App  
485 5 100.0 15 1 US-08-344-695-34 Sequence 34, Appl  
c 486 5 100.0 15 1 US-08-502-185-7 Sequence 7, Appl  
487 5 100.0 15 1 US-08-384-708A-138 Sequence 138, App  
c 488 5 100.0 15 1 US-08-388-945-7 Sequence 7, Appl  
c 489 5 100.0 15 1 US-08-220-606B-25 Sequence 25, Appl  
c 490 5 100.0 15 1 US-08-220-606B-46 Sequence 46, Appl  
491 5 100.0 15 1 US-08-090-193-35 Sequence 35, Appl  
492 5 100.0 15 1 US-08-291-932A-223 Sequence 223, App  
c 493 5 100.0 15 1 US-08-501-779-7 Sequence 7, Appl  
c 494 5 100.0 15 1 US-08-334-215-24 Sequence 24, Appl  
c 495 5 100.0 15 1 US-08-580-242-3 Sequence 3, Appl  
496 5 100.0 15 1 US-08-334-847-611 Sequence 611, App  
c 497 5 100.0 15 1 US-08-684-672-33 Sequence 33, Appl  
c 498 5 100.0 15 1 US-08-684-672-34 Sequence 34, Appl  
c 499 5 100.0 15 1 US-08-363-240A-80 Sequence 80, Appl  
c 500 5 100.0 15 5 PCT-US92-06821A-131 Sequence 131, App

## ALIGNMENTS

RESULT 1  
US-09-263-790-7/c  
; Sequence 7, Application US/09263790  
; Patent No. PP12997  
; GENERAL INFORMATION:  
; APPLICANT: Nitmal Kumar PATRA et al.  
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMOPOGON WINTERIANUS  
; FILE REFERENCE: 2761-0120P  
; CURRENT APPLICATION NUMBER: US/09/263.790  
; CURRENT FILING DATE: 1999-03-05  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: MAP 07 Primer - Primer used in RAPD analysis comparing Jal Pallav  
; OTHER INFORMATION: with Jorlab-2, Manjusha, Mandakini, Bio-13, and Ceylon.  
US-09-263-790-7

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|  
|  
|  
|  
|  
Db 5 GGGTG 1

RESULT 2  
US-09-263-790-29/c  
; Sequence 29, Application US/09263790



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; Patent No. PPI2997
; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: OPT 09 Primer - Used to develop the unique RAPD profiles of the
; OTHER INFORMATION: plant Jal Pallavi
US-09-263-790-29

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
Db      5 GGGTG 1

RESULT 3
US-09-263-790-31
; Sequence 31, Application US/09263790
; Patent No. PPI2997
; GENERAL INFORMATION:
; APPLICANT: Nirmal Kumar PATRA et al.
; TITLE OF INVENTION: JAL PALLAVI, WATER LOGGING TOLERANT CYMBOPOGON WINTERIANUS
; FILE REFERENCE: 2761-0120P
; CURRENT APPLICATION NUMBER: US/09/263,790
; CURRENT FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: OPT 12 Primer - Used to develop the unique RAPD profiles of the
; OTHER INFORMATION: plant Jal Pallavi
US-09-263-790-31

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
Db      5 GGGTG 5

RESULT 4
US-09-721-777-9/c
; Sequence 9, Application US/09721777
; Patent No. PPI3279
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Kumar, Sushil
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Dhawan, Sunita
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Nagvi, Ali Arif
; APPLICANT: Singh, Anil Kumar
; APPLICANT: Patra, Nirmal Kumar
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Bansal, Ram Prakash
```

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; TITLE OF INVENTION: Mint Plant Named Saksham
; FILE REFERENCE: 033166-002
; CURRENT APPLICATION NUMBER: US/09/721,777
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPT primer
US-09-721-777-9

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
Db      5 GGGTG 1

RESULT 5
US-09-721-777-12
; Sequence 12, Application US/09721777
; Patent No. PPI3279
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Kumar, Sushil
; APPLICANT: Shasany, Ajit Kumar
; APPLICANT: Dhawan, Sunita
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Nagvi, Ali Arif
; APPLICANT: Dhawan, Om Parkash
; APPLICANT: Singh, Anil Kumar
; APPLICANT: Patra, Nirmal Kumar
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Bansal, Ram Prakash
; TITLE OF INVENTION: Mint Plant Named Saksham
; FILE REFERENCE: 033166-002
; CURRENT APPLICATION NUMBER: US/09/721,777
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPT primer
US-09-721-777-12

Query Match          100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGTG 5
Db      1 GGGTG 5

RESULT 6
US-09-799-880-7/c
; Sequence 7, Application US/09799880
; Patent No. PPI4400
; GENERAL INFORMATION:
; APPLICANT: Kumar, Sushil
; APPLICANT: Gupta, Ritika
; APPLICANT: Sastri, Kakraparthi
; APPLICANT: Banerjee, Suchitra
; APPLICANT: Mallavarapu, Gopal
; APPLICANT: Ramesh, Srinivas
```

```

; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/061,697
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:347/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 320-7200
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-061-697-27

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No.2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels

QY 1 GGGTG 5
Db 7 GGGTG 3

RESULT 9
US-08-131-365B-27/c
; Sequence 27, Application US/08131365B
; Patent No. 5527690
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Briggs, Michael R.
; APPLICANT: Wang, Xiaodong
; APPLICANT: Goldstein, Joseph L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
; TO STEROL AND COMPOSITIONS RELATING
; TO STEROL REGULATORY ELEMENT BINDING
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/131,365B
; FILING DATE: 01-OCT-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.

```

REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-131-365B-27

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
DB 7 GGGTG 3

RESULT 10  
US-08-131-365B-43  
Sequence 43, Application US/08131365B  
Patent No. 5527690  
GENERAL INFORMATION:  
APPLICANT: Brown, Michael S.  
APPLICANT: Briggs, Michael R.  
APPLICANT: Wang, Xiaodong  
APPLICANT: Goldstein, Joseph L.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
TO STEROL REGULATORY ELEMENT BINDING  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/131.365B  
FILING DATE: 01-OCT-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-131-365B-43

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
DB 6 GGGTG 10

RESULT 11  
US-08-330-123A-11/c  
Sequence 11, Application US/08330123A  
Patent No. 5583016  
GENERAL INFORMATION:  
APPLICANT: VILLEPONTTEAU, Bryant  
APPLICANT: FENG, Junli  
APPLICANT: FUNK, Walter  
APPLICANT: ANDREWS, William H.  
TITLE OF INVENTION: HUMAN TELOMERASE  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/330.123A  
FILING DATE: 27-OCT-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/272,102  
FILING DATE: 07-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15389-000810  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-330-123A-11

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5  
DB 7 GGGTG 3

RESULT 12  
US-08-210-222-34/c  
Sequence 34, Application US/08210222  
Patent No. 5599917  
GENERAL INFORMATION:  
APPLICANT: Coppola, George R.  
APPLICANT: Beutel, Bruce A.  
APPLICANT: Bertelsen, Arthur H.  
TITLE OF INVENTION: Inhibition of Interferon- with Oligonucleotides  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,  
US-08-210-222-34/c

ADDRESSEE: Cecchi, Stewart & Olstein  
STREET: 6 Becker Farm Road  
CITY: Roseland  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch diskette  
COMPUTER: IBM  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/210,222  
FILING DATE: Unassigned  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Herron, Charles J.  
REGISTRATION NUMBER: 28,019  
REFERENCE/DOCKET NUMBER: 23550-114  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 34:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 BASES  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
HYPOTHETICAL: NO  
US-08-210-222-34

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 7 GGGTG 3

## RESULT 13

US-08-197-463-4/c  
Sequence 4, Application US/08197463  
Patent No. 5627047  
GENERAL INFORMATION:  
APPLICANT: Brenner, Michael  
APPLICANT: Besnard, Francois  
APPLICANT: Nakatani, Yoshihiro  
TITLE OF INVENTION: Astrocyte-Specific Transcription  
TITLE OF INVENTION: of Human Genes  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Birch, Stewart, Koslasch & Birch  
STREET: 301 N. Washington St.  
CITY: Falls Church  
STATE: Virginia  
COUNTRY: USA  
ZIP: 22046-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/197,463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION NUMBER: US/07/769,626  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Svensson, Leonard R.  
REGISTRATION NUMBER: 30330

REFERENCE/DOCKET NUMBER: 1173-362P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-241-1300  
TELEFAX: 703-241-2848  
TELEX: 248345  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: protein\_bind  
LOCATION: 1..10  
OTHER INFORMATION: /function= "transcription enhancer"  
OTHER INFORMATION: /bound\_moiety= "AP-2"  
OTHER INFORMATION: /standard\_name= "AP-2 site"  
US-08-197-463-4

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 8 GGGTG 4

## RESULT 14

US-08-153-051B-55  
Sequence 55, Application US/08153051B  
Patent No. 5645986  
GENERAL INFORMATION:  
APPLICANT: Michael D. West  
APPLICANT: Jerry W. Shay  
APPLICANT: Woodring E. Wright  
APPLICANT: Elizabeth Blackburn  
APPLICANT: Nam Woo Kim  
APPLICANT: Calvin B. Harley  
APPLICANT: Scott L. Weinrich  
APPLICANT: Catherine Strahl  
APPLICANT: Michael J. McEachern  
APPLICANT: Homayoun Vaziri  
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF  
TITLE OF INVENTION: CONDITIONS RELATED TO TELOMERE  
TITLE OF INVENTION: LENGTH AND/OR TELOMERASE ACTIVITY  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FastSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/153,051B  
FILING DATE: No. 5645986ember 12, 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/038,766  
FILING DATE: March 24, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 204/195  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 55:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-153-051B-55

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 2 GGGTG 6

RESULT 15  
US-08-202-927-5  
; Sequence 5, Application US/08202927  
; Patent No. 5646126  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Yung-chi  
; APPLICANT: Lukhtanov, Eugeny A.  
; APPLICANT: Meyer Jr., Rich B.  
; APPLICANT: Pai, Balakrishna S.  
; APPLICANT: Reed, Michael W.  
; APPLICANT: Zhou, James H.  
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klein & Szekeres  
; STREET: 4199 Campus Drive, Suite 700  
; CITY: Irvine  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92715  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/202,927  
; FILING DATE: 28-FEB-1994  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Szekeres, Gabor L.  
; REGISTRATION NUMBER: 28,675  
; REFERENCE/DOCKET NUMBER: 491-07-PA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 854-4897  
; TELEFAX: (714) 854-5502  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 10  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to  
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
; OTHER INFORMATION: formula 3)."

US-08-202-927-5

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 6 GGGTG 10

RESULT 16  
US-08-202-927-7  
; Sequence 7, Application US/08202927  
; Patent No. 5646126  
; GENERAL INFORMATION:  
; APPLICANT: Cheng, Yung-chi  
; APPLICANT: Lukhtanov, Eugeny A.  
; APPLICANT: Meyer Jr., Rich B.  
; APPLICANT: Pai, Balakrishna S.  
; APPLICANT: Reed, Michael W.  
; APPLICANT: Zhou, James H.  
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
; NUMBER OF SEQUENCES: 70  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klein & Szekeres  
; STREET: 4199 Campus Drive, Suite 700  
; CITY: Irvine  
; STATE: CA  
; COUNTRY: U.S.A.  
; ZIP: 92715  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/202,927  
; FILING DATE: 28-FEB-1994  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Szekeres, Gabor L.  
; REGISTRATION NUMBER: 28,675  
; REFERENCE/DOCKET NUMBER: 491-07-PA  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (714) 854-5502  
; TELEFAX: (714) 854-4897  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: modified\_base  
; LOCATION: 10  
; OTHER INFORMATION: /mod\_base= OTHER  
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises  
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to  
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached  
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from  
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see  
; OTHER INFORMATION: formula 3)."

US-08-202-927-7

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 4 GGGTG 8

```

; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
; US-08-202-927-12

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 GGGTG 5
DB 6 GGGTG 10

RESULT 19
US-08-202-927-13
; Sequence 13, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
```



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises a cholesterol moiety which has its A ring linked to the 3'-phosphate through a carbonyl group attached to the ring nitrogen of a moiety derived from 4-hydroxy-2-hydroxymethylpyrrolidine (see formula 3)."  
US-08-202-927-21

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 6 GGGTG 10

RESULT 22  
US-08-202-927-22  
Sequence 22, Application US/08202927  
Patent No. 5646126  
GENERAL INFORMATION:  
APPLICANT: Cheng, Yung-chi  
APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Meyer Jr., Rich B.  
APPLICANT: Pai, Balakrishna S.  
APPLICANT: Reed, Michael W.  
APPLICANT: Zhou, James H.  
TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
TITLE OF INVENTION: Anticancer Activity  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klein & Szekeres  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675  
REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises a cholesterol moiety which has its A ring linked to the 3'-phosphate through a carbonyl group attached to the ring nitrogen of a moiety derived from 4-hydroxy-2-hydroxymethylpyrrolidine (see formula 3)."  
US-08-202-927-22

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 6 GGGTG 10

RESULT 23  
US-08-202-927-23  
Sequence 23, Application US/08202927  
Patent No. 5646126  
GENERAL INFORMATION:  
APPLICANT: Cheng, Yung-chi  
APPLICANT: Lukhtanov, Eugeny A.  
APPLICANT: Meyer Jr., Rich B.  
APPLICANT: Pai, Balakrishna S.  
APPLICANT: Reed, Michael W.  
APPLICANT: Zhou, James H.  
TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having  
TITLE OF INVENTION: Anticancer Activity  
NUMBER OF SEQUENCES: 70  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Klein & Szekeres  
STREET: 4199 Campus Drive, Suite 700  
CITY: Irvine  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 92715  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/202,927  
FILING DATE: 28-FEB-1994  
CLASSIFICATION: 536  
ATTORNEY/AGENT INFORMATION:  
NAME: Szekeres, Gabor L.  
REGISTRATION NUMBER: 28,675  
REFERENCE/DOCKET NUMBER: 491-07-PA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (714) 854-5502  
TELEFAX: (714) 854-4897  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises a cholesterol moiety which has its A ring linked to the 3'-phosphate through a carbonyl group attached to the ring nitrogen of a moiety derived from 4-hydroxy-2-hydroxymethylpyrrolidine (see



```

; OTHER INFORMATION: formula 3)."
US-08-202-927-23

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10
|||||

RESULT 24
US-08-202-927-24
; Sequence 24, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-24

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10
|||||

US-08-202-927-25
; Sequence 25, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-25

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10
|||||

RESULT 26
US-08-202-927-26
; Sequence 26, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-26

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10
|||||
```

```
;
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
;
US-08-202-927-26

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10
|||||

RESULT 27
US-08-202-927-26/c
; Sequence 26, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
```

```
;
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
;
US-08-202-927-26

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 5 GGGTG 1
|||||

RESULT 28
US-08-202-927-27
; Sequence 27, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
; US-08-202-927-27

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Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGGTG 5
    |||||
DB 6 GGGTG 10

```

```

RESULT 29
US-08-202-927-28
; Sequence 28, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675

```

```

; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
; US-08-202-927-28

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Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGGTG 5
    |||||
DB 6 GGGTG 10

```

```

RESULT 30
US-08-202-927-29
; Sequence 29, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

```
;
; TOPOLOGY: linear
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-29

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10

RESULT 31
US-08-202-927-30
; Sequence 30, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-29

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10

RESULT 32
US-08-202-927-31
; Sequence 31, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-31

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
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;
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-30

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10

RESULT 32
US-08-202-927-31
; Sequence 31, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-31

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
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Db      |||||
        6 GGGTG 10

RESULT 33
US-08-202-927-43/c
; Sequence 43, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises a
; OTHER INFORMATION: cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
US-08-202-927-43

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
        |||||
Db      5 GGGTG 1

RESULT 34
US-08-060-952C-54
; Sequence 54, Application US/08060952C
; Patent No. 5695932
; GENERAL INFORMATION:
; APPLICANT: Michael D. West
; APPLICANT: Jerry W. Shay
; APPLICANT: Woodring E. Wright
; APPLICANT: Elizabeth Blackburn
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF CONDITIONS
; TITLE OF INVENTION: RELATED TO TELOMERE LENGTH AND/OR
; TITLE OF INVENTION: TELOMERASE ACTIVITY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/060,952C
; FILING DATE: May 13, 1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/882,438
; FILING DATE: May 13, 1992
; APPLICATION NUMBER: 08/038,766
; FILING DATE: March 24, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 202/045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-060-952C-54

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
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Db      2 GGGTG 6

RESULT 35
US-08-368-071-7/c
; Sequence 7, Application US/08368071
; Patent No. 5707853
; GENERAL INFORMATION:
; APPLICANT: MILLAN, JOSE L.
; TITLE OF INVENTION: RECOMBINANT CALF INTESTINAL ALKALINE
; TITLE OF INVENTION: PHOSPHATASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:

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;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/368,071  
;; FILING DATE: 03-JAN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CAMPBELL, CATHRYN  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 1275  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-535-9001  
;; TELEFAX: 619-535-8949  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
US-08-368-071-7

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 10 GGGTG 6

RESULT 36  
US-08-532-904-6/c  
; Sequence 6, Application US/08532904  
; Patent No. 5710367  
; GENERAL INFORMATION:  
; APPLICANT: Kindinger, Bryan K.  
; APPLICANT: Sokolov, Victor  
; TITLE OF INVENTION: Apomictic Maize  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Curtis P. Ribando  
; STREET: 1815 No. 5710367th University Street  
; CITY: Peoria  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 61604  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/532,904  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ribando, Curtis P  
; REGISTRATION NUMBER: 27976  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 309-681-6513  
; TELEFAX: 309-681-6688  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
US-08-532-904-6

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 5 GGGTG 1

RESULT 37  
US-08-463-660-13/c  
; Sequence 13, Application US/08463660  
; Patent No. 5759776  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, HELENE S.  
; APPLICANT: CHEN, LING-CHUN  
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND TREATMENT  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/463,660  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CIOTTI, THOMAS E.  
; REGISTRATION NUMBER: 21,013  
; REFERENCE/DOCKET NUMBER: 28888-20001.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-463-660-13

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 8 GGGTG 4

RESULT 38  
US-08-458-181-7/c  
; Sequence 7, Application US/08458181  
; Patent No. 5773226  
; GENERAL INFORMATION:  
; APPLICANT: MILLAN, JOSE L.  
; TITLE OF INVENTION: RECOMBINANT CALF INTESTINAL ALKALINE  
; TITLE OF INVENTION: PHOSPHATASE  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CAMPBELL AND FLORES  
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700  
; CITY: SAN DIEGO  
; STATE: CALIFORNIA

;; COUNTRY: UNITED STATES  
;; ZIP: 92122  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/458,181  
;; FILING DATE: 30-DEC-1994  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: CAMPBELL, CATHRYN  
;; REGISTRATION NUMBER: 31,815  
;; REFERENCE/DOCKET NUMBER: P-LJ 1275  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 619-535-9001  
;; TELEFAX: 619-535-8949  
;; INFORMATION FOR SEQ ID NO: 7:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-458-181-7

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 10 GGGTG 6

RESULT 39  
US-08-482-115B-11/c  
;; Sequence 11, Application US/08482115B  
;; Patent No. 5776679  
;; GENERAL INFORMATION:  
;; APPLICANT: Villeponteau, Bryant  
;; APPLICANT: Feng, Junli  
;; APPLICANT: Funk, Walter  
;; APPLICANT: Andrews, William H.  
;; TITLE OF INVENTION: Assays for the RNA Component of Human  
;; TITLE OF INVENTION: Telomerase  
;; NUMBER OF SEQUENCES: 40  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Townsend and Townsend and Crew LLP  
;; STREET: Two Embarcadero Center, Eighth Floor  
;; CITY: San Francisco  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94111-3834  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/482,115B  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/272,102  
;; FILING DATE: 07-JUL-1994  
;; APPLICATION NUMBER: US 08/330,123  
;; FILING DATE: 27-OCT-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Storella, John R.  
;; REGISTRATION NUMBER: 32,944  
;; REFERENCE/DOCKET NUMBER: 015389-000830US

;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 11:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA  
;; US-08-482-115B-11

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 7 GGGTG 3

RESULT 40  
US-08-678-280-13/c  
;; Sequence 13, Application US/08678280  
;; Patent No. 5776883  
;; GENERAL INFORMATION:  
;; APPLICANT: SMITH, HELENE S.  
;; APPLICANT: CHUN, LING-CHEN  
;; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND  
;; TITLE OF INVENTION: TREATMENT  
;; NUMBER OF SEQUENCES: 14  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: MORRISON & FOERSTER  
;; STREET: 755 Page Mill Road  
;; CITY: Palo Alto  
;; STATE: California  
;; COUNTRY: USA  
;; ZIP: 94304-1018  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent in Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/678,280  
;; FILING DATE:  
;; CLASSIFICATION: 514  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Schiff, J. Michael  
;; REGISTRATION NUMBER: 40,253  
;; REFERENCE/DOCKET NUMBER: 28888-20001.20  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 813-5600  
;; TELEFAX: (415) 494-0792  
;; TELEX: 706141  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-678-280-13

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 8 GGGTG 4

RESULT 41

```

US-08-590-804-13
; Sequence 13, Application US/08590804
; Patent No. 5780273
; GENERAL INFORMATION:
; APPLICANT: Burg, J. Lawrence
; TITLE OF INVENTION: INSERTION ELEMENTS AND AMPLIFIABLE
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amoco Corporation
; STREET: 55 Shuman Blvd., Suite 600
; CITY: Naperville
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60563
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,804
; FILING DATE: 24-JAN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,779
; FILING DATE:
; APPLICATION NUMBER: US 08/045,587
; FILING DATE: 09-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Galloway, No. 5780273val B
; REGISTRATION NUMBER: 33,595
; REFERENCE/DOCKET NUMBER: 32,468
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-717-2447
; TELEFAX: 708-717-2430
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-590-804-13

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGTG 5
Db 2 GGGTG 6

RESULT 42
US-08-729-447-3/c
; Sequence 3, Application US/08729447
; Patent No. 5789174
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DETECTION OF PERIODONTAL PATHOGENS INCLUDING
; TITLE OF INVENTION: BACTEROIDES FORSYTHUS, PORPHYROMONAS GINGIVALIS,
; TITLE OF INVENTION: PREVOTELLA INTERMEDIA AND PREVOTELLA NIGRESCENS
; NUMBER OF SEQUENCES: 20
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,447
; FILING DATE:

```



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;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-151-477A-55
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 2 GGGTG 6

RESULT 44
US-08-660-678A-11/c
; Sequence 11, Application US/08660678A
; Patent No. 5837857
; GENERAL INFORMATION:
; APPLICANT: Villeponteau, Bryant
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Andrews, William H.
; TITLE OF INVENTION: Mammalian Telomerase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,678A
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Storella, John R.
; REGISTRATION NUMBER: 32,944
; REFERENCE/DOCKET NUMBER: 015389-000811US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-660-678A-11
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 7 GGGTG 3

RESULT 45
```

```
US-08-590-571-17
; Sequence 17, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-17
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 2 GGGTG 6

RESULT 46
US-08-590-571-45
; Sequence 45, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-45

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      3 GGGTG 7

RESULT 47
US-08-286-819A-52
; Sequence 52, Application US/08286819A
; Patent No. 5871910
; GENERAL INFORMATION:
; APPLICANT: ARTHUR, MICHEL
; APPLICANT: DUKTA-MALEN, SYLVIE
; APPLICANT: MOLINAS, CATHERINE
; APPLICANT: COURVALIN, PATRICE
; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPOLYPTIDES, IN PARTICULAR
; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR
; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/286,819A
; FILING DATE: 05-AUG-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/174,682
; FILING DATE: 28-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/917,146
; FILING DATE: 10-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR/91/00855
; FILING DATE: 29-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9013579
; FILING DATE: 31-OCT-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5871910man F.
; REGISTRATION NUMBER: 24,618
```

```
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-286-819A-52

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      6 GGGTG 10

RESULT 48
US-08-485-778-42/c
; Sequence 42, Application US/08485778
; Patent No. 5876979
; GENERAL INFORMATION:
; APPLICANT: Andrews, William H.
; APPLICANT: Avilion, Ariel Athena
; APPLICANT: Feng, Junli
; APPLICANT: Funk, Walter
; APPLICANT: Greider, Carol
; APPLICANT: Marhuenda, Maria Antonia Blasco
; APPLICANT: Villeponteau, Bryant
; TITLE OF INVENTION: RNA COMPONENT OF TELOMERASE
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,778
; FILING DATE: 07-JE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,524
; FILING DATE: 13-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,123
; FILING DATE: 27-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/272,102
; FILING DATE: 07-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL94-05A4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 617-861-9540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
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```
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-485-778-42

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 7 GGGTG 3

RESULT 49
US-08-668-123-27/c
; Sequence 27, Application US/08668123
; Patent No. 5891631
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Briggs, Michael R.
; APPLICANT: Wang, Xiaodong
; APPLICANT: Goldstein, Joseph L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
; TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/668,123
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/131,365
; FILING DATE: 01-OCT-1993
; NAME: Parker, David L.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:372/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-668-123-27

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 7 GGGTG 3

RESULT 50
US-08-668-123-43
; Sequence 43, Application US/08668123
; Patent No. 5891631
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.
; APPLICANT: Briggs, Michael R.
; APPLICANT: Wang, Xiaodong
; APPLICANT: Goldstein, Joseph L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING
; TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: U.S.A.
; ZIP: 77210
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/668,123
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/131,365
; FILING DATE: 01-OCT-1993
; NAME: Parker, David L.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:372/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-668-123-43

Query Match      100.0%; Score 5; DB 2; Length 10;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 6 GGGTG 10

Search completed: January 7, 2005, 11:05:44
Job time : 61 secs
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 06:51:47 ; Search time 270.2 Seconds  
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Title: GGCTG

Perfect score: 5

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Scoring table: IDENTITY\_NUC

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Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 2912722

Minimum DB seq length: 10

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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 237	5	100.0	10	17	US-10-470-180-63	Sequence 63, Appl	Sequence 63, Appl	C 310	5	100.0	11	17	US-10-612-224-92	Sequence 4, Appl
C 238	5	100.0	10	17	US-10-745-377-19	Sequence 19, Appl	Sequence 19, Appl	C 311	5	100.0	11	17	US-10-450-797-4	Sequence 17, Appl
C 239	5	100.0	10	17	US-10-784-710-33	Sequence 33, Appl	Sequence 33, Appl	C 312	5	100.0	11	17	US-10-450-797-17	Sequence 17, Appl
C 240	5	100.0	10	17	US-10-302-547-17	Sequence 17, Appl	Sequence 17, Appl	C 313	5	100.0	11	17	US-10-450-797-53	Sequence 53, Appl
C 241	5	100.0	10	17	US-10-302-547-19	Sequence 19, Appl	Sequence 19, Appl	C 314	5	100.0	11	17	US-10-450-797-277	Sequence 277, App
C 242	5	100.0	10	17	US-10-302-547-27	Sequence 27, Appl	Sequence 27, Appl	C 315	5	100.0	11	17	US-10-450-797-277	Sequence 246, App
C 243	5	100.0	10	17	US-10-302-547-43	Sequence 43, Appl	Sequence 43, Appl	C 316	5	100.0	11	17	US-10-450-797-326	Sequence 326, App
C 244	5	100.0	10	17	US-10-302-547-63	Sequence 63, Appl	Sequence 63, Appl	C 317	5	100.0	11	17	US-10-450-797-364	Sequence 364, App
C 245	5	100.0	10	17	US-10-302-547-51	Sequence 51, Appl	Sequence 51, Appl	C 318	5	100.0	11	17	US-10-450-797-386	Sequence 386, App
C 246	5	100.0	10	17	US-10-643-752A-12	Sequence 12, Appl	Sequence 12, Appl	C 319	5	100.0	11	17	US-10-450-797-429	Sequence 429, App
C 247	5	100.0	10	18	US-10-821-568-110	Sequence 110, App	Sequence 110, App	C 320	5	100.0	11	17	US-10-450-797-431	Sequence 431, App
C 248	5	100.0	10	18	US-10-401-691-7	Sequence 7, Appl	Sequence 7, Appl	C 321	5	100.0	11	17	US-10-450-797-481	Sequence 481, App
C 249	5	100.0	10	18	US-10-61-633-54	Sequence 54, Appl	Sequence 54, Appl	C 322	5	100.0	11	17	US-10-450-797-516	Sequence 516, App
C 250	5	100.0	10	18	US-10-872-113-19	Sequence 19, Appl	Sequence 19, Appl	C 323	5	100.0	11	17	US-10-450-797-560	Sequence 560, App
C 251	5	100.0	10	18	US-10-487-934-106	Sequence 106, App	Sequence 106, App	C 324	5	100.0	11	17	US-10-450-797-597	Sequence 597, App
C 252	5	100.0	10	18	US-10-487-934-107	Sequence 107, App	Sequence 107, App	C 325	5	100.0	11	17	US-10-450-797-929	Sequence 929, App
C 253	5	100.0	10	18	US-10-487-934-108	Sequence 108, App	Sequence 108, App	C 326	5	100.0	11	17	US-10-450-797-993	Sequence 993, App
C 254	5	100.0	10	18	US-10-487-934-109	Sequence 109, App	Sequence 109, App	C 327	5	100.0	11	17	US-10-450-797-1039	Sequence 1039, Ap
C 255	5	100.0	10	18	US-10-487-934-146	Sequence 146, App	Sequence 146, App	C 328	5	100.0	11	17	US-10-450-797-1124	Sequence 1124, Ap
C 256	5	100.0	10	18	US-10-487-934-178	Sequence 178, App	Sequence 178, App	C 329	5	100.0	11	17	US-10-450-797-1153	Sequence 1153, Ap
C 257	5	100.0	10	18	US-10-487-934-212	Sequence 212, App	Sequence 212, App	C 330	5	100.0	11	17	US-10-450-797-1399	Sequence 1399, Ap
C 258	5	100.0	10	18	US-10-489-386-1	Sequence 1, Appl	Sequence 1, Appl	C 331	5	100.0	11	17	US-10-803-622-213	Sequence 213, App
C 259	5	100.0	10	18	US-10-602-494-379	Sequence 379, App	Sequence 379, App	C 332	5	100.0	11	17	US-10-803-653-213	Sequence 213, App
C 260	5	100.0	11	9	US-09-813-031-11	Sequence 11, Appl	Sequence 11, Appl	C 333	5	100.0	11	18	US-10-474-794-86	Sequence 86, Appl
C 261	5	100.0	11	9	US-09-813-031-19	Sequence 19, Appl	Sequence 19, Appl	C 334	5	100.0	11	18	US-10-474-794-93	Sequence 93, Appl
C 262	5	100.0	11	9	US-09-813-990A-11	Sequence 11, Appl	Sequence 11, Appl	C 335	5	100.0	11	18	US-10-474-794-122	Sequence 122, App
C 263	5	100.0	11	9	US-09-813-990A-19	Sequence 19, Appl	Sequence 19, Appl	C 336	5	100.0	11	18	US-10-149-109A-159	Sequence 159, App
C 264	5	100.0	11	9	US-09-879-813-20	Sequence 20, Appl	Sequence 20, Appl	C 337	5	100.0	11	18	US-10-149-109A-160	Sequence 160, App
C 265	5	100.0	11	9	US-09-879-813-42	Sequence 42, Appl	Sequence 42, Appl	C 338	5	100.0	11	18	US-10-149-109A-163	Sequence 163, App
C 266	5	100.0	11	9	US-09-945-901-9	Sequence 9, Appl	Sequence 9, Appl	C 339	5	100.0	11	18	US-10-149-109A-165	Sequence 165, App
C 267	5	100.0	11	9	US-09-745-317-79	Sequence 79, Appl	Sequence 79, Appl	C 340	5	100.0	11	18	US-10-715-844-35	Sequence 35, Appl
C 268	5	100.0	11	10	US-09-918-715-86	Sequence 86, Appl	Sequence 86, Appl	C 341	5	100.0	12	8	US-08-463-404-55	Sequence 55, Appl
C 269	5	100.0	11	10	US-09-918-715-93	Sequence 93, Appl	Sequence 93, Appl	C 342	5	100.0	12	9	US-09-365-029-23	Sequence 23, Appl
C 270	5	100.0	11	10	US-09-918-715-122	Sequence 122, App	Sequence 122, App	C 343	5	100.0	12	9	US-09-365-029-24	Sequence 24, Appl
C 271	5	100.0	11	10	US-09-943-115A-11	Sequence 11, Appl	Sequence 11, Appl	C 344	5	100.0	12	9	US-09-365-029-38	Sequence 38, Appl
C 272	5	100.0	11	10	US-09-943-115A-13	Sequence 13, Appl	Sequence 13, Appl	C 345	5	100.0	12	9	US-09-365-029-89	Sequence 89, Appl
C 273	5	100.0	11	10	US-09-249-155-7	Sequence 7, Appl	Sequence 7, Appl	C 346	5	100.0	12	9	US-09-365-029-90	Sequence 90, Appl
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C 276	5	100.0	11	10	US-09-249-155-109	Sequence 109, App	Sequence 109, App	C 349	5	100.0	12	9	US-09-263-959-907	Sequence 907, App
C 277	5	100.0	11	10	US-09-249-155-165	Sequence 165, App	Sequence 165, App	C 350	5	100.0	12	9	US-09-263-959-915	Sequence 915, App
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C 279	5	100.0	11	10	US-09-942-310-73	Sequence 73, Appl	Sequence 73, Appl	C 352	5	100.0	12	9	US-09-976-736-17	Sequence 17, Appl
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C 281	5	100.0	11	13	US-10-007-747-9	Sequence 9, Appl	Sequence 9, Appl	C 354	5	100.0	12	9	US-09-841-157A-32	Sequence 32, Appl
C 282	5	100.0	11	14	US-10-038-937-9	Sequence 9, Appl	Sequence 9, Appl	C 355	5	100.0	12	9	US-09-841-157A-33	Sequence 33, Appl
C 283	5	100.0	11	14	US-10-146-354A-13	Sequence 13, Appl	Sequence 13, Appl	C 356	5	100.0	12	10	US-09-765-061B-24	Sequence 24, Appl
C 284	5	100.0	11	14	US-10-146-354A-14	Sequence 14, Appl	Sequence 14, Appl	C 357	5	100.0	12	10	US-09-835-370-33	Sequence 33, Appl
C 285	5	100.0	11	15	US-10-146-505-20	Sequence 20, Appl	Sequence 20, Appl	C 358	5	100.0	12	10	US-09-823-005-22	Sequence 22, Appl
C 286	5	100.0	11	15	US-10-146-505-42	Sequence 42, Appl	Sequence 42, Appl	C 359	5	100.0	12	10	US-09-923-005-31	Sequence 31, Appl
C 287	5	100.0	11	15	US-10-266-138B-19	Sequence 19, Appl	Sequence 19, Appl	C 360	5	100.0	12	10	US-09-405-032-3	Sequence 3, Appl
C 288	5	100.0	11	15	US-10-214-417A-33	Sequence 33, Appl	Sequence 33, Appl	C 361	5	100.0	12	14	US-10-104-949A-14	Sequence 14, Appl
C 289	5	100.0	11	15	US-10-055-728-8	Sequence 8, Appl	Sequence 8, Appl	C 362	5	100.0	12	14	US-10-054-429A-14	Sequence 14, Appl
C 290	5	100.0	11	15	US-10-285-509B-19	Sequence 19, Appl	Sequence 19, Appl	C 363	5	100.0	12	14	US-10-054-429A-29	Sequence 29, Appl
C 291	5	100.0	11	15	US-10-084-839-3364	Sequence 3364, App	Sequence 3364, App	C 364	5	100.0	12	15	US-10-146-505-38	Sequence 38, Appl
C 292	5	100.0	11	15	US-10-277-494-100	Sequence 100, App	Sequence 100, App	C 365	5	100.0	12	15	US-10-101-030B-56	Sequence 56, Appl
C 293	5	100.0	11	15	US-10-091-281-77	Sequence 77, Appl	Sequence 77, Appl	C 366	5	100.0	12	15	US-10-101-030B-65	Sequence 65, Appl
C 294	5	100.0	11	15	US-10-091-281-170	Sequence 170, App	Sequence 170, App	C 367	5	100.0	12	15	US-10-021-425-60	Sequence 60, Appl
C 295	5	100.0	11	15	US-10-091-281-183	Sequence 183, App	Sequence 183, App	C 368	5	100.0	12	15	US-10-279-061-60	Sequence 60, Appl
C 296	5	100.0	11	15	US-10-091-281-245	Sequence 245, App	Sequence 245, App	C 369	5	100.0	12	15	US-10-084-839-3010	Sequence 3010, Ap
C 297	5	100.0	11	15	US-10-310-677-8	Sequence 8, Appl	Sequence 8, Appl	C 370	5	100.0	12	15	US-10-091-281-374	Sequence 374, App
C 298	5	100.0	11	15	US-10-314-322-7	Sequence 7, Appl	Sequence 7, Appl	C 371	5	100.0	12	15	US-10-091-281-434	Sequence 434, App
C 299	5	100.0	11	15	US-10-314-322-74	Sequence 74, Appl	Sequence 74, Appl	C 372	5	100.0	12	15	US-10-232-927A-76	Sequence 76, Appl
C 300	5	100.0	11	15	US-10-314-322-100	Sequence 100, App	Sequence 100, App	C 373	5	100.0	12	15	US-10-343-943-4	Sequence 4, Appl
C 301	5	100.0	11	15	US-10-314-322-109	Sequence 109, App	Sequence 109, App	C 374	5	100.0	12	16	US-10-182-329-45	Sequence 45, Appl
C 302	5	100.0	11	15	US-10-314-322-165	Sequence 165, App	Sequence 165, App	C 375	5	100.0	12	16	US-10-182-329-46	Sequence 46, Appl
C 303	5	100.0	11	15	US-10-314-322-318	Sequence 318, App	Sequence 318, App	C 376	5	100.0	12	16	US-10-182-329-47	Sequence 47, Appl
C 304	5	100.0	11	15	US-10-314-322-325	Sequence 325, App	Sequence 325, App	C 377	5	100.0	12	16	US-10-182-329-56	Sequence 56, Appl





; STATE: California  
 ; COUNTRY: U.S.A.  
 ; ZIP: 90071-2066  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
 ; MEDIUM TYPE: storage  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0  
 ; SOFTWARE: Word Perfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/463,404  
 ; FILING DATE: 05-JUN-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/060,952  
 ; FILING DATE: May 13, 1993  
 ; APPLICATION NUMBER: 07/882,438  
 ; FILING DATE: May 13, 1992  
 ; APPLICATION NUMBER: 08/038,766  
 ; FILING DATE: March 24, 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warburg, Richard J.  
 ; REGISTRATION NUMBER: 32,327  
 ; REFERENCE/DOCKET NUMBER: 202/045  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (213) 489-1600  
 ; TELEFAX: (213) 955-0440  
 ; TELEX: 67-3510  
 ; INFORMATION FOR SEQ ID NO: 54:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-463-404-54

Query Match 100.0%; Score 5; DB 8; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
 Db 2 GGGTG 6

RESULT 2  
 US-09-758-073-3  
 ; Sequence 3, Application US/09758073  
 ; Patent No. US20010024785A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keinath, et al.  
 ; TITLE OF INVENTION: Method of Diagnosing Gummy Stem Blight in  
 ; TITLE OF INVENTION: Plants Using a Polymerase Chain Reaction Assay  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Judy C. Jarecki-Black, Ph.D.  
 ; ADDRESSEE: Dority & Manning, P.A.  
 ; STREET: 700 E. No. US20010024785A1th Street, Suite 15  
 ; CITY: Greenville  
 ; STATE: South Carolina  
 ; COUNTRY: USA  
 ; ZIP: 29601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
 ; COMPUTER: IBM compatible  
 ; OPERATING SYSTEM: MS Dos; Windows 95  
 ; SOFTWARE: Wordperfect 6.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/758,073  
 ; FILING DATE: Filed Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/078,103

; FILING DATE: 16-MAR-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Judy C. Jarecki-Black, Ph.D.  
 ; REGISTRATION NUMBER: P44,170  
 ; REFERENCE/DOCKET NUMBER: CXU-291  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (864) 271-1592  
 ; TELEFAX: (864) 233-7342  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 10 Pairs  
 ; TYPE: Nucleic Acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: Other Nucleic Acid  
 ; DESCRIPTION: Oligonucleotide Primer  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: No  
 ; ORIGINAL SOURCE: Operon Technologies (Alameda, CA)  
 ; IMMEDIATE SOURCE: Operon Technologies  
 ; POSITION IN GENOME: No. US20010024785A1 Applicable  
 ; UNITS:  
 ; FEATURE:  
 ; OTHER INFORMATION: Commercially Available Primer  
 ; PUBLICATION INFORMATION: No. US20010024785A1 Applicable  
 ; US-09-758-073-3

Query Match 100.0%; Score 5; DB 9; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
 Db 1 GGGTG 5

RESULT 3  
 US-09-057-351-11/c  
 ; Sequence 11, Application US/09057351  
 ; Patent No. US20010034439A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Villegonteu, Bryant  
 ; APPLICANT: Feng, Junli  
 ; APPLICANT: Funk, Walter  
 ; APPLICANT: Andrews, William H.  
 ; TITLE OF INVENTION: Mammalian Telomerase  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Townsend and Townsend and Crew LLP  
 ; STREET: Two Embarcadero Center, Eighth Floor  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94111-3834  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/057,351  
 ; FILING DATE: 08-APR-1994  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/272,102  
 ; FILING DATE: 07-JUL-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/330,123  
 ; FILING DATE: 27-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/472,802  
 ; FILING DATE: 07-JUN-1995  
 ; ATTORNEY/AGENT INFORMATION:

; NAME: Storella, John R.  
; REGISTRATION NUMBER: 32,944  
; REFERENCE/DOCKET NUMBER: 015389-000821US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA  
US-09-057-351-11

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Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 7 GGGTG 3

## RESULT 4

US-09-823-699-1/c  
; Sequence 1, Application US/09823699  
; Patent No. US2002002143A1  
; GENERAL INFORMATION:  
; APPLICANT: Kano, Munehide  
; APPLICANT: Matano, Tetsuro  
; APPLICANT: Kato, Atsushi  
; APPLICANT: Nagai, Yoshiyuki  
; APPLICANT: Hasegawa, Mamoru  
; TITLE OF INVENTION: AIDS Virus Vaccines Using Sendai Virus  
; FILE REFERENCE: 50026/022002  
; CURRENT APPLICATION NUMBER: US/09/823,699  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 60/193,127  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: artificially synthesized sequence  
US-09-823-699-1

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 9 GGGTG 5

## RESULT 5

US-09-154-750A-9/c  
; Sequence 9, Application US/09154750A  
; Publication No. US20020055097A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: p53-induced Apoptosis  
; FILE REFERENCE: 1107.75357  
; CURRENT APPLICATION NUMBER: US/09/154,750A  
; CURRENT FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/059,153

; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079817  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 9  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-154-750A-9

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 6 GGGTG 2

## RESULT 6

US-09-154-750A-66/c  
; Sequence 66, Application US/09154750A  
; Publication No. US20020055097A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: p53-induced Apoptosis  
; FILE REFERENCE: 1107.75357  
; CURRENT APPLICATION NUMBER: US/09/154,750A  
; CURRENT FILING DATE: 1998-09-17  
; PRIOR APPLICATION NUMBER: 60/059,153  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079817  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 66  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-154-750A-66

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 10 GGGTG 6

## RESULT 7

US-09-785-632A-4  
; Sequence 4, Application US/09785632A  
; Patent No. US20020061512A1  
; GENERAL INFORMATION:  
; APPLICANT: Kim, Jin-Soo  
; APPLICANT: Kwon, Young Do  
; APPLICANT: Kim, Hyun-Won  
; APPLICANT: Ryu, Eun-Hyun  
; APPLICANT: Hwang, Moon-Sun  
; TITLE OF INVENTION: ZINC FINGER DOMAINS AND METHODS OF  
; FILE REFERENCE: IDENTIFYING SAME  
; FILE REFERENCE: 12279-002001  
; CURRENT APPLICATION NUMBER: US/09/785,632A  
; CURRENT FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 166  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 10  
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-03-785-632A-4

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      2 GGGTG 6

RESULT 8
US-09-989-789-97
; Sequence 97, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-97

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      5 GGGTG 9

RESULT 9
US-09-989-789-584
; Sequence 584, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 584
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-584

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      2 GGGTG 6

RESULT 10
US-09-989-789-626
; Sequence 626, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-626

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      3 GGGTG 7

RESULT 11
US-09-989-789-1287
; Sequence 1287, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1287
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1287

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      3 GGGTG 7

RESULT 12
US-09-989-789-1329
; Sequence 1329, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
```

```
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1329
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1329

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10

RESULT 13
US-09-989-789-1339
; Sequence 1339, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1339
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1339

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 6 GGGTG 10

RESULT 14
US-09-989-789-1645
; Sequence 1645, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1645
```

```
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 2 GGGTG 6

RESULT 15
US-09-989-789-1646
; Sequence 1646, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1646
```

```
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 2 GGGTG 6
```

```
RESULT 16
US-09-989-789-1660
; Sequence 1660, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1660
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1660
```

```
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5
Db 5 GGGTG 9
```

RESULT 17

```
US-09-989-789-1669
; Sequence 1669, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1669
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1669

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      3 GGGTG 7

RESULT 18
US-09-989-789-1670
; Sequence 1670, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1670
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-789-1670

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      3 GGGTG 7

RESULT 19
US-09-942-325A-5/c
; Sequence 5, Application US/09942325A
; Patent No. US20020106794A1
; GENERAL INFORMATION:
; APPLICANT: Iacovitti, Lorraine
; APPLICANT: Kessler, Mark
; TITLE OF INVENTION: The Human Tyrosine Hydroxylase Promoter
; FILE REFERENCE: IAC01.NP001
; CURRENT APPLICATION NUMBER: US/09/942,325A
; CURRENT FILING DATE: 2001-08-29
```

```
gggtg.rnpb

; PRIOR APPLICATION NUMBER: 60/228931
; PRIOR FILING DATE: 2000-02-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-942-325A-5

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      10 GGGTG 6

RESULT 20
US-09-816-763-110/c
; Sequence 110, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; NAME/KEY: misc binding
; LOCATION: (0)...(0)
; OTHER INFORMATION: non E-Box consensus binding sequence
US-09-816-763-110

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
Db      7 GGGTG 3

RESULT 21
US-09-772-719-19/c
; Sequence 19, Application US/09772719
; Patent No. US20020137910A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
```

;  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: AP-2 transcription factor  
US-09-772-719-19

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 10 GGGTG 6

RESULT 22  
US-09-772-719-20/c  
; Sequence 20, Application US/09772719  
; Patent No. US20020137910A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994

;  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; DESCRIPTION: initiator (Inr) element  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-09-772-719-20

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 6 GGGTG 2

RESULT 23  
US-09-966-277-63/c  
; Sequence 63, Application US/09966277  
; Patent No. US20020169306A1  
; GENERAL INFORMATION:  
; APPLICANT: KITAZATO, Kaio  
; APPLICANT: SHU, Tsugumine  
; APPLICANT: KUNA, Hidekazu  
; APPLICANT: UEDA, Yasuji  
; APPLICANT: ASAKAWA, Makoto  
; APPLICANT: HASEGAWA, Mamoru  
; APPLICANT: IIDA, Akihiro  
; APPLICANT: TOKITOU, Fumino  
; APPLICANT: HIRATA, Takahiro  
; APPLICANT: TOKUSUMI, Tsuyoshi  
; APPLICANT: INOUE, Makoto  
; TITLE OF INVENTION: ENVELOPE GENE-DEFICIENT PARAMYXOVIRUS  
; FILE REFERENCE: 50026/028001  
; CURRENT APPLICATION NUMBER: US/09/966,277  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/03195  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: JP 2001/283451  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: JP 11/200739  
; PRIOR FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-277-63

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 9 GGGTG 5

## RESULT 24

US-09-961-700A-48  
; Sequence 48, Application US/09961700A  
; Publication No. US20020187482A1  
; GENERAL INFORMATION:  
; APPLICANT: Liang, Zicai  
; APPLICANT: Zhang, Hong-Yan  
; APPLICANT: Wahlestedt, Claes  
; TITLE OF INVENTION: Methods and Means of RNA Analysis  
; FILE REFERENCE: 13522-003001  
; CURRENT APPLICATION NUMBER: US/09/961,700A  
; CURRENT FILING DATE: 2002-07-23  
; PRIOR APPLICATION NUMBER: 60/235,029  
; PRIOR FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 71  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated oligonucleotide  
US-09-961-700A-48

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 3 GGGTG 7

## RESULT 25

US-09-916-228-3/c  
; Sequence 3, Application US/09916228  
; Publication No. US20030008290A1  
; GENERAL INFORMATION:  
; APPLICANT: Velculescu, Victor  
; APPLICANT: Sparks, Andrew  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Vogelstein, Bert  
; TITLE OF INVENTION: Serial analysis of transcript expression  
; TITLE OF INVENTION: using long tags  
; FILE REFERENCE: 001107,00172  
; CURRENT APPLICATION NUMBER: US/09/916,228  
; CURRENT FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: 60/221,556  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: 60/233,431  
; PRIOR FILING DATE: 2000-09-18  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: tag or tag concatamer  
US-09-916-228-3

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 6 GGGTG 2

## RESULT 26

US-09-799-880-7/c

; Sequence 7, Application US/09799880  
; Publication No. US20030014799P1  
; GENERAL INFORMATION:  
; APPLICANT: Kumar, Sushil  
; APPLICANT: Gupta, Ritika  
; APPLICANT: Sastry, Kakaraparthi  
; APPLICANT: Banerjee, Suchitra  
; APPLICANT: Mallavarapu, Gopal  
; APPLICANT: Ramesh, Srinivas  
; APPLICANT: Shasany, Ajit  
; APPLICANT: Darokar, Mahendra  
; APPLICANT: Khanuja, Suman  
; TITLE OF INVENTION: A NOVEL ROSE SCENTED GERANIUM PELARCONIUM GRAVEOLENS PLANT 'SARAL'  
; FILE REFERENCE: 2734-102  
; CURRENT APPLICATION NUMBER: US/09/799,880  
; CURRENT FILING DATE: 2001-03-07  
; NUMBER OF SEQ ID NOS: 20  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 7  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-799-880-7

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 5 GGGTG 1

## RESULT 27

US-09-966-930-63/c  
; Sequence 63, Application US/09966930  
; Publication No. US20030022376A1  
; GENERAL INFORMATION:  
; APPLICANT: KITAZATO, Kaio  
; APPLICANT: SHU, Tsugumine  
; APPLICANT: KUNA, Hidekazu  
; APPLICANT: UEDA, Yasuji  
; APPLICANT: ASAKAWA, Makoto  
; APPLICANT: HASEGAWA, Mamoru  
; APPLICANT: IIDA, Akihiro  
; APPLICANT: HIRATA, Takahiro  
; APPLICANT: INOUE, Makoto  
; TITLE OF INVENTION: PARAMYXOVIRUS-DERIVED RNP  
; FILE REFERENCE: 50026/029001  
; CURRENT APPLICATION NUMBER: US/09/966,930  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/03194  
; PRIOR FILING DATE: 2000-05-18  
; PRIOR APPLICATION NUMBER: JP 2001/283451  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: JP 11/200740  
; PRIOR FILING DATE: 1999-05-18  
; NUMBER OF SEQ ID NOS: 64  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Sequence  
US-09-966-930-63

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 9 GGGTG 5

## RESULT 28

US-09-846-033B-144  
; Sequence 144, Application US/09846033B  
; Publication No. US20030044404A1  
; GENERAL INFORMATION:  
; APPLICANT: Rebar, Edward  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Liu, Qiang  
; APPLICANT: Liu, Pei-Qi  
; APPLICANT: Wolffe, Alan  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric  
; APPLICANT: Sangamo BioSciences, Inc.  
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc  
; FILE REFERENCE: 019496-005820US  
; CURRENT APPLICATION NUMBER: US/09/846,033B  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 09/733,604  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 09/736,083  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 144  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: target  
US-09-846-033B-144

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 3 GGGTG 7

## RESULT 29

US-09-846-033B-145  
; Sequence 145, Application US/09846033B  
; Publication No. US20030044404A1  
; GENERAL INFORMATION:  
; APPLICANT: Rebar, Edward  
; APPLICANT: Jamieson, Andrew  
; APPLICANT: Liu, Qiang  
; APPLICANT: Liu, Pei-Qi  
; APPLICANT: Wolffe, Alan  
; APPLICANT: Eisenberg, Stephen P.  
; APPLICANT: Jarvis, Eric  
; APPLICANT: Sangamo BioSciences, Inc.  
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc  
; FILE REFERENCE: 019496-005820US  
; CURRENT APPLICATION NUMBER: US/09/846,033B  
; CURRENT FILING DATE: 2001-04-30  
; PRIOR APPLICATION NUMBER: US 09/733,604  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 09/736,083  
; PRIOR FILING DATE: 2000-12-12  
; NUMBER OF SEQ ID NOS: 252  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 145  
; LENGTH: 10  
; TYPE: DNA

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 3 GGGTG 7

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: target  
US-09-846-033B-145

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 3 GGGTG 7

## RESULT 30

US-09-967-237-20/c  
; Sequence 20, Application US/09967237  
; Publication No. US20030049828A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; FILE REFERENCE: D-0021.SB-2  
; CURRENT APPLICATION NUMBER: US/09/967,237  
; CURRENT FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: 09/178,115  
; PRIOR FILING DATE: 1998-10-23  
; NUMBER OF SEQ ID NOS: 116  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: HUMAN  
; OTHER INFORMATION: target  
US-09-967-237-20

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 6 GGGTG 2

## RESULT 31

US-09-916-466-116/c  
; Sequence 116, Application US/09916466  
; Publication No. US20030064945A1  
; GENERAL INFORMATION:  
; APPLICANT: Ribozyme Pharmaceuticals, Inc.  
; APPLICANT: Akhtar, Saghir  
; APPLICANT: McSwiggen, Jim  
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or conditions Related to Epidermal Growth Factor Receptors  
; FILE REFERENCE: MBH00-958-J (400/032)  
; CURRENT APPLICATION NUMBER: US/09/916,466  
; CURRENT FILING DATE: 2001-07-25  
; NUMBER OF SEQ ID NOS: 446  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 116  
; LENGTH: 10  
; TYPE: RNA  
; ORGANISM: Homo sapiens  
; OTHER INFORMATION: target  
US-09-916-466-116

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||||  
Db 10 GGGTG 6



```
RESULT 32
US-09-916-466-125/c
; Sequence 125, Application US/09916466
; Publication No. US20030064945A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Akhtar, Saghir
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to Growth Factor Receptors
; FILE REFERENCE: MBH00-958-J (400/032)
; CURRENT APPLICATION NUMBER: US/09/916,466
; CURRENT FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 125
; LENGTH: 10
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-916-466-125

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
        |||||
Db      9 GGGTG 5

RESULT 33
US-09-990-186-97
; Sequence 97, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-97

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
        |||||
Db      5 GGGTG 9

RESULT 34
US-09-990-186-584
; Sequence 584, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
```

```
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 584
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-584

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
        |||||
Db      2 GGGTG 6

RESULT 35
US-09-990-186-626
; Sequence 626, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-626

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGTG 5
        |||||
Db      3 GGGTG 7

RESULT 36
US-09-990-186-1287
; Sequence 1287, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1287
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-1287
```

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|  
|  
|  
|  
|  
Db 3 GGGTG 7

RESULT 37  
US-09-990-186-1329  
; Sequence 1329, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1329  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1329

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|  
|  
|  
|  
|  
Db 6 GGGTG 10

RESULT 38  
US-09-990-186-1339  
; Sequence 1339, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1339  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1339

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|  
|  
|  
|  
|  
Db 6 GGGTG 10

RESULT 39

US-09-990-186-1645  
; Sequence 1645, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1645  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1645

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|  
|  
|  
|  
|  
Db 2 GGGTG 6

RESULT 40  
US-09-990-186-1646  
; Sequence 1646, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1646  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1646

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|  
|  
|  
|  
|  
Db 2 GGGTG 6

RESULT 41  
US-09-990-186-1660  
; Sequence 1660, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1660  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1660

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||  
Db 5 GGGTG 9

RESULT 42  
US-09-990-186-1669  
; Sequence 1669, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1669  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1669

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||  
Db 3 GGGTG 7

RESULT 43  
US-09-990-186-1670  
; Sequence 1670, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1670  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1670

Query Match 100.0%; Score 5; DB 10; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||  
Db 3 GGGTG 7

RESULT 44  
US-09-979-593-43  
; Sequence 43, Application US/09979593  
; Publication No. US20030082555A1  
; GENERAL INFORMATION:  
; APPLICANT: Genaisance Pharmaceuticals, Inc.  
; APPLICANT: Chew, Anne  
; APPLICANT: Choi, Julie Y  
; APPLICANT: Denton, R. Rex  
; APPLICANT: Klem, Stefanie B  
; APPLICANT: Lee, Helen H  
; APPLICANT: Nandabalan, Krishnan  
; TITLE OF INVENTION: HAPLOTYPES OF THE ICAM2 GENE  
; FILE REFERENCE: MMH-0425 PCT ICAM2  
; CURRENT APPLICATION NUMBER: US/09/979,593  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: PCT/US01/14714  
; PRIOR FILING DATE: 2001-05-07  
; PRIOR APPLICATION NUMBER: 60/201,946  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 83  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 43  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-979-593-43

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||  
Db 3 GGGTG 7

RESULT 45  
US-09-989-994-97  
; Sequence 97, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 97  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-97

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
|||

```
Db          5 GGGTG 9

RESULT 46
US-09-989-994-584
; Sequence 584, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 584
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-584

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGTG 5
           |||||
Db          2 GGGTG 6

RESULT 47
US-09-989-994-626
; Sequence 626, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 626
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-626

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGTG 5
           |||||
Db          3 GGGTG 7

RESULT 48
US-09-989-994-1287
; Sequence 1287, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
```

```
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1287
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1287

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGTG 5
           |||||
Db          3 GGGTG 7

RESULT 49
US-09-989-994-1329
; Sequence 1329, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1329
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1329

Query Match          100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GGGTG 5
           |||||
Db          6 GGGTG 10

RESULT 50
US-09-989-994-1339
; Sequence 1339, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1339
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
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OTHER INFORMATION: DNA  
US-09-989-994-1339

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGTG 5  
Db 6 GGGTG 10

Search completed: January 7, 2005, 11:31:28  
Job time : 272.2 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 03:37:26 ; Search time 517 Seconds  
(without alignments)  
457.347 Million cell updates/sec

Title: GTGGG

Perfect score: 5

Sequence: 1 gt999 5

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 1774806

Minimum DB seq length: 10

Maximum DB seq length: 50

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : GenEmbl.\*

1: gb\_ba.\*

2: gb\_hcg.\*

3: gb\_in.\*

4: gb\_on.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_atg.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C	3	5	100.0	10	6	A57562 Sequence 54
C	4	5	100.0	10	6	A76253 Sequence 24
C	5	5	100.0	10	6	AR016245 Sequence
C	6	5	100.0	10	6	AR017948 Sequence
C	7	5	100.0	10	6	AR017953 Sequence
C	8	5	100.0	10	6	AR020527 Sequence
C	9	5	100.0	10	6	AR030206 Sequence
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c 421	5	100.0	11	6	AX190769	Sequence	AX190769	Sequence	C 493	5	100.0	11	6	AX624473	Sequence	AX624473	Sequence
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c 423	5	100.0	11	6	AX190808	Sequence	AX190808	Sequence	C 495	5	100.0	11	6	AX624558	Sequence	AX624558	Sequence
c 424	5	100.0	11	6	AX190809	Sequence	AX190809	Sequence	C 496	5	100.0	11	6	AX624576	Sequence	AX624576	Sequence
c 425	5	100.0	11	6	AX190812	Sequence	AX190812	Sequence	C 497	5	100.0	11	6	AX624736	Sequence	AX624736	Sequence
c 426	5	100.0	11	6	AX190813	Sequence	AX190813	Sequence	C 498	5	100.0	11	6	AX624845	Sequence	AX624845	Sequence
c 427	5	100.0	11	6	AX190814	Sequence	AX190814	Sequence	C 499	5	100.0	11	6	AX625098	Sequence	AX625098	Sequence
c 428	5	100.0	11	6	AX225317	Sequence	AX225317	Sequence	500	5	100.0	11	6	AX625171	Sequence	AX625171	Sequence
c 429	5	100.0	11	6	AX380965	Sequence	AX380965	Sequence									
c 430	5	100.0	11	6	AX393163	Sequence	AX393163	Sequence									
c 431	5	100.0	11	6	AX393207	Sequence	AX393207	Sequence									
c 432	5	100.0	11	6	AX470440	Sequence	AX470440	Sequence									
c 433	5	100.0	11	6	AX470456	Sequence	AX470456	Sequence									
c 434	5	100.0	11	6	AX470504	Sequence	AX470504	Sequence									
c 435	5	100.0	11	6	AX470607	Sequence	AX470607	Sequence									
c 436	5	100.0	11	6	AX470768	Sequence	AX470768	Sequence									
c 437	5	100.0	11	6	AX470809	Sequence	AX470809	Sequence									
c 438	5	100.0	11	6	AX470837	Sequence	AX470837	Sequence									
c 439	5	100.0	11	6	AX470909	Sequence	AX470909	Sequence									
c 440	5	100.0	11	6	AX470920	Sequence	AX470920	Sequence									
c 441	5	100.0	11	6	AX470974	Sequence	AX470974	Sequence									
c 442	5	100.0	11	6	AX470983	Sequence	AX470983	Sequence									
c 443	5	100.0	11	6	AX470999	Sequence	AX470999	Sequence									
c 444	5	100.0	11	6	AX471018	Sequence	AX471018	Sequence									
c 445	5	100.0	11	6	AX471059	Sequence	AX471059	Sequence									
c 446	5	100.0	11	6	AX471115	Sequence	AX471115	Sequence									
c 447	5	100.0	11	6	AX471135	Sequence	AX471135	Sequence									
c 448	5	100.0	11	6	AX471214	Sequence	AX471214	Sequence									
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ALIGNMENTS

RESULT 1

A08938/c

LOCUS

A08938

DEFINITION

H.sapiens factor recognition motif in promoter.

ACCESSION

A08938

VERSION

A08938.1

KEYWORDS

10 bp DNA linear PAT 27-AUG-1993

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 10)

AUTHORS

Taniguchi, T.

TITLE

Improvements in and relating to the regulation of gene expression

JOURNAL

Patent: EP 0374503-A 5 27-JUN-1990;

FEATURES

Location/Qualifiers

source

1..10

/organism="Homo sapiens"

/mol\_type="unassigned DNA"

/db\_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 4.6e+07;

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 9 GTGGG 5

RESULT 2
A57560/c
LOCUS A57560 10 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 52 from Patent WO9632483.
ACCESSION A57560
VERSION A57560.1 GI:4530653
KEYWORDS .
SOURCE .
ORGANISM .
REFERENCE 1
AUTHORS Masucci, M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 52 17-OCT-1996;
COMMENT MASUCCI MARIA GRAZIA (SE)
FEATURES Other publication AU 5284296 961030.
          Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 7 GTGGG 3

RESULT 3
A57562/c
LOCUS A57562 10 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 54 from Patent WO9632483.
ACCESSION A57562
VERSION A57562.1 GI:4530654
KEYWORDS .
SOURCE .
ORGANISM .
REFERENCE 1
AUTHORS Masucci, M.G.
TITLE IMMUNE-EVADING PROTEINS
JOURNAL Patent: WO 9632483-A 54 17-OCT-1996;
COMMENT MASUCCI MARIA GRAZIA (SE)
FEATURES Other publication AU 5284296 961030.
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 7 GTGGG 3

RESULT 4
A76253
LOCUS A76253 10 bp DNA linear PAT 19-OCT-1999
DEFINITION Sequence 24 from Patent WO9319181.
ACCESSION A76253
VERSION A76253.1 GI:6088352
KEYWORDS .
SOURCE .
ORGANISM .
REFERENCE 1
AUTHORS Sandal, N. and Marcker, K.
TITLE BIOLOGICAL MATERIAL
JOURNAL Patent: WO 9319181-A 24 30-SEP-1993;
FEATURES SANDOZ AG (AT); SANDOZ AG (DE)
          Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"

ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 6 GTGGG 10

RESULT 5
AR016245/c
LOCUS AR016245 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 13 from patent US 5776683.
ACCESSION AR016245
VERSION AR016245.1 GI:3972522
KEYWORDS .
SOURCE .
ORGANISM .
REFERENCE 1
AUTHORS Smith, H.S. and Chen, L.-C.
TITLE Methods for identifying genes amplified in cancer cells
JOURNAL Patent: US 5776683-A 13 07-JUL-1998;
FEATURES Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 10 GTGGG 6

RESULT 6
AR017948
LOCUS AR017948 10 bp DNA linear PAT 05-DEC-1998
DEFINITION Sequence 13 from patent US 5780273.
ACCESSION AR017948
VERSION AR017948.1 GI:3973551
KEYWORDS .
SOURCE .
ORGANISM .
REFERENCE 1
AUTHORS Burg, J. Lawrence.
TITLE Insertion elements and amplifiable nucleic acids
JOURNAL Patent: US 5780273-A 13 14-JUL-1998;
FEATURES Location/Qualifiers

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source      1..10
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/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      4 GTGGG 8

RESULT 7
AR017953 LOCUS      AR017953      10 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION      Sequence 18 from patent US 5780273.
ACCESSION      AR017953
VERSION      AR017953.1 GI:3973556
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Burg,J.Lawrence.
TITLE      Insertion elements and amplifiable nucleic acids
JOURNAL      Patent: US 5780273-A 18 14-JUL-1998;
FEATURES
source      Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      6 GTGGG 10

RESULT 8
AR020527/c LOCUS      AR020527      10 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION      Sequence 3 from patent US 5789174.
ACCESSION      AR020527
VERSION      AR020527.1 GI:3975142
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Mouton,C., Guillot,E. and Menard,C.
TITLE      Detection of periodontal pathogens including bacteroides forsythus,
porphyromonas gingivalis, prevotella intermedia and prevotella
nigrescens
JOURNAL      Patent: US 5789174-A 3 04-AUG-1998;
FEATURES
source      Location/Qualifiers
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/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      10 GTGGG 6

RESULT 9
AR030206 LOCUS      AR030206      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 17 from patent US 5861246.
ACCESSION      AR030206
VERSION      AR030206.1 GI:5943420
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE      Multiple selection process for binding sites of DNA-binding
proteins
JOURNAL      Patent: US 5861246-A 17 19-JAN-1999;
FEATURES
source      Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      4 GTGGG 8

RESULT 10
AR030217 LOCUS      AR030217      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 28 from patent US 5861246.
ACCESSION      AR030217
VERSION      AR030217.1 GI:5943431
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE      Multiple selection process for binding sites of DNA-binding
proteins
JOURNAL      Patent: US 5861246-A 28 19-JAN-1999;
FEATURES
source      Location/Qualifiers
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ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      1 GTGGG 5

RESULT 11
AR030218 LOCUS      AR030218      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION      Sequence 29 from patent US 5861246.
ACCESSION      AR030218
VERSION      AR030218.1 GI:5943432
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Weissman,S.M., Nallur,G.N. and Kulkarni,P.
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TITLE      Multiple selection process for binding sites of DNA-binding
JOURNAL    Patent: US 5861246-A 29 19-JAN-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GTGGG 5
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Db      1 GTGGG 5

RESULT 12
AR030234 LOCUS      AR030234      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 45 from patent US 5861246.
ACCESSION AR030234
VERSION AR030234.1 GI:5943448
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE      Multiple selection process for binding sites of DNA-binding
            proteins
JOURNAL    Patent: US 5861246-A 45 19-JAN-1999;
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"
ORIGIN
Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GTGGG 5
        |||||
Db      1 GTGGG 5

RESULT 13
AR030237 LOCUS      AR030237      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 48 from patent US 5861246.
ACCESSION AR030237
VERSION AR030237.1 GI:5943451
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE      Multiple selection process for binding sites of DNA-binding
            proteins
JOURNAL    Patent: US 5861246-A 48 19-JAN-1999;
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GTGGG 5
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Db      1 GTGGG 5

TITLE      Multiple selection process for binding sites of DNA-binding
JOURNAL    Patent: US 5861246-A 29 19-JAN-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GTGGG 5
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Db      1 GTGGG 5

RESULT 14
AR030238 LOCUS      AR030238      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 49 from patent US 5861246.
ACCESSION AR030238
VERSION AR030238.1 GI:5943452
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Weissman,S.M., Nallur,G.N. and Kulkarni,P.
TITLE      Multiple selection process for binding sites of DNA-binding
            proteins
JOURNAL    Patent: US 5861246-A 49 19-JAN-1999;
FEATURES   Location/Qualifiers
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GTGGG 5
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Db      1 GTGGG 5

RESULT 15
AR032136/c LOCUS      AR032136      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5866699.
ACCESSION AR032136
VERSION AR032136.1 GI:5946425
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 10)
AUTHORS      Smyth,A.P.
TITLE      Oligonucleotides with anti-MDR-1 gene activity
JOURNAL    Patent: US 5866699-A 6 02-FEB-1999;
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"
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Query Match      100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 GTGGG 5
        |||||
Db      1 GTGGG 5

RESULT 16
AR049904 LOCUS      AR049904      10 bp      DNA      linear      PAT 29-SEP-1999
DEFINITION Sequence 9 from patent US 5824787.
ACCESSION AR049904
VERSION AR049904.1 GI:5971896
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unknown.
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Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Singer,P.A.
TITLE Polynucleotide sizing reagent
JOURNAL Patent: US 5824787-A 9 20-OCT-1998;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 6 GTGGG 10

RESULT 17
LOCUS AR069288/c 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 27 from patent US 5891631.
ACCESSION AR069288
VERSION AR069288.1 GI:7220176
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Goldstein,J.L., Brown,M.S., Briggs,M.R. and Wang,X.
TITLE Methods relating tosterol regulatory element binding proteins
JOURNAL Patent: US 5891631-A 27 06-APR-1999;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 10 GTGGG 6

RESULT 18
LOCUS AR069301 10 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 43 from patent US 5891631.
ACCESSION AR069301
VERSION AR069301.1 GI:7220189
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Goldstein,J.L., Brown,M.S., Briggs,M.R. and Wang,X.
TITLE Methods relating tosterol regulatory element binding proteins
JOURNAL Patent: US 5891631-A 43 06-APR-1999;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 8 GTGGG 4

Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Singer,P.A.
TITLE Polynucleotide sizing reagent
JOURNAL Patent: US 5824787-A 9 20-OCT-1998;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 6 GTGGG 10

RESULT 19
LOCUS AR074300 10 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 108 from patent US 5952490.
ACCESSION AR074300
VERSION AR074300.1 GI:10001055
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hanecak,R.C., Anderson,K.P., Bennett,C.Frank., Chiang,M.-Y., Brown-Driver,V.D., Ecker,D.J., Vickers,T.A., Wyatt,J.R. and Imbach,J.Louis.
TITLE Oligonucleotides having a conserved G4 core sequence
JOURNAL Patent: US 5952490-A 108 14-SEP-1999;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 3 GTGGG 7

RESULT 20
LOCUS AR074448/c 10 bp DNA linear PAT 28-AUG-2000
DEFINITION Sequence 19 from patent US 5955075.
ACCESSION AR074448
VERSION AR074448.1 GI:10001203
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Method of inhibiting tumor growth using antibodies to MN protein
JOURNAL Patent: US 5955075-A 19 21-SEP-1999;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 21
LOCUS AR081128/c 10 bp DNA linear PAT 31-AUG-2000
DEFINITION Sequence 19 from patent US 5972353.
ACCESSION AR081128
VERSION AR081128.1 GI:10007856
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides
JOURNAL Patent: US 592353-A 19 26-OCT-1999;
FEATURES
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    Best Local Similarity 100.0%; Pred. No. 4.6e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 22
LOCUS AR085325/c
DEFINITION Sequence 19 from patent US 5981711.
ACCESSION AR085325
VERSION AR085325.1 GI:10012094
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 19 09-NOV-1999;
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    Best Local Similarity 100.0%; Pred. No. 4.6e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 23
LOCUS AR088073/c
DEFINITION Sequence 19 from patent US 5989838.
ACCESSION AR088073
VERSION AR088073.1 GI:10014836
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 19 23-NOV-1999;
FEATURES
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    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 24
LOCUS AR092703
DEFINITION Sequence 15 from patent US 5998193.
ACCESSION AR092703
VERSION AR092703.1 GI:10019455
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
    embedded ribozymes and compositions thereof
JOURNAL Patent: US 5998193-A 15 07-DEC-1999;
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    Best Local Similarity 100.0%; Pred. No. 4.6e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 5 GTGGG 9

RESULT 25
LOCUS AR098894/c
DEFINITION Sequence 30 from patent US 6077685.
ACCESSION AR098894
VERSION AR098894.1 GI:12808660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofater,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE Tumor suppressor merlin and antibodies thereof
JOURNAL Patent: US 6077685-A 30 20-JUN-2000;
FEATURES
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    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 26
LOCUS AR102396/c
DEFINITION Sequence 21 from patent US 6083923.
ACCESSION AR102396
VERSION AR102396.1 GI:12813194
KEYWORDS
SOURCE Unknown.

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Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 24
LOCUS AR092703
DEFINITION Sequence 15 from patent US 5998193.
ACCESSION AR092703
VERSION AR092703.1 GI:10019455
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
    embedded ribozymes and compositions thereof
JOURNAL Patent: US 5998193-A 15 07-DEC-1999;
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    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 5 GTGGG 9

RESULT 25
LOCUS AR098894/c
DEFINITION Sequence 30 from patent US 6077685.
ACCESSION AR098894
VERSION AR098894.1 GI:12808660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Trofater,J.A., MacCollin,M.M. and Gusella,J.F.
TITLE Tumor suppressor merlin and antibodies thereof
JOURNAL Patent: US 6077685-A 30 20-JUN-2000;
FEATURES
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    Query Match      100.0%; Score 5; DB 6; Length 10;
    Best Local Similarity 100.0%; Pred. No. 4.6e+07;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 26
LOCUS AR102396/c
DEFINITION Sequence 21 from patent US 6083923.
ACCESSION AR102396
VERSION AR102396.1 GI:12813194
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hardee,G.E., Geary,R.S., Levin,A., Templin,M.V., Howard,R. and
Mehta,R.C.
TITLE Liposomal oligonucleotide compositions for modulating RAS gene
expression
JOURNAL Patent: US 6083923-A 21 04-JUL-2000;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 8 GTGGG 4
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RESULT 27
LOCUS ARI02399/c 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 24 from patent US 6083923.
ACCESSION ARI02399
VERSION ARI02399.1 GI:12813197
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Hardee,G.E., Geary,R.S., Levin,A., Templin,M.V., Howard,R. and
Mehta,R.C.
TITLE Liposomal oligonucleotide compositions for modulating RAS gene
expression
JOURNAL Patent: US 6083923-A 24 04-JUL-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 8 GTGGG 4
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RESULT 28
LOCUS ARI04232/c 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 19 from patent US 6093548.
ACCESSION ARI04232
VERSION ARI04232.1 GI:12816940
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Detection and quantitation of MN-specific antibodies
JOURNAL Patent: US 6093548-A 19 25-JUL-2000;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.6e+07;
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Qy 1 GTGGG 5
Db 8 GTGGG 4
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RESULT 29
LOCUS ARI06687 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 15 from patent US 6107078.
ACCESSION ARI06687
VERSION ARI06687.1 GI:12821217
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
embedded ribozymes and compositions thereof
JOURNAL Patent: US 6107078-A 15 22-AUG-2000;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
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Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 5 GTGGG 9
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RESULT 30
LOCUS ARI07349 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 38 from patent US 6109776.
ACCESSION ARI07349
VERSION ARI07349.1 GI:12822836
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Haas,J.
TITLE Method and system for computationally identifying clusters within a
set of sequences
JOURNAL Patent: US 6109776-A 38 29-AUG-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.6e+07;
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Qy 1 GTGGG 5
Db 2 GTGGG 6
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RESULT 31
LOCUS ARI19493 10 bp DNA linear PAT 16-MAY-2001
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DEFINITION Sequence 16 from patent US 6153382.
ACCESSION AR119493
VERSION AR119493.1 GI:14102192
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Karn,J., Gait,M.John., Heaphy,S. and Dingwall,C.
TITLE Viral growth inhibition
JOURNAL Patent: US 6153382-A 16 28-NOV-2000;
FEATURES
    Location/Qualifiers
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Query Match          100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 2 GTGGG 6

RESULT 32
LOCUS AR137926
DEFINITION Sequence 2 from patent US 6197580.
ACCESSION AR137926
VERSION AR137926.1 GI:14479435
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Susulic,V.S. and Dusic,B.
TITLE Transcriptional regulation of the human .beta.3-adrenergic receptor
JOURNAL Patent: US 6197580-A 2 06-MAR-2001;
FEATURES
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Query Match          100.0%; Score 5; DB 6; Length 10;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 3 GTGGG 7

RESULT 33
LOCUS AR143496/c
DEFINITION Sequence 19 from patent US 6204370.
ACCESSION AR143496
VERSION AR143496.1 GI:15104782
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 19 20-MAR-2001;
FEATURES
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Qy 1 GTGGG 5
Db 3 GTGGG 7

RESULT 34
LOCUS AR168826
DEFINITION Sequence 52 from patent US 6288042.
ACCESSION AR168826
VERSION AR168826.1 GI:17904948
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL Patent: US 6288042-A 52 11-SEP-2001;
FEATURES
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Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 35
LOCUS AR175405/c
DEFINITION Sequence 128 from patent US 6309823.
ACCESSION AR175405
VERSION AR175405.1 GI:17916704
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A., Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes for analyzing biotransformation genes
JOURNAL Patent: US 6309823-A 128 30-OCT-2001;
FEATURES
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Qy 1 GTGGG 5
Db 9 GTGGG 5

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ORIGIN
Query Match          100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 34
LOCUS AR168826
DEFINITION Sequence 52 from patent US 6288042.
ACCESSION AR168826
VERSION AR168826.1 GI:17904948
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Rando,R.F., Ojwaug,J.O., Hogan,M.E., Wallace,T.L. and Cossum,P.A.
TITLE Anti-viral guanosine-rich tetrad forming oligonucleotides
JOURNAL Patent: US 6288042-A 52 11-SEP-2001;
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Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 35
LOCUS AR175405/c
DEFINITION Sequence 128 from patent US 6309823.
ACCESSION AR175405
VERSION AR175405.1 GI:17916704
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 10)
AUTHORS Cronin,M.T., Miyada,C.G., Hubbell,E.A., Chee,M., Fodor,S.P.A., Huang,X.C., Lipshutz,R.J., Lobban,P.E., Morris,M.S. and Sheldon,E.L.
TITLE Arrays of nucleic acid probes for analyzing biotransformation genes
JOURNAL Patent: US 6309823-A 128 30-OCT-2001;
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Qy 1 GTGGG 5
Db 9 GTGGG 5

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RESULT 36
BD225179/c
LOCUS
DEFINITION
  Use of DNA identification technique for determining gene substances
  in fermented or roasted beans and cocoa in chocolate.
ACCESSION
  BD225179
VERSION
  JP 2002529105-A/5.
KEYWORDS
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SOURCE
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ORGANISM
  unclassified.
REFERENCE
  1 (bases 1 to 10)
AUTHORS
  Petiard,V. and Crouzillat,D.
TITLE
  Use of DNA identification technique for determining gene substances
  in fermented or roasted beans and cocoa in chocolate
JOURNAL
  Patent: JP 2002529105-A 5 10-SEP-2002;
  SOCIETE DES PRODUITS NESTLE SA
COMMENT
  OS Theobroma cacao L. (cacao)
  PN JP 2002529105-A/5
  PD 10-SEP-2002
  PF 29-OCT-1999 JP 2000581244
  PR 05-NOV-1998 EP 98121043.8
  PT VINCENT PETIARD,DOMINIQUE CROUZILLAT
  PC C12N15/09,C12Q1/68,C12N15/00
  CC Use of DNA identification technique for determining gene CC
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  CC fermented or roasted beans and cocoa in chocolate FH Key
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  Qy 1 GTGGG 5
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RESULT 37
BD238592/c
LOCUS
DEFINITION
  Preparation and use of superior vaccines.
ACCESSION
  BD238592
VERSION
  BD238592.1 GI:33048362
KEYWORDS
  JP 2002534056-A/10.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 10)
  Roberts,B.L. and Shankara,S.
  Preparation and use of superior vaccines
  Patent: JP 2002534056-A 10 15-OCT-2002;
  GENZYME CORP
COMMENT
  OS Homo sapiens (human)
  PN JP 2002534056-A/10
  PD 15-OCT-2002
  PF 18-JUN-1999 JP 2000554749
  PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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  19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089994,19-JUN-1998 US 60/089833 PR
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  19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
  08-DEC-1998 US 60/111715
  PI BRUCE L ROBERTS,SRINIVAS SHANKARA
  PC C12N15/09,C12N15/05,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
  C12N1/19,
  C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
  PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC

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  Qy 1 GTGGG 5
  Db 9 GTGGG 5

RESULT 38
BD238727/c
LOCUS
DEFINITION
  Preparation and use of superior vaccines.
ACCESSION
  BD238727
VERSION
  BD238727.1 GI:33048497
KEYWORDS
  JP 2002534056-A/145.
SOURCE
  Homo sapiens (human)
ORGANISM
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  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 10)
  Roberts,B.L. and Shankara,S.
  Preparation and use of superior vaccines
  Patent: JP 2002534056-A 145 15-OCT-2002;
  GENZYME CORP
COMMENT
  OS Homo sapiens (human)
  PN JP 2002534056-A/145
  PD 15-OCT-2002
  PF 18-JUN-1999 JP 2000554749
  PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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  19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
  19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
  08-DEC-1998 US 60/111715
  PI BRUCE L ROBERTS,SRINIVAS SHANKARA
  PC C12N15/09,C12N15/05,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
  C12N1/19,
  C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
  PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC

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G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
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ORIGIN
Query Match 100.0%; Score 5; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+07;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 8 GTGGG 4
RESULT 39
BD238733
LOCUS BD238733 10 bp DNA linear PAT 17-JUL-2003
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238733
VERSION BD238733.1 GI:33048503
KEYWORDS JP 2002534056-A/151.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 151 15-OCT-2002;
GENZYME CORP
COMMENT OS Homo sapiens (human)
PN JP 2002534056-A/151
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
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19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,
PC C12N15/00,C12N5/00,C12N15/00
CC Preparation and use of superior vaccines
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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238817
VERSION BD238817.1 GI:33048587
KEYWORDS JP 2002534056-A/235.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 10)
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 235 15-OCT-2002;
GENZYME CORP
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REFERENCE	Roberts,B.L. and Shankara,S.									
AUTHORS	Preparation and use of superior vaccines									
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REFERENCE
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
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JOURNAL Patent: JP 2002534056-A 319 15-OCT-2002;
GENZYME CORP
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VERSION BD238903.1 GI:33048673
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1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
AUTHORS
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 321 15-OCT-2002;
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TITLE     Preparation and use of superior vaccines
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ACCESSION  BD238992
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AUTHORS   Roberts,B.L. and Shankara,S.

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GenCore version 5.1.6  
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9	5	100.0	10	2	AaQ61967 Phospholi
10	5	100.0	10	2	AaQ63558 C11 3' sp
11	5	100.0	10	2	AaQ63553 C22 5' sp
12	5	100.0	10	2	AaQ79252 Guanosine
13	5	100.0	10	2	AaQ73141 Mutant ra
14	5	100.0	10	2	AaQ73134 TAF-1 bin
C 15	5	100.0	10	2	AaX32620 Anticance
16	5	100.0	10	2	AaX32638 Anticance
C 17	5	100.0	10	2	AaX32638 Anticance
18	5	100.0	10	2	AaQ96493 HIV-1 NL4
19	5	100.0	10	2	AaQ96488 HIV-1 NL4
20	5	100.0	10	2	AaQ96596 HIV-1 NL4
21	5	100.0	10	2	AaQ96600 HIV-1 NL4

22	5	100.0	10	2	AAQ96492 HIV-1 NL4
C 23	5	100.0	10	2	AAQ96491 HIV-1 NL4
C 24	5	100.0	10	2	AAQ97088 HIV-1 NL4
25	5	100.0	10	2	AAQ96601 HIV-1 NL4
C 26	5	100.0	10	2	AAQ97086 HIV-1 NL4
C 27	5	100.0	10	2	AAQ97089 HIV-1 NL4
C 28	5	100.0	10	2	AAQ97090 HIV-1 NL4
29	5	100.0	10	2	AAQ96597 HIV-1 NL4
30	5	100.0	10	2	AAQ96490 HIV-1 NL4
31	5	100.0	10	2	AAQ96489 HIV-1 NL4
C 32	5	100.0	10	2	AAQ96599 HIV-1 NL4
C 33	5	100.0	10	2	AAQ97091 HIV-1 NL4
C 34	5	100.0	10	2	AAQ96598 HIV-1 NL4
C 35	5	100.0	10	2	AAQ97087 HIV-1 NL4
C 36	5	100.0	10	2	AAQ79835 H-ras mod
C 37	5	100.0	10	2	AAQ79834 H-ras mod
38	5	100.0	10	2	AAQ79834 H-ras mod
39	5	100.0	10	2	AAQ79863 Core-bind
40	5	100.0	10	2	AAQ79860 Core-bind
41	5	100.0	10	2	AAQ79847 Binding s
42	5	100.0	10	2	AAQ798837 Binding s
43	5	100.0	10	2	AAQ79848 Binding s
44	5	100.0	10	2	AAQ798864 Core-bind
45	5	100.0	10	2	AAQ79864 Core-bind
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C 48	5	100.0	10	2	AAQ79864 Core-bind
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C 57	5	100.0	10	2	AAQ79864 Core-bind
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83	5	100.0	10	2	AAQ79864 Core-bind
C 84	5	100.0	10	2	AAQ79864 Core-bind
C 85	5	100.0	10	2	AAQ79864 Core-bind
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C 91	5	100.0	10	2	AAQ79864 Core-bind
92	5	100.0	10	2	AAQ79864 Core-bind
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C 94	5	100.0	10	2	AAQ79864 Core-bind

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96 5 100.0 10 3 AAZ79653 Aaz79653 Human den  
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c 98 5 100.0 10 3 AAZ79668 Aaz79668 Human den  
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C 241	5	100.0	10	3	Az282897	Aaz82897	Metastati
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C 244	5	100.0	10	3	Az285227	Aaz85227	Metastati
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C 248	5	100.0	10	3	Az284106	Aaz84106	Metastati
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C 254	5	100.0	10	3	Az2893870	Aaz93870	Oligonucle
C 255	5	100.0	10	3	Az2874192	Aaz74192	Human mon
C 256	5	100.0	10	3	Az2874198	Aaz74198	Human mon
C 257	5	100.0	10	3	Az2874131	Aaz74131	Human mon
C 258	5	100.0	10	3	Az2874116	Aaz74116	Human mon
C 259	5	100.0	10	3	Az2874140	Aaz74140	Human mon
C 260	5	100.0	10	3	Az2874146	Aaz74146	Human mon
C 261	5	100.0	10	3	Az2873943	Aaz73943	Human den
C 262	5	100.0	10	3	Az2856447	Aaz56447	Human mac
C 263	5	100.0	10	3	Az2856470	Aaz56470	Human mac
C 264	5	100.0	10	3	Az2856510	Aaz56510	Human mac
C 265	5	100.0	10	3	Az2856127	Aaz56127	Human mon
C 266	5	100.0	10	3	Az2856427	Aaz56427	Human mac
C 267	5	100.0	10	3	Az2856255	Aaz56255	Human mac
C 268	5	100.0	10	3	Az2856439	Aaz56439	Human mac
C 269	5	100.0	10	3	Az2856516	Aaz56516	Human mac
C 270	5	100.0	10	3	Az2856350	Aaz56350	Human mac
C 271	5	100.0	10	3	Az2856458	Aaz56458	Human mac
C 272	5	100.0	10	3	Az2856210	Aaz56210	Human mac
C 273	5	100.0	10	3	Az2856190	Aaz56190	Human mon
C 274	5	100.0	10	3	Az2856366	Aaz56366	Human mac
C 275	5	100.0	10	3	Az2856506	Aaz56506	Human mac
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C 281	5	100.0	10	3	Az2853295	Aaz53295	Putative
C 282	5	100.0	10	3	Az2879727	Aaz79727	Human col
C 283	5	100.0	10	3	Az2879795	Aaz79795	Human cys
C 284	5	100.0	10	3	Az2879914	Aaz79914	Human den
C 285	5	100.0	10	3	Az288680	Aaz8680	Ras RNA b
C 286	5	100.0	10	3	Az288681	Aaz8681	Ras RNA b
C 287	5	100.0	10	3	Az288692	Aaz8692	Ras RNA b
C 288	5	100.0	10	3	Az288686	Aaz8686	Ras RNA b
C 289	5	100.0	10	3	Az288683	Aaz8683	Ras RNA b
C 290	5	100.0	10	3	Az28359	Aaz20359	Human eos
C 291	5	100.0	10	3	Az28312	Aaz20312	Human end
C 292	5	100.0	10	3	Az2861026	Aaz61026	Protein b
C 293	5	100.0	10	3	Az2861030	Aaz61030	Protein b
C 294	5	100.0	10	3	Az2861002	Aaz61002	Protein b
C 295	5	100.0	10	3	Az2861012	Aaz61012	Protein b
C 296	5	100.0	10	3	Az2861029	Aaz61029	Protein b
C 297	5	100.0	10	3	Az2861013	Aaz61013	Protein b
C 298	5	100.0	10	3	Az2867903	Aaz87903	Human bet
C 299	5	100.0	10	3	Az2874367	Aaz74367	Mouse tra
C 300	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly
C 301	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly
C 302	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly
C 303	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly
C 304	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly
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C 308	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly
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C 310	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly
C 311	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly
C 312	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly
C 313	5	100.0	10	4	Az2861026	Aaz61026	UCP3 poly

C 314	5	100.0	10	4	Az2863932	Aah63932	Human ubi
C 315	5	100.0	10	4	Az2863985	Aah63985	Human ubi
C 316	5	100.0	10	4	Az2864002	Aah64002	Human ubi
C 317	5	100.0	10	4	Az2864452	Aah64452	Human ubi
C 318	5	100.0	10	4	Az2864467	Aah64467	Human ubi
C 319	5	100.0	10	4	Az2863172	Aah63172	Human col
C 320	5	100.0	10	4	Az2863774	Aah63774	Human ubi
C 321	5	100.0	10	4	Az2863829	Aah63829	Human ubi
C 322	5	100.0	10	4	Az2864056	Aah64056	Human ubi
C 323	5	100.0	10	4	Az2864167	Aah64167	Human ubi
C 324	5	100.0	10	4	Az2864218	Aah64218	Human ubi
C 325	5	100.0	10	4	Az2864363	Aah64363	Human ubi
C 326	5	100.0	10	4	Az2864508	Aah64508	Human ubi
C 327	5	100.0	10	4	Az2864261	Aah64261	Human ubi
C 328	5	100.0	10	4	Az2864312	Aah64312	Human ubi
C 329	5	100.0	10	4	Az2864704	Aah64704	Human kid
C 330	5	100.0	10	4	Az2863380	Aah63380	Human kid
C 331	5	100.0	10	4	Az2864062	Aah64062	Human ubi
C 332	5	100.0	10	4	Az2864228	Aah64228	Human ubi
C 333	5	100.0	10	4	Az2864005	Aah64005	Human ubi
C 334	5	100.0	10	4	Az2864110	Aah64110	Human ubi
C 335	5	100.0	10	4	Az2864153	Aah64153	Human ubi
C 336	5	100.0	10	4	Az2864175	Aah64175	Human ubi
C 337	5	100.0	10	4	Az2864296	Aah64296	Human ubi
C 338	5	100.0	10	4	Az2864628	Aah64628	Human col
C 339	5	100.0	10	4	Az2863625	Aah63625	Human ubi
C 340	5	100.0	10	4	Az2864142	Aah64142	Human ubi
C 341	5	100.0	10	4	Az2864165	Aah64165	Human ubi
C 342	5	100.0	10	4	Az2863434	Aah63434	Human ubi
C 343	5	100.0	10	4	Az2864006	Aah64006	Human ubi
C 344	5	100.0	10	4	Az2864170	Aah64170	Human ubi
C 345	5	100.0	10	4	Az2863931	Aah63931	Human ubi
C 346	5	100.0	10	4	Az2863437	Aah63437	Human ubi
C 347	5	100.0	10	4	Az2864007	Aah64007	Human ubi
C 348	5	100.0	10	4	Az2864313	Aah64313	Human ubi
C 349	5	100.0	10	4	Az2864340	Aah64340	Human ubi
C 350	5	100.0	10	4	Az2864479	Aah64479	Human ubi
C 351	5	100.0	10	4	Az2864483	Aah64483	Human ubi
C 352	5	100.0	10	4	Az2863542	Aah63542	Human ubi
C 353	5	100.0	10	4	Az2863272	Aah63272	Human col
C 354	5	100.0	10	4	Az2857300	Aah57300	Human chr
C 355	5	100.0	10	4	Az2857302	Aah57302	Human chr
C 356	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 357	5	100.0	10	4	Az2857297	Aah57297	Human chr
C 358	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 359	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 360	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 361	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 362	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 363	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 364	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 365	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 366	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 367	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 368	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 369	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 370	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 371	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 372	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 373	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 374	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 375	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 376	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 377	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 378	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 379	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 380	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 381	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 382	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 383	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 384	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 385	5	100.0	10	4	Az2857322	Aah57322	Human chr
C 386	5	100.0	10	4	Az2857322	Aah57322	Human chr

c 387 5 100.0 10 5 AAF69621 Human IL4  
c 388 5 100.0 10 5 AAF74057 Human SLC  
c 389 5 100.0 10 5 AAF74045 Human SLC  
c 390 5 100.0 10 5 AAF74009 Human SLC  
c 391 5 100.0 10 5 ABA83159 Apolipop  
c 392 5 100.0 10 5 ABA83152 Leukocyte  
c 393 5 100.0 10 5 ABA83181 Human ova  
c 394 5 100.0 10 5 AAF37432 Yeast NOR  
c 395 5 100.0 10 5 AAF37976 Yeast NOR  
c 396 5 100.0 10 5 AAF39447 Yeast NOR  
c 397 5 100.0 10 5 AAF39820 Yeast NOR  
c 398 5 100.0 10 5 AAF40013 Yeast NOR  
c 399 5 100.0 10 5 AAF35350 Yeast NOR  
c 400 5 100.0 10 5 AAF37938 Yeast NOR  
c 401 5 100.0 10 5 AAF40211 Yeast NOR  
c 402 5 100.0 10 5 AAF42869 Yeast NOR  
c 403 5 100.0 10 5 AAF42871 Yeast NOR  
c 404 5 100.0 10 5 AAF33385 Yeast NOR  
c 405 5 100.0 10 5 AAF33917 Yeast NOR  
c 406 5 100.0 10 5 AAF34850 Yeast NOR  
c 407 5 100.0 10 5 AAF40921 Yeast NOR  
c 408 5 100.0 10 5 AAF43725 Yeast NOR  
c 409 5 100.0 10 5 AAF36503 Yeast NOR  
c 410 5 100.0 10 5 AAF37657 Yeast NOR  
c 411 5 100.0 10 5 AAF38182 Yeast NOR  
c 412 5 100.0 10 5 AAF41877 Yeast NOR  
c 413 5 100.0 10 5 AAF33958 Yeast NOR  
c 414 5 100.0 10 5 AAF35176 Yeast NOR  
c 415 5 100.0 10 5 AAF43379 Yeast NOR  
c 416 5 100.0 10 5 AAF34255 Yeast NOR  
c 417 5 100.0 10 5 AAF38950 Yeast NOR  
c 418 5 100.0 10 5 AAF40918 Yeast NOR  
c 419 5 100.0 10 5 AAF40920 Yeast NOR  
c 420 5 100.0 10 5 AAF41626 Yeast NOR  
c 421 5 100.0 10 5 AAF43293 Yeast NOR  
c 422 5 100.0 10 5 AAF43762 Yeast NOR  
c 423 5 100.0 10 5 AAF33918 Yeast NOR  
c 424 5 100.0 10 5 AAF34643 Yeast NOR  
c 425 5 100.0 10 5 AAF39821 Yeast NOR  
c 426 5 100.0 10 5 AAF40922 Yeast NOR  
c 427 5 100.0 10 5 AAF42078 Yeast NOR  
c 428 5 100.0 10 5 AAF43603 Yeast NOR  
c 429 5 100.0 10 5 AAF35838 Yeast NOR  
c 430 5 100.0 10 5 AAF36522 Yeast NOR  
c 431 5 100.0 10 5 AAF37164 Yeast NOR  
c 432 5 100.0 10 5 AAF39252 Yeast NOR  
c 433 5 100.0 10 5 AAF40919 Yeast NOR  
c 434 5 100.0 10 5 AAF42060 Yeast NOR  
c 435 5 100.0 10 5 AAF42118 Yeast NOR  
c 436 5 100.0 10 5 AAF37459 Yeast NOR  
c 437 5 100.0 10 5 AAF37691 Yeast NOR  
c 438 5 100.0 10 5 AAF42861 Yeast NOR  
c 439 5 100.0 10 5 AAF38128 Yeast NOR  
c 440 5 100.0 10 5 AAF43380 Yeast NOR  
c 441 5 100.0 10 5 AAF35354 Yeast NOR  
c 442 5 100.0 10 5 AAF36493 Yeast NOR  
c 443 5 100.0 10 5 AAF33916 Yeast NOR  
c 444 5 100.0 10 5 AAF39535 Yeast NOR  
c 445 5 100.0 10 5 AAF40917 Yeast NOR  
c 446 5 100.0 10 5 AAF37936 Yeast NOR  
c 447 5 100.0 10 5 AAF34394 Yeast NOR  
c 448 5 100.0 10 5 AAF37937 Yeast NOR  
c 449 5 100.0 10 5 AAF41499 Yeast NOR  
c 450 5 100.0 10 5 AAF42059 Yeast NOR  
c 451 5 100.0 10 5 AAF42804 Yeast NOR  
c 452 5 100.0 10 5 AAF37786 Yeast NOR  
c 453 5 100.0 10 5 AAF38496 Yeast NOR  
c 454 5 100.0 10 5 AAF40576 Yeast NOR  
c 455 5 100.0 10 5 AAF43044 Yeast NOR  
c 456 5 100.0 10 5 AAF43607 Yeast NOR  
c 457 5 100.0 10 5 AAF43738 Yeast NOR  
c 458 5 100.0 10 5 ABA89321 Zif268 zi  
c 459 5 100.0 10 5 ABA42236 Nucleotid

Abn86238 Nucleotid  
Aas18734 Primer-ex  
Aas18736 Primer-ex  
Aas18717 Primer-ex  
Aad25082 Primer #9  
Aas98399 Galanin r  
Aas98402 Human GPR  
Aad26712 Human LCA  
Abk51085 Human CCR  
Abk97527 Human LCA  
AbL59314 Primer fo  
Aas18299 Primer-ex  
Aad26032 Primer #3  
Aad26002 Primer #8  
Aad26022 Primer #2  
AbL88354 Human CHR  
AbL88334 Human CHR  
AbL88338 Human CHR  
AbL52190 Human PER  
AbL52194 Human PER  
Aal39611 SSTR4 gen  
Aal39596 SSTR4 gen  
Abk81951 Human CYP  
Abk81956 Human CYP  
Abk95844 Solute Ca  
AbL01210 Human AKR  
Aas98880 Colony st  
Aas98913 Colony st  
Aas98907 Colony st  
Aas98911 Colony st  
AbL42719 Human mat  
AbL42816 Human mat  
AbL42705 Mouse neu  
AbL19904 Mouse neu  
AbL60214 Human MUC  
Abk93934 Human pro  
Abk93939 Human pro  
Abk93918 Human pro  
Abk93925 Human pro  
Abk93941 Human pro  
Adi13733 Cytoplasm

460 5 100.0 10 6 ABN86238  
c 461 5 100.0 10 6 AAS18734  
c 462 5 100.0 10 6 AAS18736  
c 463 5 100.0 10 6 AAS18717  
c 464 5 100.0 10 6 AAD25082  
c 465 5 100.0 10 6 AAS98399  
c 466 5 100.0 10 6 AAS98402  
c 467 5 100.0 10 6 AAD26712  
c 468 5 100.0 10 6 ABK51085  
c 469 5 100.0 10 6 ABK97527  
c 470 5 100.0 10 6 ABL59314  
c 471 5 100.0 10 6 AAS18299  
c 472 5 100.0 10 6 AAD26032  
c 473 5 100.0 10 6 AAD26006  
c 474 5 100.0 10 6 AAD26022  
c 475 5 100.0 10 6 ABL88354  
c 476 5 100.0 10 6 ABL88334  
c 477 5 100.0 10 6 ABL88338  
c 478 5 100.0 10 6 ABL52190  
c 479 5 100.0 10 6 ABL52194  
c 480 5 100.0 10 6 AAL39611  
c 481 5 100.0 10 6 AAL39596  
c 482 5 100.0 10 6 ABK81951  
c 483 5 100.0 10 6 ABK81956  
c 484 5 100.0 10 6 ABK95844  
c 485 5 100.0 10 6 ABL01210  
c 486 5 100.0 10 6 AAS98880  
c 487 5 100.0 10 6 AAS98913  
c 488 5 100.0 10 6 AAS98907  
c 489 5 100.0 10 6 AAS98911  
c 490 5 100.0 10 6 ABL42719  
c 491 5 100.0 10 6 ABL42816  
c 492 5 100.0 10 6 ABL42705  
c 493 5 100.0 10 6 ABL19904  
c 494 5 100.0 10 6 ABL60214  
c 495 5 100.0 10 6 ABK93934  
c 496 5 100.0 10 6 ABK93939  
c 497 5 100.0 10 6 ABK93918  
c 498 5 100.0 10 6 ABK93925  
c 499 5 100.0 10 6 ABK93941  
c 500 5 100.0 10 12 ADI13733

## ALIGNMENTS

## RESULT 1

AAQ49540  
ID AAQ49540 standard; DNA; 10 BP.  
AC AAQ49540;  
XX  
XX  
DT 25-MAR-2003 (revised)  
DT 20-APR-1994 (first entry)  
XX  
XX  
DE Primer to amplify BCNR locus marker Y10.  
XX  
XX  
KW Phytopathogenic nematode; beet cyst nematode resistance; BCNR locus;  
KW sugar beet; ss.  
XX  
OS Synthetic.  
XX  
XX  
PN WO9319181-A1.  
XX  
PD 30-SEP-1993.  
XX  
PF 23-MAR-1993; 93WO-EP000702.  
XX  
PR 25-MAR-1992; 92DK-0000396.  
XX  
PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.  
PA (SANO ) SANDOZ PATENT GMBH.  
PA (SANO ) SANDOZ LTD.



CC selected 2'-O-methyl oligonucleotides are characterised by microbore  
 CC HPLC. Complete and limited fragmentation of the recovered 2'-O-methyl  
 CC oligonucleotides can be accomplished by appropriate base and nuclease  
 CC treatment to facilitate sequence reconstruction in comparison to pre-  
 CC calibrated retention times of standard mono, di, and tri 2'-O-methyl  
 CC standards. (Updated on 25-MAR-2003 to correct PN field.)  
 SQ Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
 DB 8 GTGGG 4  
 |||||

RESULT 4  
 AAQ38704/c  
 ID AAQ38704 standard; RNA; 10 BP.  
 XX  
 AC AAQ38704;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 15-JUL-1993 (first entry)  
 XX  
 DE 2'-O-methyl oligonucleotide for calibration of ras binding.  
 XX  
 KW oligonucleotide binding; nucleotide binding; DNA detection; binding DNA;  
 KW treatment; diagnosis; testing; assay; Candida; papillomavirus;  
 KW cytomegalovirus; Epstein-Barr virus; rhinovirus; hepatitis virus;  
 KW liver disease; human immunodeficiency virus; herpes simplex virus; HSV;  
 KW human immunodeficiency virus; HIV; AIDS; influenza virus;  
 KW genetic disease; genetic abnormalities.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9305182-A1.  
 XX  
 PD 18-MAR-1993.  
 XX  
 PF 04-SEP-1992; 92WO-US007489.  
 XX  
 PR 05-SEP-1991; 91US-00755485.  
 XX  
 PA (ISIS-) ISIS PHARM INC.  
 XX  
 PI Bruce TW;  
 XX  
 WPI; 1993-101001/12.  
 XX  
 XX Determn. of oligo:nucleotide(s) with specific activity for a bio:molecule  
 PT - for use in therapeutics, diagnostics and research reagents.  
 XX  
 XX Example 12; Page 37; 61pp; English.  
 PS  
 XX This sequence was used as a calibration oligonucleotide to investigate  
 CC random 2'-O-methyl oligonucleotide binding to ras RNA using continuous  
 CC flow mass transport methodology to effect stringent binding selection.  
 CC The oligonucleotides are added to a PPLC column together with a mixture  
 CC of calibration oligonucleotides that have been incubated with ras RNA to  
 CC form any possible hybridisation complexes. This is to enable an elution  
 CC profile to be obtained. Following calibration, either the random  
 CC oligonucleotide pool is loaded onto the column followed by the ras RNA or  
 CC the pool and ras RNA are pre-incubated prior to loading on the column.  
 CC Bound oligonucleotide/ras RNA complexes are dissociated using stepwise or  
 CC gradient low salt and/or increased temperature and the oligonucleotides  
 CC are recovered by RNase treatment to selectively degrade the ras RNA. The  
 CC selected 2'-O-methyl oligonucleotides are characterised by microbore  
 CC HPLC. Complete and limited fragmentation of the recovered 2'-O-methyl  
 CC oligonucleotides can be accomplished by appropriate base and nuclease  
 CC treatment to facilitate sequence reconstruction in comparison to pre-

CC calibrated retention times of standard mono, di, and tri 2'-O-methyl  
 CC standards. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
 DB 8 GTGGG 4  
 |||||

RESULT 5  
 AAQ79368  
 ID AAQ79368 standard; DNA; 10 BP.  
 XX  
 AC AAQ79368;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-JUN-1995 (first entry)  
 XX  
 DE Regulatory element AP2/Rev located at posn. 708 of the extended 3'  
 DE flanking region of human erythropoietin.  
 XX  
 KW Erythropoietin; erythropoiesis; red blood cell; regulatory element; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN WO9423570-A1.  
 XX  
 PD 27-OCT-1994.  
 XX  
 PF 15-APR-1994; 94WO-US004141.  
 XX  
 PR 15-APR-1993; 93US-00046295.  
 PR 23-JUN-1993; 93US-00082850.  
 XX  
 PA (UTNY ) UNIV NEW YORK STATE.  
 XX  
 PI Lee-Huang S;  
 XX  
 WPI; 1994-341353/42.  
 XX  
 DR New regulatory regions of human erythropoietin gene - used for studying  
 PT and treating diseases and for prodn. of transgenic animal models (Eng).  
 PT  
 PS Disclosure; Table II, page 14; 81pp; English.  
 XX  
 CC AAQ79353 shows the nt. sequence of the entire 9.3 kb genomic clone  
 CC hEpsLH. This nucleic acid sequence includes a coding sequence, a 5'  
 CC flanking region contg. multiple regulatory elements and a 3' flanking  
 CC region contg. multiple regulatory elements. AAQ79355 consists of the last  
 CC 1777 bases of AAQ79753. It corresp. to the non-coding 3' flanking region  
 CC of AAQ79753 and includes all the regulatory elements contained therein.  
 CC It extends from the 5'-most PstI site 3' of the end of the coding  
 CC sequence to a BamHI site. It comprises 1777 bp exhibiting many stem-loop  
 CC structures. It also contains TATA boxes in forward and reverse  
 CC orientation, and at least about 184 potential transcriptional regulatory  
 CC elements. AAQ79365-Q79369 list several of these elements and their  
 CC positions. The nucleotide posns. are measured from first nucleotide at  
 CC the extended 3' end of hEpsLH as shown in AAQ79355. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 SQ Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
 |||||



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PD 07-SEP-1994.
PF
XX 25-FEB-1994; 94EP-00301367.
XX
PR 25-FEB-1993; 93US-00022034.
PR 04-MAR-1993; 93US-00026063.
PR 19-AUG-1993; 93US-00108808.
PR 22-DEC-1993; 93US-00171718.
XX
PA (GEO) GEN HOSPITAL CORP.
XX
PI Trofatter JA, Maccollin MM, Gusella JF;
XX WPI; 1994-272992/34.
XX
DR
XX The tumour suppressor gene merlin - for treatment and diagnosis of
PT tumours and neurofibromatosis (NF2).
XX
XX Example 6; Page 26; 86pp; English.
XX
CC The sequences given in AAQ01078-109 represent the splice donor and
CC acceptor sites of the 17 exons of the NF2 gene. NF2 is a neuro-
CC fibromatosis which is characterised by bi-lateral schwannomas. The NF2
CC "gene" has been shown by linkage studies to be assigned to chromosome 22.
CC The missing or mutated gene in NF2 patients has been shown to be the
CC merlin gene. The gene encodes a protein, merlin (moesin-erzin-radixin-
CC like protein), which possesses tumour suppressor activity, and whose
CC tumour suppressor activity is mediated by inter- actions with the
CC cytoskeleton. The merlin gene is found on chromosome 22 between the known
CC markers D22S1 and D22S28. In patients suffering from NF2, the merlin gene
CC is either lost or mutated. A mutant merlin protein may be encoded by a
CC gene in which a mutation of A to T at the first position of the codon
CC encoding amino acid 220 causes the substitution of Tyr for Asn. The
CC merlin gene may be used in gene therapy for the treatment of a merlin-
CC associated tumour or NF2, or for prevention of schwannoma, meningioma,
CC posterior capsular lens opacities, deafness or hearing loss, balance
CC disorders or paralysis. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 2 A; 6 C; 1 G; 1 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 9
AAQ01967
ID AAQ01967 standard; DNA; 10 BP.
XX
AC AAQ01967;
XX
DT 25-MAR-2003 (revised)
DT 04-NOV-1994 (first entry)
XX
DE Phospholipase A2 inhibiting oligomer, ISIS no 4962.
XX
KW Inhibition; replication; herpes simplex virus; HSV; HIV; aging;
KW human cytomegalovirus; influenza virus; inflammation; telomere length;
KW neurological disorders; phospholipase A2 activity; hyperproliferation;
KW malignancy; cardiovascular disease; snake bite; malignancy; retard; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..10
FT /*tag= a
FT /note= "Phosphorothioate intersugar linkages"
XX
PN WO9408053-A1.

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XX 14-APR-1994.
XX
XX 29-SEP-1993; 93WO-US009297.
XX
XX 29-SEP-1992; 92US-00954185.
XX (ISIS-) ISIS PHARM INC.
XX
PI Hanecak RC, Anderson KP, Bennett CF, Chiang M, Brown-Driver VL;
PI Ecker DJ, Vickers TA, Wyatt JR, Imbach JL;
XX WPI; 1994-135613/16.
XX
PT New modified oligo-nucleotide contg guanine quartet - inhibits activity
PT of viruses, e.g. HIV, and phospholipase A2 and modulates telomere length
PT of chromosomes.
XX
PS Disclosure; Page 29; 144pp; English.
XX
CC The sequences given in AAQ61956-67 are oligonucleotides which represent
CC the core sequences of G4 containing oligos which may be used for
CC inhibiting phospholipase A2 enzyme activity. Oligonucleotides such as
CC these may also be used for inhibiting activity of HSV, HIV, human
CC cytomegalovirus or influenza virus, or for treating inflammatory and
CC neurological disorders caused by phospholipase A2 activity in cases of
CC hyperproliferation, malignancy, cardiovascular disease and snake bite.
CC They may also be used for inhibiting division of malignant cells by
CC modulating telomere length, which may also retard aging. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 3 GTGGG 7

RESULT 10
AAQ63558
ID AAQ63558 standard; DNA; 10 BP.
XX
AC AAQ63558;
XX
DT 25-MAR-2003 (revised)
DT 21-DEC-1994 (first entry)
XX
DE C11 3' spacer element.
XX
KW Insertion element; junk DNA; spacer element; functional DNA sequence;
KW primer binding site; reaction product; binding specificity; primer;
KW recombinant molecule; structural stress; hybridisation assay; ss.
XX
OS Synthetic.
XX
PN WO9409159-A2.
XX
PD 28-APR-1994.
XX
PF 08-OCT-1993; 93WO-US009702.
XX
PR 09-OCT-1992; 92US-00959939.
PR 09-APR-1993; 93US-00045587.
XX
XX (STAD ) AMOCO CORP.
XX
XX Burg J;
XX
XX WPI; 1994-151343/18.

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XX Insertion elements an amplifiable nucleic acids - for use as probes in  
PT hybridisation assays and for the prepn. of libraries used to identify  
PT preferred insertion elements.  
XX  
XX Disclosure; Page 23; 39pp; English.  
XX  
CC The sequences given in AAQ63549-60 are spacer elements used within the  
CC insertion elements of the invention. These insertion elements contain  
CC junk DNA, two spacer elements, a functional DNA sequence and a primer  
CC binding site. They also contain an MluI site, an MluI/NheI site and a  
CC NheI site. The junk DNA serves to keep the MluI site from being at the  
CC extreme end of the molecule and also allows determination that the MluI  
CC cleavage has occurred because the extended DNA will be reduced in size by  
CC the length of the junk sequence and the junk sequence will appear as a  
CC reaction product. The nucleotides making up the spacer elements are  
CC chosen randomly and the functional nucleotide sequence is chosen to  
CC achieve the binding specificity required of the amplifiable nucleic acid.  
CC The primer binding site can be any nucleotide sequence for which a  
CC complementary primer is available or can be synthesised. However, the  
CC primer and primer binding site are chosen such that the primer itself  
CC does not bind to any other portion of the insertion element under  
CC construction. Insertion sequences such as these can be used to insert a  
CC functional molecule into a host molecule to form a recombinant molecule.  
CC The spacer elements are thought to relieve structural stresses imposed on  
CC the host by addition of the functional nucleotide sequence. The insertion  
CC elements can be used with nucleic acid hybridisation assays. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 2 A; 1 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 6 GTGGG 10

RESULT 11  
AAQ63553  
ID AAQ63553 standard; DNA; 10 BP.  
XX  
AC AAQ63553;  
XX  
DT 25-MAR-2003 (revised)  
DT 21-DEC-1994 (first entry)  
XX  
DE C22 5' spacer element.  
XX  
KW Insertion element; junk DNA; spacer element; functional DNA sequence;  
KW primer binding site; reaction product; binding specificity; primer;  
KW recombinant molecule; structural stress; hybridisation assay; ss.  
XX  
OS Synthetic.  
XX  
XX WO9409159-A2.  
XX  
XX 28-APR-1994.  
XX  
XX 08-OCT-1993; 93WO-US009702.  
XX  
XX 09-OCT-1992; 92US-00959939.  
PR 09-APR-1993; 93US-00045587.  
XX  
XX (STAD ) AMOCO CORP.  
PA  
XX Burg J;  
XX  
XX WPI; 1994-151343/18.  
DR  
XX Insertion elements an amplifiable nucleic acids - for use as probes in

PT hybridisation assays and for the prepn. of libraries used to identify  
PT preferred insertion elements.  
XX  
XX Disclosure; Page 23; 39pp; English.  
XX  
CC The sequences given in AAQ63549-60 are spacer elements used within the  
CC insertion elements of the invention. These insertion elements contain  
CC junk DNA, two spacer elements, a functional DNA sequence and a primer  
CC binding site. They also contain an MluI site, an MluI/NheI site and a  
CC NheI site. The junk DNA serves to keep the MluI site from being at the  
CC extreme end of the molecule and also allows determination that the MluI  
CC cleavage has occurred because the extended DNA will be reduced in size by  
CC the length of the junk sequence and the junk sequence will appear as a  
CC reaction product. The nucleotides making up the spacer elements are  
CC chosen randomly and the functional nucleotide sequence is chosen to  
CC achieve the binding specificity required of the amplifiable nucleic acid.  
CC The primer binding site can be any nucleotide sequence for which a  
CC complementary primer is available or can be synthesised. However, the  
CC primer and primer binding site are chosen such that the primer itself  
CC does not bind to any other portion of the insertion element under  
CC construction. Insertion sequences such as these can be used to insert a  
CC functional molecule into a host molecule to form a recombinant molecule.  
CC The spacer elements are thought to relieve structural stresses imposed on  
CC the host by addition of the functional nucleotide sequence. The insertion  
CC elements can be used with nucleic acid hybridisation assays. (Updated on  
CC 25-MAR-2003 to correct PN field.)  
XX  
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 4 GTGGG 8

RESULT 12  
AAQ79252  
ID AAQ79252 standard; DNA; 10 BP.  
XX  
AC AAQ79252;  
XX  
DT 25-MAR-2003 (revised)  
DT 18-JUL-1995 (first entry)  
XX  
DE Guanosine rich oligonucleotide used to treat viral infection.  
XX  
KW Guanosine; tetrad; inhibition; replication; virus; treatment; therapy;  
KW infection; herpes simplex virus; human papilloma virus;  
KW Epstein-Barr virus; HIV; adenovirus; respiratory syncytial virus;  
KW hepatitis B virus; human cytomegalovirus; ss.  
XX  
OS Synthetic.  
XX  
XX Key Location/Qualifiers  
FH misc\_feature 10  
FT /\*tag= a  
FT /mod\_base  
FT /note= "Propanolamine group attached to this base."  
XX  
XX WO9425037-A1.  
XX  
XX 10-NOV-1994.  
XX  
XX 25-APR-1994; 94WO-US004529.  
XX  
XX 23-APR-1993; 93US-00053027.  
PR 28-OCT-1993; 93US-00145704.  
XX  
XX (TRIP-) TRIPLEX PHARM CORP.  
PA (BAYU ) BAYLOR COLLEGE MEDICINE.  
PA

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XX Rando RF, Fennwald S, Zendequi JG, Ojwang JO, Hogan ME;
XX WPI; 1994-357890/44.
XX
XX Oligo-nucleotide(s) rich in guanosine which form guanosine tetrads - used
XX to treat viral infections, e.g. herpes-virus and HIV.
XX
XX Claim 41; Page 71; 101pp; English.
XX
XX The oligonucleotides (See AAQ79201-52) can be used to treat viral
XX infections. The oligonucleotides inhibit viral replication by forming
XX guanosine tetrads which form a stabilised 3D structure. Preferred
XX oligonucleotides contain at least 2 runs of at least 2 guanosine bases
XX and may be capped at the 3' terminus with a modifier selected from
XX polyamine, poly-L-lysine, cholesterol and propanolamine. They may also
XX have a modified phosphodiester linkage or be modified to contain a
XX phosphorothioate linkage. They are used to treat infections with viruses
XX such as herpes simplex virus, human papilloma virus, Epstein-Barr virus,
XX HIV, adenovirus, respiratory syncytial virus, hepatitis B virus or human
XX cytomegalovirus. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GTGGG 5
DB 1 GTGGG 5
|||||
1 GTGGG 5

RESULT 13
AAQ73141
ID AAQ73141 standard; cDNA; 10 BP.
XX
XX AAQ73141;
XX
XX 26-MAY-1995 (first entry)
XX
XX Mutant rab16 motif I probe M5.
XX
XX Transactivating factor; TAF-1; transcription activator; transgenic plant;
XX gene expression; G-box motif; rab16 motif I; tobacco; probe; ds.
XX
XX Synthetic.
XX
XX US5362864-A.
XX
XX 08-NOV-1994.
XX
XX 06-FEB-1991; 91US-00651710.
XX
XX 06-FEB-1991; 91US-00651710.
XX
XX (UVRQ ) UNIV ROCKEFELLER.
XX
XX Chua N;
XX
XX WPI; 1994-357424/44.
XX
XX Isolated trans:activating factor, TAF-1 and encoding DNA - useful to
XX increase gene expression in plants.
XX
XX Disclosure; Col 29; 39pp; English.
XX
XX Partial cDNA clone p5a, encoding a C-terminal portion of transactivating
XX factor TAF-1 was isolated from a tobacco cDNA expression library. The
XX truncated TAF-1 protein (AAR62822) binds to rab16 motif I and the B-box
XX motif, and can be used to modulate gene expression in transgenic plants
XX or cell cultures. Tetramers of wild-type motif I (given in AAQ73135) and
XX of mutants M1-M5 (AAQ73137-41) were assayed for their ability to interact
XX
CC with recombinant TAF-1 protein produced in Escherichia coli by gel
CC mobility shift
XX
XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GTGGG 5
DB 5 GTGGG 9
|||||
5 GTGGG 9

RESULT 14
AAQ73134
ID AAQ73134 standard; cDNA; 10 BP.
XX
XX AAQ73134;
XX
XX 16-OCT-2003 (revised)
XX 26-MAY-1995 (first entry)
XX
XX TAF-1 binding motif.
XX
XX Transactivating factor; TAF-1; transcription activator; transgenic plant;
XX gene expression; binding motif; tobacco; ds.
XX
XX Nicotiana tabacum; cv. SR1.
XX
XX US5362864-A.
XX
XX 08-NOV-1994.
XX
XX 06-FEB-1991; 91US-00651710.
XX
XX 06-FEB-1991; 91US-00651710.
XX
XX (UVRQ ) UNIV ROCKEFELLER.
XX
XX Chua N;
XX
XX WPI; 1994-357424/44.
XX
XX Isolated trans:activating factor, TAF-1 and encoding DNA - useful to
XX increase gene expression in plants.
XX
XX Claim 9; Col 45; 39pp; English.
XX
XX Partial cDNA clone p5a (given in AAQ73130), encoding a C-terminal portion
XX of transactivating factor TAF-1 (AAR62822), was isolated from a tobacco
XX cDNA expression library. In host cells or transgenic plants, the TAF-1
XX sequence is controlled by a regulatory sequence containing 1 or more
XX copies of a binding site (e.g. AAQ73131-34) for TAF-1, so that expression
XX of a gene of interest is increased when TAF-1 is expressed. (Updated on
XX 16-OCT-2003 to standardise OS field)
XX
XX Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GTGGG 5
DB 6 GTGGG 10
|||||
6 GTGGG 10

RESULT 15
AAQ32620/c
ID AAQ32620 standard; DNA; 10 BP.
XX
XX AAQ32620;

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XX DT 23-JUN-1999 (first entry)
XX DE Anticancer duplex forming oligonucleotide SEQ ID #20.
XX KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
XX KW multiple drug resistance; MDR; ss.
XX OS Synthetic.
XX PN WO9523162-A1.
XX PD 31-AUG-1995.
XX PF 27-FEB-1995; 95WO-US002419.
XX PR 28-FEB-1994; 94US-00202927.
XX PA (MICR-) MICROPROBE CORP.
XX PA (UYIA ) UNIV YALE.
XX PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX DR WPI; 1995-311501/40.
XX PT New stable oligo:nucleotide duplex with 3'-steroid gp - including
XX PT intramolecular duplex with hairpin loop region, having selective
XX PT cytotoxicity against some tumour cells.
XX PS Disclosure; Page 52; 107pp; English.
XX CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
XX CC and which have a steroid structure attached to the 3'-end through a
XX CC linker attached to the A-ring of the steroid skeleton. In particular, the
XX CC present sequence has a cholesterol moiety attached by its A-ring to to
XX CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
XX CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
XX CC oligonucleotides form stable duplexes at physiological temperature and
XX CC have selective cytotoxic activity against certain tumour cell lines,
XX CC including some with multiple drug resistance
XX SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 5 GTGGG 1

RESULT 16
AAX32638
ID AAX32638 standard; DNA; 10 BP.
XX AC AAX32638;
XX DT 23-JUN-1999 (first entry)
XX DE Anticancer duplex forming oligonucleotide SEQ ID #38.
XX KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
XX KW multiple drug resistance; MDR; ss.
XX OS Synthetic.
XX PN WO9523162-A1.
XX PD 31-AUG-1995.
XX PF 27-FEB-1995; 95WO-US002419.
XX PR 28-FEB-1994; 94US-00202927.
XX PA (MICR-) MICROPROBE CORP.
XX PA (UYIA ) UNIV YALE.
XX PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX DR WPI; 1995-311501/40.
XX PT New stable oligo:nucleotide duplex with 3'-steroid gp - including
XX PT intramolecular duplex with hairpin loop region, having selective
XX PT cytotoxicity against some tumour cells.
XX PS Disclosure; Page 52; 107pp; English.
XX CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
XX CC and which have a steroid structure attached to the 3'-end through a
XX CC linker attached to the A-ring of the steroid skeleton. In particular, the
XX CC present sequence has a cholesterol moiety attached by its A-ring to to
XX CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
XX CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
XX CC oligonucleotides form stable duplexes at physiological temperature and
XX CC have selective cytotoxic activity against certain tumour cell lines,
XX CC including some with multiple drug resistance
XX SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 5 GTGGG 1

RESULT 17
AAX32638/c
ID AAX32638 standard; DNA; 10 BP.
XX AC AAX32638;
XX DT 23-JUN-1999 (first entry)
XX DE Anticancer duplex forming oligonucleotide SEQ ID #38.
XX KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
XX KW multiple drug resistance; MDR; ss.
XX OS Synthetic.
XX PN WO9523162-A1.
XX PD 31-AUG-1995.
XX PF 27-FEB-1995; 95WO-US002419.
XX PR 28-FEB-1994; 94US-00202927.
XX PA (MICR-) MICROPROBE CORP.
XX PA (UYIA ) UNIV YALE.
XX PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX DR WPI; 1995-311501/40.
XX PT New stable oligo:nucleotide duplex with 3'-steroid gp - including
XX PT intramolecular duplex with hairpin loop region, having selective
XX PT cytotoxicity against some tumour cells.
XX PS Disclosure; Page 59; 107pp; English.
XX CC New oligonucleotides are disclosed which are 8-18 nucleotides in length

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PR 28-FEB-1994; 94US-00202927.
XX (MICR-) MICROPROBE CORP.
XX PA (UYIA ) UNIV YALE.
XX PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX DR WPI; 1995-311501/40.
XX PT New stable oligo:nucleotide duplex with 3'-steroid gp - including
XX PT intramolecular duplex with hairpin loop region, having selective
XX PT cytotoxicity against some tumour cells.
XX PS Disclosure; Page 59; 107pp; English.
XX CC New oligonucleotides are disclosed which are 8-18 nucleotides in length
XX CC and which have a steroid structure attached to the 3'-end through a
XX CC linker attached to the A-ring of the steroid skeleton. In particular, the
XX CC present sequence has a cholesterol moiety attached by its A-ring to to
XX CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen
XX CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The
XX CC oligonucleotides form stable duplexes at physiological temperature and
XX CC have selective cytotoxic activity against certain tumour cell lines,
XX CC including some with multiple drug resistance
XX SQ Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 1 GTGGG 5

RESULT 17
AAX32638/c
ID AAX32638 standard; DNA; 10 BP.
XX AC AAX32638;
XX DT 23-JUN-1999 (first entry)
XX DE Anticancer duplex forming oligonucleotide SEQ ID #38.
XX KW Steroid; anticancer; antitumour; cytotoxic; duplex; linker;
XX KW multiple drug resistance; MDR; ss.
XX OS Synthetic.
XX PN WO9523162-A1.
XX PD 31-AUG-1995.
XX PF 27-FEB-1995; 95WO-US002419.
XX PR 28-FEB-1994; 94US-00202927.
XX PA (MICR-) MICROPROBE CORP.
XX PA (UYIA ) UNIV YALE.
XX PI Cheng Y, Lukhtanov EA, Meyer RB, Pai BS, Reed MW, Zhou JH;
XX DR WPI; 1995-311501/40.
XX PT New stable oligo:nucleotide duplex with 3'-steroid gp - including
XX PT intramolecular duplex with hairpin loop region, having selective
XX PT cytotoxicity against some tumour cells.
XX PS Disclosure; Page 59; 107pp; English.
XX CC New oligonucleotides are disclosed which are 8-18 nucleotides in length

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CC and which have a steroid structure attached to the 3'-end through a  
 CC linker attached to the A-ring of the steroid skeleton. In particular, the  
 CC present sequence has a cholesterol moiety attached by its A-ring to to  
 CC the 3'-phosphate through a carbonyl group attached to the ring nitrogen  
 CC of a moiety derived from 4-hydroxy-2-hydroxymethyl- pyrrolidine. The  
 CC oligonucleotides form stable duplexes at physiological temperature and  
 CC have selective cytotoxic activity against certain tumour cell lines,  
 CC including some with multiple drug resistance  
 XX  
 XX Sequence 10 BP; 1 A; 4 C; 4 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
 Db 10 GTGGG 6

RESULT 18  
 AAQ96493  
 ID AAQ96493 standard; DNA; 10 BP.

XX AC AAQ96493;  
 XX  
 XX 16-OCT-2003 (revised)  
 DT 20-MAR-1996 (first entry)  
 XX  
 XX HIV-1 NL4-3 nef gene nucleotide deletion 88.  
 DE  
 XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 KW  
 XX Human immunodeficiency virus 1.

OS  
 XX WO9521912-A1.  
 PN  
 XX 17-AUG-1995.

XX PF 14-FEB-1995; 95WO-AU0000063.  
 XX  
 XX 14-FEB-1994; 94AU-00003864.  
 PR 21-FEB-1994; 94AU-00004002.  
 PR 23-DEC-1994; 94AU-00000284.  
 XX  
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 PI  
 XX WPI; 1995-293115/38.

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.

PS Claim 13; Page 189; 301pp; English.

XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)

XX Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
 Db 1 GTGGG 5

RESULT 19  
 AAQ96488  
 ID AAQ96488 standard; DNA; 10 BP.  
 XX AC AAQ96488;  
 XX  
 XX 16-OCT-2003 (revised)  
 DT 20-MAR-1996 (first entry)  
 XX  
 XX HIV-1 NL4-3 nef gene nucleotide deletion 83.

XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 KW  
 XX Human immunodeficiency virus 1.  
 OS  
 XX WO9521912-A1.

XX 17-AUG-1995.

XX PF 14-FEB-1995; 95WO-AU0000063.

XX 14-FEB-1994; 94AU-00003864.

PR 21-FEB-1994; 94AU-00004002.

PR 23-DEC-1994; 94AU-00000284.

XX (MACF-) MACFARLANE BURNET CENT MEDICAL.

PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;

XX WPI; 1995-293115/38.

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.

PS Claim 13; Page 189; 301pp; English.

XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)

XX Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
 Db 6 GTGGG 10

RESULT 20  
 AAQ96596  
 ID AAQ96596 standard; DNA; 10 BP.

XX AC AAQ96596;

XX 16-OCT-2003 (revised)

DT 20-MAR-1996 (first entry)

XX HIV-1 NL4-3 nef gene nucleotide deletion 191.

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XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX DR New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 190; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 6 GTGGG 10
RESULT 21
AAQ96600
ID AAQ96600 standard; DNA; 10 BP.
XX AC AAQ96600;
XX 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX HIV-1 NL4-3 nef gene nucleotide deletion 195.
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX DR New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 190; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 3 A; 0 C; 6 G; 1 T; 0 U; 0 Other;
Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 6 GTGGG 10
RESULT 22
AAQ96492
ID AAQ96492 standard; DNA; 10 BP.
XX AC AAQ96492;
XX 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX HIV-1 NL4-3 nef gene nucleotide deletion 87.
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX DR New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 189; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more

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CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 10 BP; 2 A; 1 C; 6 G; 1 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      2 GTGGG 6

RESULT 23
AAQ96491
ID AAQ96491 standard; DNA; 10 BP.
XX
AC AAQ96491;
XX
DT 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 86.
DE
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX Human immunodeficiency virus 1.
OS
XX WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
DR New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
PF Claim 13; Page 189; 301pp; English.
XX
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 10 BP; 1 A; 1 C; 7 G; 1 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      2 GTGGG 6

RESULT 24
AAQ97088/c
ID AAQ97088 standard; DNA; 10 BP.
XX
AC AAQ97088;
XX
DT 16-OCT-2003 (revised)
DT 27-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 LTR nucleotide deletion 70.
DE
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
KW
XX Human immunodeficiency virus 1.
OS
XX WO9521912-A1.
XX
PD 17-AUG-1995.
XX
PF 14-FEB-1995; 95WO-AU0000063.
XX
PR 14-FEB-1994; 94AU-00003864.
PR 21-FEB-1994; 94AU-00004002.
PR 23-DEC-1994; 94AU-00000284.
XX
PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX
PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX WPI; 1995-293115/38.
XX
DR New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX LTR region - can be used in a vaccine to inhibit/reduce productive
XX infection in an individual by a pathogenic strain.
XX
PF Claim 14; Page 197; 301pp; English.
XX
CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
CC resulting avirulent HIV strains are still capable of inducing an immune
CC response in humans, and enable the generation of therapeutic, diagnostic
CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;

Query Match      100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      8 GTGGG 4

RESULT 25
AAQ96601
ID AAQ96601 standard; DNA; 10 BP.
XX
AC AAQ96601;
XX
DT 16-OCT-2003 (revised)
DT 20-MAR-1996 (first entry)
XX
XX HIV-1 NL4-3 nef gene nucleotide deletion 196.
DE
XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

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XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX XX
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX XX
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 190; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 0 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GTGGG 5
XX DB |||||
XX 1 GTGGG 5
XX RESULT 26
XX AAQ97086/c
XX ID AAQ97086 standard; DNA; 10 BP.
XX AC AAQ97086;
XX XX
XX DT 16-OCT-2003 (revised)
XX DT 27-MAR-1996 (first entry)
XX XX
XX DE HIV-1 NL4-3 LTR nucleotide deletion 68.
XX XX
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX XX
XX PD 17-AUG-1995.
XX XX
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX XX
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 190; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 0 A; 1 C; 4 G; 5 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GTGGG 5
XX DB |||||
XX 1 GTGGG 5
XX RESULT 26
XX AAQ97086/c
XX ID AAQ97086 standard; DNA; 10 BP.
XX AC AAQ97086;
XX XX
XX DT 16-OCT-2003 (revised)
XX DT 27-MAR-1996 (first entry)
XX XX
XX DE HIV-1 NL4-3 LTR nucleotide deletion 68.
XX XX
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX XX
XX PD 17-AUG-1995.
XX XX
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX XX
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 14; Page 197; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 3 A; 4 C; 3 G; 0 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 5; DB 2; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 1.7e+06;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 GTGGG 5
XX DB |||||
XX 10 GTGGG 6
XX RESULT 27
XX AAQ97089/c
XX ID AAQ97089 standard; DNA; 10 BP.
XX AC AAQ97089;
XX XX
XX DT 16-OCT-2003 (revised)
XX DT 27-MAR-1996 (first entry)
XX XX
XX DE HIV-1 NL4-3 LTR nucleotide deletion 71.
XX XX
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX XX
XX PD 17-AUG-1995.
XX XX
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX XX
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 14; Page 197; 301pp; English.
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The

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CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)

XX SQ Sequence 10 BP; 3 A; 5 C; 1 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
 |||||  
 Db 7 GTGGG 3

RESULT 28  
 AAQ97090/c  
 ID AAQ97090 standard; DNA; 10 BP.

XX AC AAQ97090;  
 XX DT 16-OCT-2003 (revised)  
 XX DT 27-MAR-1996 (first entry)  
 XX DE HIV-1 NL4-3 LTR nucleotide deletion 72.  
 XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 XX OS Human immunodeficiency virus 1.

XX PN W09521912-A1.  
 XX PD 17-AUG-1995.

XX PF 14-FEB-1995; 95WO-AU0000063.  
 XX PR 14-FEB-1994; 94AU-00003864.  
 XX PR 21-FEB-1994; 94AU-00004002.  
 XX PR 23-DEC-1994; 94AU-00000284.

XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 XX PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 XX WPI; 1995-293115/38.

XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.

XX PS Claim 14; Page 197; 30lpp; English.

XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)

XX SQ Sequence 10 BP; 2 A; 5 C; 1 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
 |||||  
 Db 6 GTGGG 2

RESULT 29  
 AAQ96597  
 ID AAQ96597 standard; DNA; 10 BP.  
 XX AC AAQ96597;  
 XX DT 16-OCT-2003 (revised)  
 XX DT 20-MAR-1996 (first entry)  
 XX DE HIV-1 NL4-3 nef gene nucleotide deletion 192.  
 XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 XX OS Human immunodeficiency virus 1.

XX PN W09521912-A1.

XX PD 17-AUG-1995.

XX PF 14-FEB-1995; 95WO-AU0000063.

XX PR 14-FEB-1994; 94AU-00003864.

XX PR 21-FEB-1994; 94AU-00004002.

XX PR 23-DEC-1994; 94AU-00000284.

XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.

XX PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;

XX WPI; 1995-293115/38.

XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.

XX PS Claim 13; Page 190; 30lpp; English.

XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)

XX SQ Sequence 10 BP; 2 A; 0 C; 6 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5

Db 5 GTGGG 9

RESULT 30

AAQ96490

ID AAQ96490 standard; DNA; 10 BP.

XX AC AAQ96490;

XX DT 16-OCT-2003 (revised)

XX DT 20-MAR-1996 (first entry)

XX DE HIV-1 NL4-3 nef gene nucleotide deletion 85.

XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.

XX OS Human immunodeficiency virus 1.



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XX PN WO9521912-A1.
XX PD 17-AUG-1995.
XX PT
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX SQ
XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 189; 301pp; English.
XX
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 1 A; 0 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db |||||
4 GTGGG 8

RESULT 31
AAQ96489
ID AAQ96489 standard; DNA; 10 BP.
XX AC AAQ96489;
XX
XX DT 16-OCT-2003 (revised)
XX DT 20-MAR-1996 (first entry)
XX
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 84.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX
XX PD 17-AUG-1995.
XX
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;

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XX WPI; 1995-293115/38.
XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 189; 301pp; English.
XX
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic
XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to
XX CC standardise OS field)
XX SQ Sequence 10 BP; 1 A; 0 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db |||||
5 GTGGG 9

RESULT 32
AAQ96599
ID AAQ96599 standard; DNA; 10 BP.
XX AC AAQ96599;
XX
XX DT 16-OCT-2003 (revised)
XX DT 20-MAR-1996 (first entry)
XX
XX DE HIV-1 NL4-3 nef gene nucleotide deletion 194.
XX KW HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.
XX OS Human immunodeficiency virus 1.
XX PN WO9521912-A1.
XX
XX PD 17-AUG-1995.
XX PF 14-FEB-1995; 95WO-AU0000063.
XX PR 14-FEB-1994; 94AU-00003864.
XX PR 21-FEB-1994; 94AU-00004002.
XX PR 23-DEC-1994; 94AU-00000284.
XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.
XX PA (AURE-) AUSTRALIAN RED CROSS SOC.
XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;
XX DR WPI; 1995-293115/38.
XX
XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or
XX PT LTR region - can be used in a vaccine to inhibit/reduce productive
XX PT infection in an individual by a pathogenic strain.
XX PS Claim 13; Page 190; 301pp; English.
XX
XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or
XX CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more
XX CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of
XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The
XX CC resulting avirulent HIV strains are still capable of inducing an immune
XX CC response in humans, and enable the generation of therapeutic, diagnostic

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CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 XX standardise OS field)  
 SQ Sequence 10 BP; 1 A; 0 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 3 GTGGG 7

RESULT 33  
 AAQ97091/c  
 ID AAQ97091 standard; DNA; 10 BP.

XX AAQ97091;  
 AC  
 XX 16-OCT-2003 (revised)  
 DT 27-MAR-1996 (first entry)  
 XX  
 XX HIV-1 NL4-3 LTR nucleotide deletion 73.  
 DE  
 XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 KW  
 XX Human immunodeficiency virus 1.  
 OS  
 XX WO9521912-A1.

PD 17-AUG-1995.  
 XX  
 PF 14-FEB-1995; 95WO-AU0000063.  
 XX  
 PR 14-FEB-1994; 94AU-00003864.  
 PR 21-FEB-1994; 94AU-00004002.  
 PR 23-DEC-1994; 94AU-00000284.  
 XX  
 XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 PI WPI; 1995-293115/38.

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.

XX Claim 14; Page 197; 301pp; English.

XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)

XX Sequence 10 BP; 1 A; 5 C; 1 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 5 GTGGG 1

RESULT 34

AAQ96598  
 ID AAQ96598 standard; DNA; 10 BP.

XX AAQ96598;  
 AC  
 XX 16-OCT-2003 (revised)  
 DT 20-MAR-1996 (first entry)  
 XX  
 XX HIV-1 NL4-3 nef gene nucleotide deletion 193.  
 DE  
 XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 KW  
 XX Human immunodeficiency virus 1.  
 OS  
 XX WO9521912-A1.

PD 17-AUG-1995.  
 XX  
 PF 14-FEB-1995; 95WO-AU0000063.  
 XX  
 PR 14-FEB-1994; 94AU-00003864.  
 PR 21-FEB-1994; 94AU-00004002.  
 PR 23-DEC-1994; 94AU-00000284.

XX (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 PA (AURE-) AUSTRALIAN RED CROSS SOC.

XX Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 PI WPI; 1995-293115/38.

XX New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 PT infection in an individual by a pathogenic strain.

XX Claim 13; Page 190; 301pp; English.

XX Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 CC more decanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 CC decanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 CC resulting avirulent HIV strains are still capable of inducing an immune  
 CC response in humans, and enable the generation of therapeutic, diagnostic  
 CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 CC standardise OS field)

XX Sequence 10 BP; 1 A; 0 C; 6 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 4 GTGGG 8

RESULT 35  
 AAQ97087/c  
 ID AAQ97087 standard; DNA; 10 BP.

XX AAQ97087;  
 AC  
 XX 16-OCT-2003 (revised)  
 DT 27-MAR-1996 (first entry)  
 XX  
 XX HIV-1 NL4-3 LTR nucleotide deletion 69.  
 DE  
 XX HIV-1; AIDS; attenuation; vaccine; nef gene; avirulence; ss.  
 KW  
 XX Human immunodeficiency virus 1.  
 OS  
 XX WO9521912-A1.

XX PD 17-AUG-1995.  
 XX XX  
 XX PF 14-FEB-1995; 95WO-AU000063.  
 XX XX  
 XX PR 14-FEB-1994; 94AU-00003864.  
 XX PR 21-FEB-1994; 94AU-00004002.  
 XX PR 23-DEC-1994; 94AU-00000284.  
 XX XX  
 XX PA (MACF-) MACFARLANE BURNET CENT MEDICAL.  
 XX PA (AURE-) AUSTRALIAN RED CROSS SOC.  
 XX XX  
 XX PI Deacon NJ, Learmont JC, Mcphee DA, Crowe S, Cooper D;  
 XX XX  
 XX DR WPI; 1995-293115/38.  
 XX XX  
 XX PT New non-pathogenic HIV-1 strain carrying a deletion in its nef gene or  
 XX PT LTR region - can be used in a vaccine to inhibit/reduce productive  
 XX PT infection in an individual by a pathogenic strain.  
 XX XX  
 XX PS Claim 14; Page 197; 301pp; English.  
 XX XX  
 XX CC Attenuation of pathogenic HIV-1 strain NL4-3 involves deletion of 1 or  
 XX CC more dezanucleotides (AAQ96406-Q97018) from the nef gene and/or 1 or more  
 XX CC dezanucleotides (AAQ97019-Q97166) from the LTR region; the sequence of  
 XX CC AAQ96406 corresponds to nucleotides 1-10 of the nef gene (AAQ96141). The  
 XX CC resulting avirulent HIV strains are still capable of inducing an immune  
 XX CC response in humans, and enable the generation of therapeutic, diagnostic  
 XX CC and targeting agents against HIV-1 infection. (Updated on 16-OCT-2003 to  
 XX CC standardise OS field)  
 XX XX  
 XX SQ Sequence 10 BP; 3 A; 4 C; 2 G; 1 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTGGG 5  
 Db 9 GTGGG 5

RESULT 36  
 AAQ99835/c  
 ID AAQ99835 standard; RNA; 10 BP.  
 XX AC  
 XX AC AAQ99835;  
 XX XX  
 XX DT 25-MAR-2003 (revised)  
 XX DT 04-SEP-1995 (first entry)  
 XX XX  
 XX DE H-ras modulating sequence, targetted to hairpin loop.  
 XX XX  
 XX KW Peptide nucleic acid; PNA; ligand; peptide backbone; human; H-ras; K-ras;  
 XX KW expression; ras gene; mutation; tumour; cancer; ss.  
 XX OS Synthetic.  
 XX XX  
 XX XX Key Location/Qualifiers  
 XX FT modified\_base 1..10  
 XX FT /\*tag= a  
 XX FT /note= "Each base is attached to a N-acetyl(2-amino-  
 XX FT ethyl)Gly residue through the N-acetyl group"  
 XX XX  
 XX PN W09428720-A1.  
 XX XX  
 XX PD 22-DEC-1994.  
 XX XX  
 XX PF 10-JUN-1994; 94WO-US006620.  
 XX PF  
 XX PR 11-JUN-1993; 93US-00076234.  
 XX PR  
 XX XX (ISIS-) ISIS PHARM INC.  
 XX XX  
 XX XX Lima W, Monia B, Freier S, Ecker D;  
 XX XX WPI; 1995-035955/05.  
 XX XX  
 XX PT New peptide nucleic acid oligomers for ras oncogene modulation -  
 XX PT including specific inhibition of the activated gene, for diagnosis and  
 XX PT treatment esp. of tumours.

XX Lima W, Monia B, Freier S, Ecker D;  
 XX WPI; 1995-035955/05.  
 XX  
 XX PT New peptide nucleic acid oligomers for ras oncogene modulation -  
 XX PT including specific inhibition of the activated gene, for diagnosis and  
 XX PT treatment esp. of tumours.  
 XX  
 XX PS Claim 1; Page 133; 148pp; English.  
 XX XX  
 XX CC The sequences given in AAQ79822-57 represent peptide nucleic acids (PNA)  
 XX CC that bind to complementary ssDNA and RNA strands through their  
 XX CC oligoribonucleotide ligands which are linked to a peptide backbone. These  
 XX CC sequences are directed to the human H-ras and K-ras genes and they  
 XX CC modulate the expression of the ras gene in cells or tissues and  
 XX CC specifically modulate the expression of the activated ras in cells or  
 XX CC tissues suspected of harbouring a mutated gene. These sequences are  
 XX CC designed to hybridise with the mRNA from the H-ras and K-ras genes which  
 XX CC interferes with the normal role of mRNA causing a loss of function in the  
 XX CC cell. These sequences are used in the treatment of tumours. (Updated on  
 XX CC 25-MAR-2003 to correct PN field.)  
 XX XX  
 XX SQ Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTGGG 5  
 Db 8 GTGGG 4

RESULT 37  
 AAQ79834/c  
 ID AAQ79834 standard; DNA; 10 BP.  
 XX AC  
 XX AC AAQ79834;  
 XX XX  
 XX DT 25-MAR-2003 (revised)  
 XX DT 04-SEP-1995 (first entry)  
 XX XX  
 XX DE H-ras modulating sequence, targetted to hairpin stem.  
 XX XX  
 XX KW Peptide nucleic acid; PNA; ligand; peptide backbone; human; H-ras; K-ras;  
 XX KW expression; ras gene; mutation; tumour; cancer; ss.  
 XX OS Synthetic.  
 XX XX  
 XX XX Key Location/Qualifiers  
 XX FT modified\_base 1..10  
 XX FT /\*tag= a  
 XX FT /note= "Each base is attached to a N-acetyl(2-amino-  
 XX FT ethyl)Gly residue through the N-acetyl group"  
 XX XX  
 XX PN W09428720-A1.  
 XX XX  
 XX PD 22-DEC-1994.  
 XX XX  
 XX PF 10-JUN-1994; 94WO-US006620.  
 XX PF  
 XX PR 11-JUN-1993; 93US-00076234.  
 XX PR  
 XX XX (ISIS-) ISIS PHARM INC.  
 XX XX  
 XX XX Lima W, Monia B, Freier S, Ecker D;  
 XX XX WPI; 1995-035955/05.  
 XX XX  
 XX PT New peptide nucleic acid oligomers for ras oncogene modulation -  
 XX PT including specific inhibition of the activated gene, for diagnosis and  
 XX PT treatment esp. of tumours.

XX Claim 1; Page 133; 148pp; English.

PS The sequences given in AAQ79822-57 represent peptide nucleic acids (PNA)

CC that bind to complementary ssDNA and RNA strands through their

CC oligonucleotide ligands which are linked to a peptide backbone. These

CC sequences are directed to the human H-ras and K-ras genes and they

CC modulate the expression of the ras gene in cells or tissues and

CC specifically modulate the expression of the activated ras in cells or

CC tissues suspected of harbouring a mutated gene. These sequences are

CC designed to hybridise with the mRNA from the H-ras and K-ras genes which

CC interferes with the normal role of mRNA causing a loss of function in the

CC cell. These sequences are used in the treatment of tumours. (Updated on

CC 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 10 BP; 2 A; 6 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5

DB 8 GTGGG 4

RESULT 38

AAT14316

ID AAT14316 standard; RNA; 10 BP.

XX

AC AAT14316;

XX

DT 21-NOV-1996 (first entry)

XX

DE IgE binding ligand group B consensus sequence.

XX

KW Immunoglobulin E; RNA ligand; inhibitor; IgE receptor; therapy; asthma;

KW IgE dependent reaction; allergic disease; allergic rhinitis; hay fever;

KW atopic dermatitis; chronic skin irritation; anaphylactic shock; IgE; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT modified\_base 1..10

FT /\*tag= a

FT /note= "all C's are 2'NH2 cytosine, and all U's are 2'NH2

FT uracil"

XX

PN WO9610576-A1.

XX

PD 11-APR-1996.

XX

PF 27-SEP-1995; 95WO-US012401.

XX

PR 03-OCT-1994; 94US-00317403.

PR 06-JUN-1995; 95US-00471985.

XX

PA (NEXS-) NEXSTAR PHARM INC.

XX

PI Wiegand TW, Tasset D, Gold L;

XX

DR WPI; 1996-209316/21.

XX

PT Identification of high-affinity IgE oligo:nucleotide ligands - which

PT inhibit interaction of IgE with its receptor, which are therefore useful

PT in diagnostic and therapeutic applications.

XX

PS Claim 9; Page 39; 88pp; English.

XX

CC AAT14280-T14320 represent RNA ligands for immunoglobulin E (IgE). These

CC sequences are non-naturally occurring RNA ligands, and were isolated and

CC purified using the method of the invention. In this method, a candidate

CC mixture of nucleic acids is prepared, and contacted with IgE. The

CC sequences with an increased affinity to IgE relative to the mixture are

CC partitioned off from the rest of the mixture. The partitioned sequences

CC are then amplified, to yield a mixture of nucleic acids enriched for

CC those with relatively higher affinity and specificity for IgE binding.

CC The steps of this method can be repeated in order to obtain a mixture of

CC higher specificity for IgE binding. This method can be carried out with

CC RNA or DNA. AAT14240-T14243, and AAT14431-T14487 represent the DNA

CC ligands identified by this method. The IgE ligands inhibit the function

CC of IgE by preventing the IgE/receptor interaction. The ligands are

CC therefore useful in diagnostic and therapeutic applications for diseases

CC associated with IgE dependent reactions. The IgE dependent reactions

CC include allergic diseases such as allergic rhinitis (hay fever), asthma,

CC atopic dermatitis (chronic skin irritations), and anaphylactic shock

XX

SQ Sequence 10 BP; 0 A; 1 C; 7 G; 0 T; 2 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 1.7e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5

DB 3 GUGGG 7

RESULT 39

AAT98863

ID AAT98863 standard; DNA; 10 BP.

XX

AC AAT98863;

XX

DT 20-MAR-1998 (first entry)

XX

DE Core-binding site clone 6-11-2.

XX

KW Protein-binding site isolation; transcription factor modification;

KW DNA-binding protein; inhibitor identification; ss.

XX

OS Synthetic.

XX

PN WO9727330-A1.

XX

PD 31-JUL-1997.

XX

PF 24-JAN-1997; 97WO-US001230.

XX

PR 24-JAN-1996; 96US-00590571.

XX

PA (UYYA ) UNIV YALE.

XX

PI Weissman SM, Kulkarni P, Nallur GN;

XX

DR WPI; 1997-393714/36.

XX

PT Identifying protein-binding sites for DNA-binding proteins - using

PT duplexes having 5' and 3' sequences for annealing to amplification

PT primers with an internal potential protein-binding site sequence.

XX

PS Example 3; Page 22; 52pp; English.

XX

CC This sequence represents a core-binding site identified using the method

CC of the invention. This sequence was identified using the 32P-labelled

CC oligonucleotide duplex shown in AAT76581 and the primers shown in

CC AAT76582-T76583 in the method of the invention. The method is for

CC simultaneously isolating protein-binding sites for DNA-binding proteins.

CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes

CC having 5' and 3' sequences capable of annealing to primers for

CC amplification and an internal sequence having a potential protein-binding

CC site, a non-specific inhibitor and a sample containing DNA-binding

CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed

CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form

CC amplified duplexes; thereby isolating protein-binding sites for the DNA-

CC binding proteins. The methods can be used to identify protein-binding

CC sites which can be used to identify corresponding DNA-binding proteins in  
 CC an expression library. They can also be used to develop products to  
 CC inhibit the function of a given DNA-binding protein or for the  
 CC modification of transcription factors

XX SQ Sequence 10 BP; 0 A; 1 C; 8 G; 1 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 1 GTGGG 5

RESULT 40  
 AAT98860  
 ID AAT98860 standard; DNA; 10 BP.  
 XX AC AAT98860;  
 XX DT 20-MAR-1998 (first entry)  
 XX DE Core-binding site clone 6-7-1.  
 XX KW Protein-binding site isolation; transcription factor modification;  
 XX KW DNA-binding protein; inhibitor identification; ss.  
 XX OS Synthetic.  
 XX PN WO9727330-A1.  
 XX PD 31-JUL-1997.  
 XX PF 24-JAN-1997; 97WO-US001230.  
 XX PR 24-JAN-1996; 96US-00590571.  
 XX PA (UYUA ) UNIV YALE.  
 XX PI Weissman SM, Kulkarni P, Nallur GN;  
 XX DR WPI; 1997-393714/36.

XX CC This sequence represents a core-binding site identified using the method  
 of the invention. This sequence was identified using the 32P-labelled  
 oligonucleotide duplex shown in AAT98581 and the primers shown in  
 CC AAT98582-T76583 in the method of the invention. The method is for  
 CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
 CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
 CC having 5' and 3' sequences capable of annealing to primers for  
 CC amplification and an internal sequence having a potential protein-binding  
 CC site, a non-specific inhibitor and a sample containing DNA-binding  
 CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
 CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
 CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
 CC binding proteins. The methods can be used to identify protein-binding  
 CC sites which can be used to identify corresponding DNA-binding proteins in  
 CC an expression library. They can also be used to develop products to  
 CC inhibit the function of a given DNA-binding protein or for the  
 CC modification of transcription factors

XX SQ Sequence 10 BP; 0 A; 1 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 1 GTGGG 5

RESULT 42  
 AAT98837

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTGGG 5  
 |||||  
 Db 1 GTGGG 5

RESULT 41  
 AAT98847  
 ID AAT98847 standard; DNA; 10 BP.  
 XX AC AAT98847;  
 XX DT 20-MAR-1998 (first entry)  
 XX DE Binding site BSN1 identified using the method of the invention.  
 XX DE Protein-binding site isolation; transcription factor modification;  
 XX KW DNA-binding protein; inhibitor identification; ss.  
 XX OS Synthetic.  
 XX PN WO9727330-A1.  
 XX PD 31-JUL-1997.  
 XX PF 24-JAN-1997; 97WO-US001230.  
 XX PR 24-JAN-1996; 96US-00590571.  
 XX PA (UYUA ) UNIV YALE.  
 XX PI Weissman SM, Kulkarni P, Nallur GN;  
 XX DR WPI; 1997-393714/36.

XX CC This sequence represents a binding site identified using the method of  
 the invention. This sequence was identified using the 32P-labelled  
 oligonucleotide duplex shown in AAT98581 and the primers shown in  
 CC AAT98582-T76583 in the method of the invention. The method is for  
 CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
 CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
 CC having 5' and 3' sequences capable of annealing to primers for  
 CC amplification and an internal sequence having a potential protein-binding  
 CC site, a non-specific inhibitor and a sample containing DNA-binding  
 CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
 CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
 CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
 CC binding proteins. The methods can be used to identify protein-binding  
 CC sites which can be used to identify corresponding DNA-binding proteins in  
 CC an expression library. They can also be used to develop products to  
 CC inhibit the function of a given DNA-binding protein or for the  
 CC modification of transcription factors

XX SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 1 GTGGG 5

RESULT 42  
 AAT98837

```

ID  AAT98837 standard; DNA; 10 BP.
AC  AAT98837;
DT  20-MAR-1998 (first entry)
XX
DE  Binding site BSN7 identified using the method of the invention.
XX
DE  Protein-binding site isolation; transcription factor modification;
KW  DNA-binding protein; inhibitor identification; ss.
XX
OS  Synthetic.
XX
PN  WO9727330-A1.
XX
PD  31-JUL-1997.
XX
PF  24-JAN-1997; 97WO-US001230.
XX
PR  24-JAN-1996; 96US-00590571.
XX
PA  (UYUA ) UNIV YALE.
XX
PI  Weissman SM, Kulkarni P, Nallur GN;
XX
DR  WPI; 1997-393714/36.
XX
PT  Identifying protein-binding sites for DNA-binding proteins - using
PT  duplexes having 5' and 3' sequences for annealing to amplification
PT  primers with an internal potential protein-binding site sequence.
XX
PS  Example 3; Page 19; 52pp; English.
XX
CC  This sequence represents a binding site identified using the method of
CC  the invention. This sequence was identified using the 32P-labelled
CC  oligonucleotide duplex shown in AAT76581 and the primers shown in
CC  AAT76582-T76583 in the method of the invention. The method is for
CC  simultaneously isolating protein-binding sites for DNA-binding proteins.
CC  The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC  having 5' and 3' sequences capable of annealing to primers for
CC  amplification and an internal sequence having a potential protein-binding
CC  site, a non-specific inhibitor and a sample containing DNA-binding
CC  proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC  with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC  amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC  binding proteins. The methods can be used to identify protein-binding
CC  sites which can be used to identify corresponding DNA-binding proteins in
CC  an expression library. They can also be used to develop products to
CC  inhibit the function of a given DNA-binding protein or for the
CC  modification of transcription factors
XX
SQ  Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 4 GTGGG 8

RESULT 43
AAT98848
ID AAT98848 standard; DNA; 10 BP.
AC AAT98848;
XX
DT 20-MAR-1998 (first entry)
XX
DE Binding site BSN6 identified using the method of the invention.
XX
DE Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
XX
PD 31-JUL-1997.
XX
PF 24-JAN-1997; 97WO-US001230.
XX
PR 24-JAN-1996; 96US-00590571.
XX
PA (UYUA ) UNIV YALE.
XX
PI Weissman SM, Kulkarni P, Nallur GN;
XX
DR WPI; 1997-393714/36.
XX
PT Identifying protein-binding sites for DNA-binding proteins - using
PT duplexes having 5' and 3' sequences for annealing to amplification
PT primers with an internal potential protein-binding site sequence.
XX
PS Example 3; Page 19; 52pp; English.
XX
CC This sequence represents a binding site identified using the method of
CC the invention. This sequence was identified using the 32P-labelled
CC oligonucleotide duplex shown in AAT76581 and the primers shown in
CC AAT76582-T76583 in the method of the invention. The method is for
CC simultaneously isolating protein-binding sites for DNA-binding proteins.
CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes
CC having 5' and 3' sequences capable of annealing to primers for
CC amplification and an internal sequence having a potential protein-binding
CC site, a non-specific inhibitor and a sample containing DNA-binding
CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed
CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form
CC amplified duplexes; thereby isolating protein-binding sites for the DNA-
CC binding proteins. The methods can be used to identify protein-binding
CC sites which can be used to identify corresponding DNA-binding proteins in
CC an expression library. They can also be used to develop products to
CC inhibit the function of a given DNA-binding protein or for the
CC modification of transcription factors
XX
SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 4 GTGGG 8

RESULT 44
AAT98864
ID AAT98864 standard; DNA; 10 BP.
AC AAT98864;
XX
DT 20-MAR-1998 (first entry)
XX
DE Core-binding site clone 6-12-2R.
XX
DE Protein-binding site isolation; transcription factor modification;
KW DNA-binding protein; inhibitor identification; ss.
XX
OS Synthetic.
XX
PN WO9727330-A1.
XX
PD 31-JUL-1997.
XX
PF 24-JAN-1997; 97WO-US001230.

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XX PR 24-JAN-1996; 96US-00590571.  
 XX PA (UYUA ) UNIV YALE.  
 XX PI Weiseman SM, Kulkarni P, Nallur GN;  
 XX DR WPI; 1997-393714/36.  
 XX PT Identifying protein-binding sites for DNA-binding proteins - using  
 PT duplexes having 5' and 3' sequences for annealing to amplification  
 PT primers with an internal potential protein-binding site sequence.  
 XX PS Example 3; Page 22; 52pp; English.  
 XX CC This sequence represents a core-binding site identified using the method  
 CC of the invention. This sequence was identified using the 32P-labelled  
 CC oligonucleotide duplex shown in AAT76581 and the primers shown in  
 CC AAT76582-T76583 in the method of the invention. The method is for  
 CC simultaneously isolating protein-binding sites for DNA-binding proteins.  
 CC The method comprises: (a) mixing a set of oligonucleotide (ON) duplexes  
 CC having 5' and 3' sequences capable of annealing to primers for  
 CC amplification and an internal sequence having a potential protein-binding  
 CC site, a non-specific inhibitor and a sample containing DNA-binding  
 CC proteins; (b) separating unbound ON duplexes from ON duplexes complexed  
 CC with the DNA-binding proteins; (c) amplifying complexed duplexes to form  
 CC amplified duplexes; thereby isolating protein-binding sites for the DNA-  
 CC binding proteins. The methods can be used to identify protein-binding  
 CC sites which can be used to identify corresponding DNA-binding proteins in  
 CC an expression library. They can also be used to develop products to  
 CC inhibit the function of a given DNA-binding protein or for the  
 CC modification of transcription factors  
 XX SQ Sequence 10 BP; 0 A; 2 C; 6 G; 2 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTGGG 5  
 Db 1 GTGGG 5  
 |||||  
 RESULT 45  
 AAT51668  
 ID AAT51668 standard; DNA; 10 BP.  
 AC AAT51668;  
 XX 12-NOV-1997 (first entry)  
 XX Viral integrase inhibiting oligonucleotide.  
 XX Human immunodeficiency virus; HIV; Epstein Barr virus; EBV;  
 KW herpes simplex virus; HSV; human papilloma virus; HPV; adenovirus;  
 KW respiratory syncytial virus; RSV; cytomegalovirus; CMV; hepatitis B;  
 KW integrase inhibition; guanosine tetrad; ss.  
 XX Synthetic.  
 OS WO9703997-A1.  
 XX 06-FEB-1997.  
 XX 17-JUL-1996; 96WO-US011786.  
 XX 19-JUL-1995; 95US-0001505P.  
 PR 23-OCT-1995; 95US-00535168.  
 PR 19-MAR-1996; 96US-0013688P.  
 PR 25-MAR-1996; 96US-0014007P.  
 PR 17-APR-1996; 96US-0015714P.  
 PR 23-APR-1996; 96US-0016271P.

XX PA (ARON-) ARONEX PHARM INC.  
 XX Rando RF, Fennewald S, Zendegui JG, Ojwang JO, Hogan ME;  
 XX PI Pommier Y, Mazumder A;  
 XX DR WPI; 1997-132569/12.  
 XX PT Oligonucleotide(s) capable of forming guanosine tetrads - inhibit viral  
 PT enzyme responsible for integrating viral nucleic acid into the host  
 PT genome.  
 XX PS Claim 3; Page 168; 245pp; English.  
 XX CC AAT51619-T51698 are oligonucleotides used to inhibit the production of  
 CC viruses within a host cell. The oligonucleotides may form guanosine  
 CC tetrads (structures formed of eight hydrogen bonds by coordination of the  
 CC four oxygen atoms of guanine with alkali cations believed to bind to the  
 CC centre of a quadruplex, and by strong stacking interactions) and are used  
 CC to prevent the integration of viral nucleic acid into a host genome. The  
 CC oligonucleotides inhibit functioning of the integrase enzyme and hence  
 CC prevent viral infection. Viral infections that may be treated include  
 CC human immunodeficiency virus (HIV), Epstein Barr virus (EBV), herpes  
 CC simplex virus (HSV), human papilloma virus (HPV), adenovirus, respiratory  
 CC syncytial virus (RSV), cytomegalovirus (CMV) and hepatitis B virus (HBV),  
 CC especially HIV-1 infection  
 XX SQ Sequence 10 BP; 0 A; 0 C; 7 G; 3 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GTGGG 5  
 Db 1 GTGGG 5  
 |||||  
 RESULT 46  
 AAT59107/C  
 ID AAT59107 standard; RNA; 10 BP.  
 XX AAT59107;  
 AC AAT59107;  
 XX 25-MAR-2003 (revised)  
 DT 23-APR-1997 (first entry)  
 XX Activated H-ras mRNA antisense oligonucleotide 3283.  
 XX Activated H-ras; antisense; oligonucleotide; inhibition; affinity; ss.  
 KW Synthetic.  
 OS US5582972-A.  
 PN 10-DEC-1996.  
 PD 14-DEC-1992; 92US-00990303.  
 PF 14-JUN-1991; 91US-00715196.  
 PR (ISIS-) ISIS PHARM INC.  
 XX Ecker D, Freier S, Lima W, Monia B;  
 XX WPI; 1997-042296/04.  
 XX Anti-sense oligonucleotide(s) targeted to hairpin structure - of  
 PT activated H-ras mRNA, useful for inhibiting functions of Ras derived DNA  
 PT or RNA.  
 XX Claim 4; Col 13; 16pp; English.

CC Oligonucleotides AAT59103-8 are antisense sequences targeted to  
 CC nucleotides 18-64 of the activated H-ras mRNA (AAT59102). The  
 CC oligonucleotides inhibit the function of RNA or DNA derived from the Ras  
 CC gene. The oligonucleotides are selected by comparing the affinities of  
 CC the oligonucleotides for their target region with the affinities for an  
 CC oligonucleotide complement with the same number of nucleotides. Those  
 CC oligonucleotides which have affinity for the target region not less than  
 CC one thousandth of the affinity for the oligonucleotide complement are  
 CC used to inhibit the H-ras sequence. (Updated on 25-MAR-2003 to correct PF  
 CC field.)

XX  
 SQ Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 8 GTGGG 4

RESULT 47  
 AAT59104/c  
 ID AAT59104 standard; DNA; 10 BP.

XX  
 AC AAT59104;

XX  
 DT 25-MAR-2003 (revised)  
 DT 23-APR-1997 (first entry)

XX  
 DE Activated H-ras mRNA antisense oligonucleotide 3271.

XX  
 KW Activated H-ras; antisense; oligonucleotide; inhibition; affinity; ss.

XX  
 OS Synthetic.

XX  
 PN US5582972-A.

XX  
 PD 10-DEC-1996.

XX  
 PF 14-DEC-1992; 92US-00990303.

XX  
 PR 14-JUN-1991; 91US-00715196.

XX  
 PA (ISIS-) ISIS PHARM INC.

XX  
 PI Ecker D, Freier S, Lima W, Monia B;

XX  
 DR WPI; 1997-042296/04.

XX  
 PT Anti-sense oligo:nucleotide(s) targeted to hairpin structure - of  
 PT activated H-ras mRNA, useful for inhibiting functions of Ras derived DNA  
 PT or RNA.

XX  
 PS Claim 4; Col 11; 16pp; English.

XX  
 CC Oligonucleotides AAT59103-8 are antisense sequences targeted to  
 CC nucleotides 18-64 of the activated H-ras mRNA (AAT59102). The  
 CC oligonucleotides inhibit the function of RNA or DNA derived from the Ras  
 CC gene. The oligonucleotides are selected by comparing the affinities of  
 CC the oligonucleotides for their target region with the affinities for an  
 CC oligonucleotide complement with the same number of nucleotides. Those  
 CC oligonucleotides which have affinity for the target region not less than  
 CC one thousandth of the affinity for the oligonucleotide complement are  
 CC used to inhibit the H-ras sequence. (Updated on 25-MAR-2003 to correct PF  
 CC field.)

XX  
 SQ Sequence 10 BP; 2 A; 5 C; 2 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 8 GTGGG 4

RESULT 48  
 AAV10687/c  
 ID AAV10687 standard; DNA; 10 BP.

XX  
 AC AAV10687;

XX  
 DT 21-JUL-1998 (first entry)

XX  
 DE Human breast cancer gene differential display primer #5.

XX  
 KW Breast cancer; malignant transformation; diagnostic; therapeutic;  
 KW screening; primer; ss.

XX  
 OS Synthetic.

XX  
 OS Homo sapiens.

XX  
 PN WO9738085-A2.

XX  
 PD 16-OCT-1997.

XX  
 PF 09-APR-1997; 97WO-US005930.

XX  
 PR 10-APR-1996; 96US-0015167P.

XX  
 PR 05-JUN-1996; 96WO-US009286.

XX  
 PR 06-JUN-1996; 96US-0019202P.

XX  
 PR 11-JUL-1996; 96US-00678280.

XX  
 PA (CALP-) CALIFORNIA PACIFIC MEDICAL CENT RES INST.

XX  
 PI Smith H, Chen L;

XX  
 DR WPI; 1997-512705/47.

XX  
 PT Breast cancer genes - used to develop products to design or screen  
 PT diagnostic reagents or therapeutic compounds.

XX  
 PS Example 2; Page 46; 118pp; English.

XX  
 CC Primers AAV10683-V10688 are used to obtain novel human breast cancer  
 CC genes by differential display. The identified genes or fragments of these  
 CC genes can be used for identifying genes and gene products that are  
 CC intimately related to malignant transformation or maintenance of the  
 CC malignant properties of cancer cells. It can also be used to design or  
 CC screen diagnostic reagents or therapeutic compounds. Kits are included  
 CC within the scope of the invention

XX  
 SQ Sequence 10 BP; 3 A; 6 C; 1 G; 0 T; 0 U; 0 Other;

Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 10 GTGGG 6

RESULT 49

AAT96115

ID AAT96115 standard; RNA; 10 BP.

XX  
 AC AAT96115;

XX  
 DT 31-MAR-1998 (first entry)

XX  
 DE Target site 1 sequence.

XX



KW Determination; oligonucleotide; specific activity; therapy;  
 KW target biomolecule; randomised oligonucleotide; diagnosis; research;  
 KW target site; ss.  
 XX  
 OS Synthetic.  
 XX  
 XX US5686242-A.  
 PN  
 XX 11-NOV-1997.  
 PD  
 XX 27-OCT-1994; 94US-00330000.  
 XX  
 PF  
 XX 05-SEP-1991; 91US-00755485.  
 PR  
 XX 04-SEP-1992; 92WO-US007489.  
 PR  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX Lima WF, Bruice TW;  
 PI  
 XX WPI; 1997-558135/51.  
 DR  
 XX Determination of oligo-nucleotide with specific activity for target bio-  
 PT molecule - using set of randomised oligo-nucleotide(s).  
 XX  
 XX Example 17; Col 31-32; 22pp; English.  
 PS  
 XX The present sequence was used in the development of a method of  
 CC determining an oligonucleotide having specific activity for a target  
 CC biomolecule. The method comprises assaying a set of randomised  
 CC oligonucleotides for activity against a target biomolecule, separating  
 CC active from inactive oligonucleotides and recovering, amplifying and  
 CC determining the nucleic acid sequence of the active oligonucleotides. The  
 CC oligonucleotides can be used for therapeutic, diagnostic and research  
 CC purposes  
 XX  
 XX Sequence 10 BP; 0 A; 2 C; 6 G; 0 T; 2 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 80.0%; Pred. NO. 1.7e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGGG 5  
 Db |::|||  
 3 GUGGG 7  
 RESULT 50  
 AAT96109/c  
 ID AAT96109 standard; RNA; 10 BP.  
 XX  
 XX AAT96109;  
 AC  
 XX 31-MAR-1998 (first entry)  
 DT  
 XX Calibration oligonucleotide.  
 DE  
 XX Determination; oligonucleotide; specific activity; therapy;  
 KW target biomolecule; randomised oligonucleotide; diagnosis; research;  
 KW calibration oligonucleotide; ss.  
 XX  
 OS Synthetic.  
 OS  
 XX US5686242-A.  
 PN  
 XX 11-NOV-1997.  
 PD  
 XX 27-OCT-1994; 94US-00330000.  
 XX  
 PF  
 XX 05-SEP-1991; 91US-00755485.  
 PR  
 XX 04-SEP-1992; 92WO-US007489.  
 PR  
 XX (ISIS-) ISIS PHARM INC.  
 PA  
 XX Lima WF, Bruice TW;  
 PI  
 XX WPI; 1997-558135/51.  
 DR  
 XX Determination of oligo-nucleotide with specific activity for target bio-  
 PT molecule - using set of randomised oligo-nucleotide(s).  
 XX  
 XX Example 17; Col 31-32; 22pp; English.  
 PS  
 XX The present sequence was used in the development of a method of  
 CC determining an oligonucleotide having specific activity for a target  
 CC biomolecule. The method comprises assaying a set of randomised  
 CC oligonucleotides for activity against a target biomolecule, separating  
 CC active from inactive oligonucleotides and recovering, amplifying and  
 CC determining the nucleic acid sequence of the active oligonucleotides. The  
 CC oligonucleotides can be used for therapeutic, diagnostic and research  
 CC purposes  
 XX  
 XX Sequence 10 BP; 0 A; 2 C; 6 G; 0 T; 2 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 80.0%; Pred. NO. 1.7e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGGG 5  
 Db |::|||  
 3 GUGGG 7

PI Lima WF, Bruice TW;  
 XX  
 DR WPI; 1997-558135/51.  
 XX  
 XX Determination of oligo-nucleotide with specific activity for target bio-  
 PT molecule - using set of randomised oligo-nucleotide(s).  
 XX  
 XX Example 12; Col 27-28; 22pp; English.  
 PS  
 XX The present sequence was used in the development of a method of  
 CC determining an oligonucleotide having specific activity for a target  
 CC biomolecule. The method comprises assaying a set of randomised  
 CC oligonucleotides for activity against a target biomolecule, separating  
 CC active from inactive oligonucleotides and recovering, amplifying and  
 CC determining the nucleic acid sequence of the active oligonucleotides. The  
 CC oligonucleotides can be used for therapeutic, diagnostic and research  
 CC purposes  
 XX  
 XX Sequence 10 BP; 2 A; 5 C; 1 G; 0 T; 2 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 5; DB 2; Length 10;  
 Best Local Similarity 100.0%; Pred. NO. 1.7e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGGG 5  
 Db |::|||  
 8 GTGGG 4  
 Search completed: January 7, 2005, 07:12:05  
 Job time : 258.4 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 04:56:02 ; Search time 2222.4 Seconds  
 (without alignments)  
 81.983 Million cell updates/sec

Title: GTGGG  
 Perfect score: 5  
 Sequence: 1 gtggg 5

Scoring table: IDENTITY NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 156772

Minimum DB seq length: 10  
 Maximum DB seq length: 50

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 500 summaries

Database : EST:  
 1: gb\_est1:\*  
 2: gb\_est2:\*  
 3: gb\_hc:\*  
 4: gb\_est3:\*  
 5: gb\_est4:\*  
 6: gb\_est5:\*  
 7: gb\_est6:\*  
 8: gb\_gsa1:\*  
 9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	5	100.0	10	9	CL436411
C 2	5	100.0	10	9	CL436420
C 3	5	100.0	10	9	CL652677
C 4	5	100.0	11	5	BO593914
C 5	5	100.0	11	9	CL675669
C 6	5	100.0	12	5	BO592925
C 7	5	100.0	12	5	BO594497
C 8	5	100.0	12	5	BO595544
C 9	5	100.0	12	9	CL423646
C 10	5	100.0	13	1	AA910741
C 11	5	100.0	13	4	EG810452
C 12	5	100.0	13	5	BO592041
C 13	5	100.0	13	5	BO593629
C 14	5	100.0	13	5	BO593844
C 15	5	100.0	13	5	BO594526
C 16	5	100.0	13	5	BO595480
C 17	5	100.0	13	7	CF542943
C 18	5	100.0	13	9	AJ588888
C 19	5	100.0	13	9	AJ593426
C 20	5	100.0	14	4	BM395358
C 21	5	100.0	14	5	BO595292
C 22	5	100.0	14	5	BQ605961
C 23	5	100.0	14	9	AJ587271
C 24	5	100.0	15	1	AJ682954

25	5	100.0	15	5	BO594756
26	5	100.0	15	5	BO595235
C 27	5	100.0	15	6	CA851710
C 28	5	100.0	15	7	CF543306
C 29	5	100.0	15	7	CF543404
C 30	5	100.0	16	1	AA937364
C 31	5	100.0	16	1	AI248882
C 32	5	100.0	16	1	AI564478
C 33	5	100.0	16	1	AI569544
C 34	5	100.0	16	1	AI590540
C 35	5	100.0	16	1	AI684114
C 36	5	100.0	16	1	AI735054
C 37	5	100.0	16	1	AI749229
C 38	5	100.0	16	2	BE586084
C 39	5	100.0	16	4	BM396802
C 40	5	100.0	16	4	BM399406
C 41	5	100.0	16	5	BO592176
C 42	5	100.0	16	5	BO593213
C 43	5	100.0	16	5	BO595114
C 44	5	100.0	16	7	CF543332
C 45	5	100.0	16	9	AJ596548
C 46	5	100.0	17	1	AJ666397
C 47	5	100.0	17	4	BM395627
C 48	5	100.0	17	4	BM397301
C 49	5	100.0	17	5	BO590447
C 50	5	100.0	17	5	BO594949
C 51	5	100.0	17	7	CF921142
C 52	5	100.0	17	9	AJ592362
C 53	5	100.0	17	9	AJ597423
C 54	5	100.0	18	4	BG925569
C 55	5	100.0	18	4	BM399785
C 56	5	100.0	18	4	BM401236
C 57	5	100.0	18	5	BO593882
C 58	5	100.0	18	5	BO594466
C 59	5	100.0	18	5	BO901245
C 60	5	100.0	18	9	AJ591945
C 61	5	100.0	18	9	AJ595830
C 62	5	100.0	18	9	CL436272
C 63	5	100.0	19	1	AA878747
C 64	5	100.0	19	1	AA909236
C 65	5	100.0	19	1	AA911671
C 66	5	100.0	19	1	AA928040
C 67	5	100.0	19	1	AI058541
C 68	5	100.0	19	1	AI364573
C 69	5	100.0	19	1	AI431460
C 70	5	100.0	19	1	AI537209
C 71	5	100.0	19	1	AI641650
C 72	5	100.0	19	1	AI718147
C 73	5	100.0	19	1	AI807936
C 74	5	100.0	19	1	AJ649686
C 75	5	100.0	19	1	AJ662060
C 76	5	100.0	19	1	AJ686305
C 77	5	100.0	19	2	AW063940
C 78	5	100.0	19	4	BM397569
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C 81	5	100.0	19	5	BO589613
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C 85	5	100.0	19	8	AZ307733
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C 94	5	100.0	19	8	AZ355195
C 95	5	100.0	19	8	AZ368655
C 96	5	100.0	19	8	AZ369361
C 97	5	100.0	19	8	AZ369369

BO594756	E012441-0
BO595235	E012708-0
CA851710	D16F12_L2
CF543306	S014668-0
CF543404	S014668-0
AA937364	OJ08F10.8
AI248882	QU73E07.X
AI564478	TS57G09.X
AI569544	TO28D10.X
AI590540	TLW1C02.X
AI684114	TX79D02.X
AI735054	AS88B02.X
AI749229	AT41A02.X
BE586084	EST8P77
BM396802	S009-0-25
BM399406	S009-0-57
BO592176	E012696-0
BO593213	E012795-0
BO595114	E012708-0
CF543332	S014665-0
AJ596548	Arabidops
AJ666397	AJ666397
BM395627	S009-0-1-
BM397301	S009-0-30
BO590447	E012839-0
BO594949	S012554-0
CF921142	gmfrhrw3-
AJ587423	Arabidops
AJ592362	Arabidops
BG925569	HNC5-1-E2
BM399785	S009-0-61
BM401236	S009-0-84
BO593882	E012763-0
BO594466	E012442-0
BO901245	hasp002xj
AJ591945	Arabidops
AJ595830	Arabidops
CL436272	PST2635-N
AA878747	OF85B01.8
AA909236	OL08A11.8
AA911671	OL49F08.8
AA928040	OI58G09.8
AI058541	OY98C11.X
AI364573	QW37G03.X
AI431460	TH4OC01.X
AI537209	TP06F07.X
AI641650	FC22A01.X
AI718147	AB42F11.X
AI807936	WFS2A09.X
AJ649686	AJ649686
AJ662060	AJ662060
AJ686305	AJ686305
AW063940	DP0975.KR
BM397569	S009-0-34
BM399684	S009-0-60
BM399791	S009-0-61
BO589613	E012681-0
BO589692	E012679-0
CF293217	30DGS--02
D44776	HUMSUPY214
AZ307733	LM0009C12
AZ314143	LM0030K16
AZ314511	LM0031B20
AZ323681	LM0045B13
AZ324165	LM0046C06
AZ324865	LM0047G10
AZ341989	LM0074H13
AZ343228	LM0076M05
AZ351194	LM0089A08
AZ355195	LM0094G22
AZ368655	LM0118P13
AZ369361	LM0119I23
AZ369369	LM0119K19

c	98	5	100.0	19	8	A3375581	AZ375581	1M0129805	171	5	100.0	20	8	AZ498694	AZ498694	1M0336808
	99	5	100.0	19	8	A3379786	AZ379786	1M0135X09	172	5	100.0	20	8	AZ511017	AZ511017	1M0355C19
	100	5	100.0	19	8	A3381798	AZ381798	1M0138G01	173	5	100.0	20	8	AZ511024	AZ511024	1M0355D22
	101	5	100.0	19	8	A2412553	AZ412553	1M0186M03	c 174	5	100.0	20	8	AZ514611	AZ514611	1M0361M20
	102	5	100.0	19	8	A2422531	AZ422531	1M0201E16	c 175	5	100.0	20	8	AZ579536	AZ579536	1M0367I03
	103	5	100.0	19	8	A2435252	AZ435252	1M0222D11	c- 176	5	100.0	20	8	AZ582391	AZ582391	1M0374F17
	c 104	5	100.0	19	8	A2442378	AZ442378	1M0236K18	177	5	100.0	20	8	AZ583699	AZ583699	1M0378G15
	c 105	5	100.0	19	8	A2445563	AZ445563	1M0241P18	178	5	100.0	20	8	AZ590476	AZ590476	1M0400P06
	c 106	5	100.0	19	8	A2447936	AZ447936	1M0245O18	179	5	100.0	20	8	AZ601843	AZ601843	1M0420M13
	c 107	5	100.0	19	8	A2452087	AZ452087	1M0251F18	180	5	100.0	20	8	AZ609449	AZ609449	1M0434D20
	108	5	100.0	19	8	A2453412	AZ453412	1M0254I10	181	5	100.0	20	8	AZ627848	AZ627848	1M0474G14
	109	5	100.0	19	8	A2466725	AZ466725	1M0277C09	c 182	5	100.0	20	8	AZ628809	AZ628809	1M0481C17
	c 110	5	100.0	19	8	A2478164	AZ478164	1M0298I05	183	5	100.0	20	8	AZ651800	AZ651800	1M0522N07
	111	5	100.0	19	8	A2478277	AZ478277	1M0298B16	184	5	100.0	20	8	AZ652975	AZ652975	1M0526I20
	112	5	100.0	19	8	A2478905	AZ478905	1M0299B18	185	5	100.0	20	8	AZ653361	AZ653361	1M0527D04
	113	5	100.0	19	8	A2482050	AZ482050	1M0306H20	186	5	100.0	20	8	AZ663955	AZ663955	1M0543D22
	114	5	100.0	19	8	A2485264	AZ485264	1M0312D02	187	5	100.0	20	8	AZ665998	AZ665998	1M0547F17
	115	5	100.0	19	8	A2489548	AZ489548	1M0322L05	c 188	5	100.0	20	8	AZ666896	AZ666896	1M0549A24
	c 116	5	100.0	19	8	A2510143	AZ510143	1M0354F21	189	5	100.0	20	8	AZ770749	AZ770749	1M0572B01
	117	5	100.0	19	8	A2512762	AZ512762	1M0358M04	c 190	5	100.0	20	8	AZ776456	AZ776456	2M0100Q03
	c 118	5	100.0	19	8	A2514405	AZ514405	1M0361L03	c 191	5	100.0	20	8	AZ776807	AZ776807	2M0010H14
	c 119	5	100.0	19	8	A2579133	AZ579133	1M0363B04	192	5	100.0	20	8	AZ782314	AZ782314	2M0012D03
	120	5	100.0	19	8	A2585820	AZ585820	1M0391I15	193	5	100.0	20	8	AZ782816	AZ782816	2M0024F05
	121	5	100.0	19	8	A2626573	AZ626573	1M0466J24	194	5	100.0	20	8	AZ793982	AZ793982	2M0047I05
	122	5	100.0	19	8	A2644418	AZ644418	1M0508B20	195	5	100.0	20	8	AZ802167	AZ802167	2M0061A07
	c 123	5	100.0	19	8	A2646713	AZ646713	1M0512D20	196	5	100.0	20	8	AZ808291	AZ808291	2M0071D09
	124	5	100.0	19	8	A2651870	AZ651870	1M0522M15	197	5	100.0	20	8	AZ808381	AZ808381	2M0071F23
	125	5	100.0	19	8	A2656937	AZ656937	1M0532K13	198	5	100.0	20	8	AZ828544	AZ828544	2M0105O04
	126	5	100.0	19	8	A2761834	AZ761834	1M0556E19	c 199	5	100.0	20	8	AZ828665	AZ828665	2M0105L16
	127	5	100.0	19	8	A2768418	AZ768418	1M0568H23	c 200	5	100.0	20	8	AZ830013	AZ830013	2M0109C05
	128	5	100.0	19	8	A2780591	AZ780591	2M0018B09	201	5	100.0	20	8	AZ833488	AZ833488	2M0115B12
	129	5	100.0	19	8	A2782026	AZ782026	2M0021I23	c 202	5	100.0	20	8	AZ835099	AZ835099	2M0129I07
	c 130	5	100.0	19	8	A2785573	AZ785573	2M0029L02	203	5	100.0	20	8	AZ836147	AZ836147	2M0130Q14
	131	5	100.0	19	8	A2786308	AZ786308	2M0031B17	204	5	100.0	20	8	AZ846437	AZ846437	2M0146E10
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	137	5	100.0	19	8	A2822954	AZ822954	2M0096I10	210	5	100.0	20	9	CL660020	CL660020	PR10135d
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	139	5	100.0	19	8	A2834875	AZ834875	2M0117L13	212	5	100.0	20	9	AG199663	AG199663	Pan trogl
	c 140	5	100.0	19	8	A2837373	AZ837373	2M0132C07	c 213	5	100.0	21	1	AJ662932	AJ662932	AJ662932
	141	5	100.0	19	8	A2859728	AZ859728	2M0165M22	214	5	100.0	21	1	AJ662980	AJ662980	AJ662980
	c 142	5	100.0	19	8	A2864599	AZ864599	2M0174G17	215	5	100.0	21	1	AU254493	AU254493	AU254493
	143	5	100.0	19	8	A2967656	AZ967656	2M0238M09	216	5	100.0	21	2	AU257028	AU257028	AU257028
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C 451	5	100.0	23	8	AZ628572	AZ628572 1M0480D16								
C 452	5	100.0	23	8	AZ643860	AZ643860 1M0507J04								
C 453	5	100.0	23	8	AZ647047	AZ647047 1M0513B22								
C 454	5	100.0	23	8	AZ654389	AZ654389 1M0528H06								
C 455	5	100.0	23	8	AZ759994	AZ759994 1M0553N14								
C 456	5	100.0	23	8	AZ762598	AZ762598 1M0557I12								
C 457	5	100.0	23	8	AZ766803	AZ766803 1M0564B12								
C 458	5	100.0	23	8	AZ768060	AZ768060 1M0567P13								
C 459	5	100.0	23	8	AZ774668	AZ774668 2M0004N08								
C 460	5	100.0	23	8	AZ775223	AZ775223 2M0007I20								
C 461	5	100.0	23	8	AZ783602	AZ783602 2M0025F02								
C 462	5	100.0	23	8	AZ785926	AZ785926 2M0030K08								

RESULT 1

CL436411/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CL436411

10 bp

DNA

linear

GSS 18-MAR-2004

PST292-1.seq

MICB1 Mus musculus genomic clone

PST292-1.seq

similar

to D1VERTD808E, genomic survey sequence.

CL436411

GSS.

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Hicks, G.G.

1 (bases 1 to 10)

www.EScells.ca

Unpublished (2002)

Contact: Hicks GG

Mammalian Functional Genomics Centre

Manitoba Institute of Cell Biology, University of Manitoba

ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada

Tel: 204 787 2133

Fax: 204 787 2190

Email: hicksgg@cc.umanitoba.ca

U3NeosV1 gene trap. Tag generated by plasmid rescue. Additional

sequence information and target gene cloning can be generated. ES

cell line harboring insertion mutation of target gene is available.

Sequence analysis available from

http://140.193.242.7/esdb/public\_search\_frame.php?PST=PST292-1.seq

Class: Gene Trap.

Location/Qualifiers

FEATURES

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/db_xref="taxon:10090"
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/sex="Male"
/cell_type="Embryonic stem cell"
/cell_lines="D3H (J1 subclone)"
/clone_lib="M1CB1"
/note="Vector: U3NeoSV1"

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Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 9 GTGGG 5

RESULT 2
CL436420/c
LOCUS      CL436420      10 bp      DNA      linear      GSS 18-WAR-2004
DEFINITION PST2947-NR.Seq M1CB1 Mus musculus genomic clone PST2947-NR.Seq
similar to D130048F08RIK, genomic survey sequence.
ACCESSION  CL436420
VERSION     CL436420.1 GI:45571196
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    1 (bases 1 to 10)
AUTHORS      Hicks G.G.
TITLE        www.Escells.ca
JOURNAL      Unpublished (2002)
COMMENT      Contact: Hicks GG
              Mammalian Functional Genomics Centre
              Manitoba Institute of Cell Biology, University of Manitoba
              ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
              Tel: 204 787 2133
              Fax: 204 787 2190
              Email: hicksgg@cc.umanitoba.ca
              U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
              sequence information and target gene cloning can be generated. ES
              cell line harboring insertion mutation of target gene is available.
              Sequence analysis available from
              http://140.193.242.7/esdb/public_search_frame.php?PST=PST2947-NR.Se
              q
              Class: Gene Trap.

FEATURES             Location/Qualifiers
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                     /clone="PST2947-NR.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_lines="D3H (J1 subclone)"
                     /clone_lib="M1CB1"
                     /note="Vector: U3NeoSV1"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 5 GTGGG 1

RESULT 3
CL652677/c
LOCUS      CL652677      10 bp      DNA      linear      GSS 09-JUL-2004
DEFINITION PR10115c.A09 - PR10115c.B21 (10) Mixed stage fosmid library of P.
pacificus var. California Pristionchus pacificus genomic, genomic
survey sequence.
ACCESSION  CL652677
VERSION     CL652677.1 GI:50131455
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
ORGANISM    Pristionchus pacificus
REFERENCE    1 (bases 1 to 10)
AUTHORS      Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE        AppaDB: an AcedB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL      Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT      Contact: Sommer RJ
              Evolutionary Biology
              Max-Planck-Institute for Developmental Biology
              Spemannstr. 37-39, Tuebingen D-72076, Germany
              Tel: 00497071601371
              Fax: 00497071601498
              Email: ralf.sommer@tuebingen.mpg.de
              This library was generated at Caltech, Pasadena, USA and end
              sequenced at Vancouver, Canada.
              Seq primer: T7
              Class: fosmid ends.

FEATURES             Location/Qualifiers
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                     /strain="California"
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                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 10 GTGGG 6

RESULT 4
BQ593914
LOCUS      BQ593914      11 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION S015507-024-025-N20-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-025-N20 5-PRIME, mRNA sequence.
ACCESSION  BQ593914
VERSION     BQ593914.1 GI:26123497
KEYWORDS    EST.
SOURCE      Beta vulgaris
ORGANISM    Beta vulgaris
REFERENCE    1 (bases 1 to 11)
AUTHORS      Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
              Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
              and Radelof,U.
              Construction of a 'unigene' cDNA clone set by oligonucleotide
              fingerprinting allows access to 25 000 potential sugar beet genes
              Plant J. 32 (5), 845-857 (2002)
JOURNAL      22362189
MEDLINE     12472698
PUBMED

```

COMMENT	CONTACT: Weishaar B ADIS DNA core facility at MPiZ Max-Planck-Institute for Plant Breeding Research Carl-von-Linne Weg 10, 50829 Koeln, Germany Fax: 00492215062851 Email: weishaar@mpiz-koeln.mpg.de Insert Length: 11 Std Error: 0.00 Plate: 25 row: N column: 20 Seq primer: SP6; CATACGATTAGTGACACTATAG. Location/Qualifiers 1. .11 /organism="Beta vulgaris" /mol_type="mRNA" /cultivar="KWS2320 (double haploid, monogerm breeding line)" /db_xref="GABI:192937" /db_xref="taxon:161934" /clone="024-025-N20" /tissue_type="developing root" /lab_host="EMDH10B" /clone_lib="MPiZ-ADIS-024-developing root" /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites Sali-NotI, primer sites and orientation: SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN	Query Match 100.0%; Score 5; DB 5; Length 11; Best Local Similarity 100.0%; Pred. No. 9.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 GTGGG 5       Db 7 GTGGG 11
FEATURES	source CL675669.1 GI:50180372 Pristionchus pacificus Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. 1 (bases 1 to 11) Srinivasan,J., Otto G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppADB: an AcedB database for the nematode satellite organism Nucleic Acids Res. 32 (1), D421-D422 (2004) Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada. Seq primer: T7 Class: fosmid ends. Location/Qualifiers 1. .11
ORIGIN	Query Match 100.0%; Score 5; DB 5; Length 11; Best Local Similarity 100.0%; Pred. No. 9.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 GTGGG 5       Db 7 GTGGG 11
FEATURES	source CL675669/c LOCUS DEFINITION CL675669.1 GI:50180372 Pristionchus pacificus Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. 1 (bases 1 to 11) Srinivasan,J., Otto G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppADB: an AcedB database for the nematode satellite organism Nucleic Acids Res. 32 (1), D421-D422 (2004) Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada. Seq primer: T7 Class: fosmid ends. Location/Qualifiers 1. .11
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FEATURES	source CL675669/c LOCUS DEFINITION CL675669.1 GI:50180372 Pristionchus pacificus Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. 1 (bases 1 to 11) Srinivasan,J., Otto G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppADB: an AcedB database for the nematode satellite organism Nucleic Acids Res. 32 (1), D421-D422 (2004) Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada. Seq primer: T7 Class: fosmid ends. Location/Qualifiers 1. .11
ORIGIN	Query Match 100.0%; Score 5; DB 5; Length 11; Best Local Similarity 100.0%; Pred. No. 9.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 GTGGG 5       Db 7 GTGGG 11
FEATURES	source CL675669/c LOCUS DEFINITION CL675669.1 GI:50180372 Pristionchus pacificus Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. 1 (bases 1 to 11) Srinivasan,J., Otto G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppADB: an AcedB database for the nematode satellite organism Nucleic Acids Res. 32 (1), D421-D422 (2004) Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada. Seq primer: T7 Class: fosmid ends. Location/Qualifiers 1. .11
ORIGIN	Query Match 100.0%; Score 5; DB 5; Length 11; Best Local Similarity 100.0%; Pred. No. 9.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 GTGGG 5       Db 7 GTGGG 11
FEATURES	source CL675669/c LOCUS DEFINITION CL675669.1 GI:50180372 Pristionchus pacificus Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. 1 (bases 1 to 11) Srinivasan,J., Otto G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppADB: an AcedB database for the nematode satellite organism Nucleic Acids Res. 32 (1), D421-D422 (2004) Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada. Seq primer: T7 Class: fosmid ends. Location/Qualifiers 1. .11
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ORIGIN	Query Match 100.0%; Score 5; DB 5; Length 11; Best Local Similarity 100.0%; Pred. No. 9.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 GTGGG 5       Db 7 GTGGG 11
FEATURES	source CL675669/c LOCUS DEFINITION CL675669.1 GI:50180372 Pristionchus pacificus Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. 1 (bases 1 to 11) Srinivasan,J., Otto G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppADB: an AcedB database for the nematode satellite organism Nucleic Acids Res. 32 (1), D421-D422 (2004) Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada. Seq primer: T7 Class: fosmid ends. Location/Qualifiers 1. .11
ORIGIN	Query Match 100.0%; Score 5; DB 5; Length 11; Best Local Similarity 100.0%; Pred. No. 9.4e+06; Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 1 GTGGG 5       Db 7 GTGGG 11
FEATURES	source CL675669/c LOCUS DEFINITION CL675669.1 GI:50180372 Pristionchus pacificus Pristionchus pacificus Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus. 1 (bases 1 to 11) Srinivasan,J., Otto G.W., Kahlow,U., Geisler,R. and Sommer,R.J. AppADB: an AcedB database for the nematode satellite organism Nucleic Acids Res. 32 (1), D421-D422 (2004) Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 004



Query Match 100.0%; Score 5; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
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 Db 5 GTGGG 1

RESULT 7  
 BQ594497/c  
 LOCUS  
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 cDNA clone 024-024-P14 5-PRIME, mRNA sequence.

ACCESSION BQ594497  
 VERSION BQ594497.1 GI:26124080  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 12)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE  
 PUBMED 22362189  
 COMMENT 12472698

CONTACT: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
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 Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES  
 Location/Qualifiers  
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 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
 Query Match 100.0%; Score 5; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
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Qy 1 GTGGG 5  
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 Db 5 GTGGG 1

RESULT 8  
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 LOCUS  
 DEFINITION E012691-024-022-A12-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
 cDNA clone 024-022-A12 5-PRIME, mRNA sequence.

ACCESSION BQ595544  
 VERSION BQ595544.1 GI:26125127  
 KEYWORDS EST.  
 SOURCE  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.

REFERENCE 1 (bases 1 to 12)  
 AUTHORS Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)

JOURNAL MEDLINE  
 PUBMED 22362189  
 COMMENT 12472698

CONTACT: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 12 Std Error: 0.00  
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 Seq primer: SP6; CATACGATTAGTGACACTATAG.

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 line)"  
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 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN  
 Query Match 100.0%; Score 5; DB 5; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 9.4e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 8 GTGGG 12

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Weishaar B

ADIS DNA core facility at MP1Z

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 12 Std Error: 0.00

Plate: 24 row: P column: 14

Seq primer: SP6; CATACGATTAGTGACACTATAG.

FEATURES

Location/Qualifiers

1..12

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/mol\_type="mRNA"

/cultivar="KWS2320 (double haploid, monogerm breeding

line)"

/db\_xref="GABI:191314"

/db\_xref="taxon:161934"

/clone="024-022-A12"

/tissue\_type="developing root"

/lab\_host="EMDH10B"

/clone\_lib="MP1Z-ADIS-024-developing root"

/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;

cDNA library from sugar beet, library provided by KWS

Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:

b.schulz@kws.de; cloning sites Sali-NotI, primer sites and

orientation:

SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:

Sequencing granted in the context of the GABI-Beet

project, local PI: Dr. Katharina Schneider, coordinator:

Prof. Christian Jung; Sequence submission managed by

RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 12;

Best Local Similarity 100.0%; Pred. No. 9.4e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5

|||||

Db 8 GTGGG 12

RESULT 9

CL423646/c

LOCUS

DEFINITION O1S0726-07C1-E03 UniformMu MUTAIL Library Zea mays genomic clone

CL423646

O1S0726-07C1-E03, genomic survey sequence.

ACCESSION

CL423646

VERSION

CL423646.1 GI:45501690

KEYWORDS

GSS.

SOURCE

Zea mays



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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 13 GTGGG 9

RESULT 12
BQ592041/c
LOCUS
DEFINITION E012696-024-021-A18-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
ACCESSION BQ592041
VERSION E012696-024-021-A18 5-PRIME, mRNA sequence.
KEYWORDS
SOURCE BQ592041.1 GI:26121624
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 13)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Location/Qualifiers
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line)"
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/db_xref="taxon:161934"
/clone="024-021-A18"
/tissue_type="developing root"
/lab_host="EMDH10B"
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/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match 100.0%; Score 5; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 5 GTGGG 1

RESULT 13
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LOCUS
DEFINITION E012766-024-026-M06-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
ACCESSION BQ593629
VERSION E012766-024-026-M06 5-PRIME, mRNA sequence.
KEYWORDS
SOURCE BQ593629.1 GI:26123212
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 13)
AUTHORS Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
Plate: 26 row: N column: 02
Seq primer: SP6; CATACGATTAGTGACACTATAG.
Location/Qualifiers
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line)"
/db_xref="GABI:193221"
/db_xref="taxon:161934"
/clone="024-026-M06"
/tissue_type="developing root"
/lab_host="EMDH10B"
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/notes="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match 100.0%; Score 5; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 5 GTGGG 1

RESULT 14
BQ593844/c
LOCUS
DEFINITION E012764-024-026-M06-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
ACCESSION BQ593844
VERSION E012764-024-026-M06 5-PRIME, mRNA sequence.
KEYWORDS
SOURCE BQ593844.1 GI:26123427
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
COMMENT

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 13)  
Herwig,R.; Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)  
22362189  
12472698

Contact: Weisshaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 13 Std Error: 0.00  
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Seq primer: SP6: CATACGATTAGTGACACTATAG.

FEATURES  
source

Location/Qualifiers  
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line)"  
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/note="vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
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Db 5 GTGGG 9

RESULT 15  
BQ594526/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

BQ594526  
E012443-024-024-L11-SP6 MPiZ-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-024-L11 5-PRIME, mRNA sequence.  
BQ594526  
EST.  
Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 13)  
Herwig,R.; Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

MEDLINE  
PUBMED  
COMMENT

22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 13 Std Error: 0.00  
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Seq primer: SP6: CATACGATTAGTGACACTATAG.

FEATURES  
source

Location/Qualifiers  
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cDNA library from sugar beet, library provided by KWS  
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
orientation:  
SP6-Sali-CCACGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
Sequencing granted in the context of the GABI-Beet  
project, local PI: Dr. Katharina Schneider, coordinator:  
Prof. Christian Jung; Sequence submission managed by  
RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 13;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 5 GTGGG 1

RESULT 16  
BQ595480  
LOCUS  
DEFINITION

BQ595480  
E012690-024-022-G15-SP6 MPiZ-ADIS-024-developing root Beta vulgaris  
cDNA clone 024-022-G15 5-PRIME, mRNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

BQ595480  
BQ595480  
EST.  
Beta vulgaris  
Beta vulgaris

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.  
1 (bases 1 to 13)  
Herwig,R.; Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,  
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
and Radelof,U.

Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

JOURNAL  
MEDLINE  
PUBMED  
COMMENT

22362189  
12472698  
Contact: Weisshaar B  
ADIS DNA core facility at MPiZ  
Max-Planck-Institute for Plant Breeding Research  
Carl-von-Linne Weg 10, 50829 Koeln, Germany  
Fax: 00492215062851  
Email: weisshaar@mpiz-koeln.mpg.de  
Insert Length: 13 Std Error: 0.00

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Location/Qualifiers
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/tissue_type="developing root"
/lab_host="EMDH10B"
/culture="MP1Z-ADIS-024-developing root"
/notes="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN
Query Match 100.0%; Score 5; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
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Db 8 GTGGG 12

RESULT 17
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LOCUS S014678-024-030-114-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone
DEFINITION 024-030-114 5-PRIME, mRNA sequence.
ACCESSION CF542943
VERSION CF542943.1 GI:34891383
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 13)
AUTHORS Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpi-z-koeln.mpg.de
Insert Length: 13 Std Error: 0.00
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Location/Qualifiers
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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
Query Match 100.0%; Score 5; DB 7; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
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Db 7 GTGGG 11

RESULT 18
AJ588888
LOCUS Arabidopsis thaliana T-DNA flanking sequence, right border, clone
DEFINITION 540D02, genomic survey sequence.
ACCESSION AJ588888
VERSION AJ588888.1 GI:37938512
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Crisard,C., DeRose,R., Pelleier,G.,
Lepiniec,I., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 13)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (6) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
FEATURES
source
location/Qualifiers
1. .13
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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/db_xref="taxon:3702"
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/misc_feature 1. .13
Arabidopsis thaliana T-DNA insertion lines"

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/note="T-DNA flanking sequence
right border"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 12

RESULT 19
AJ593426
LOCUS      13 bp      DNA      linear      GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
380B04, genomic survey sequence.
ACCESSION  AJ593426
VERSION     AJ593426.1 GI:37943050
KEYWORDS   GSS; left border; T-DNA flanking sequence.
SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE   1
AUTHORS    Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepintec, L., Caboche, M., and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE    2236355
PUBMED     1246565
REFERENCE   2 (bases 1 to 13)
AUTHORS    Balzerque, S.
DIRECT SUBMISSION
TITLES     Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).

FEATURES             Location/Qualifiers
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                     /organism="Arabidopsis thaliana"
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                     /clone="380B04"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
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                     left border"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 5 GTGGG 9

/note="T-DNA flanking sequence
right border"

ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 12

RESULT 20
BM395358
LOCUS      14 bp      mRNA      linear      EST 17-JAN-2002
DEFINITION Tetrachyena thermophila cDNA, mRNA sequence.
50072-2-8-G03.f.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrachyena thermophila cDNA, mRNA sequence.
ACCESSION  BM395358
VERSION     BM395358.1 GI:18195411
KEYWORDS   EST.
SOURCE     Tetrachyena thermophila
ORGANISM   Tetrachyena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrachymena; Tetrachymena.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Turkewitz, A.P., Karrer, K.M., Jahn, C., Orlas, E., Kirk, K.E.,
Frankel, J., and Klobutcher, L.
EST from Tetrachymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
TITLES     Contact: Turkewitz AP
JOURNAL    Molecular Genetics and Cell Biology
COMMENT    University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES             Location/Qualifiers
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                     /organism="Tetrachymena thermophila"
                     /mol_type="mRNA"
                     /strain="CU428.1"
                     /db_xref="taxon:5911"
                     /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
                     /note="Vector: Bluescript2 SK+; Details on library
                     preparation can be found in Chilcoat and Turkewitz (2001)
                     Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match      100.0%; Score 5; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 2 GTGGG 6

RESULT 21
BQ595292
LOCUS      14 bp      mRNA      linear      EST 06-DEC-2002
DEFINITION B012710-024-023-H07-SP6 MP12-ADIS-024-developing root Beta vulgaris
cDNA clone 024-023-H07 5-PRIME, mRNA sequence.
ACCESSION  BQ595292
VERSION     BQ595292.1 GI:26124875
KEYWORDS   EST.
SOURCE     Beta vulgaris
ORGANISM   Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1 (bases 1 to 14)
AUTHORS    Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.,
and Radelof, U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
MEDLINE    22362189
PUBMED     12472698
CONTACT    Contact: Weishaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851

```

```

Email: weishaa@piz-koeln.mpg.de
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Location/Qualifiers
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            /mol_type="mRNA"
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            /lab_host="EMDH10B"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation: SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"
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Qy 1 GTGGG 5
    |||||
Db 8 GTGGG 12

RESULT 22
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LOCUS
DEFINITION
    BRY 1556 wheat EST endosperm library Triticum aestivum cDNA 5',
    mRNA sequence.
ACCESSION
    BQ605961
VERSION
    BQ605961.1 GI:21555112
KEYWORDS
    EST.
SOURCE
    Triticum aestivum (bread wheat)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Pooideae; Triticeae; Triticum.
REFERENCE
    1 (bases 1 to 14)
    Clarke, B., Lambrecht, M. and Rhee, S.Y.
    Arabidopsis genomic information for interpreting wheat EST
    sequences
JOURNAL
    Funct. Integr. Genomics 3 (1-2), 33-38 (2003)
MEDLINE
    22478026
PUBMED
    12590341
COMMENT
    Contact: Lambrecht M
    The Arabidopsis Information Resource
    Carnegie Institution of Washington, Dept. of Plant Biology
    260 Panama Street, Stanford, CA 94305, USA
    Tel: 1 650 325 1521 x 251
    Fax: 1 650 325 3748
    Email: rhee@acoma.stanford.edu.
    Location/Qualifiers
FEATURES
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            /organism="Triticum aestivum"
            /mol_type="mRNA"
            /cultivar="Wyuana"
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/clone_lib="wheat EST endosperm library"
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Qy 1 GTGGG 5
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Db 6 GTGGG 2

RESULT 23
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LOCUS
DEFINITION
    Arabidopsis thaliana T-DNA flanking sequence, left border, clone
    257B04, genomic survey sequence.
ACCESSION
    AJ587271
VERSION
    AJ587271.1 GI:37936860
KEYWORDS
    GSS; left border; T-DNA flanking sequence.
SOURCE
    Arabidopsis thaliana (thale cress)
ORGANISM
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; euroside II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
    1
    Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
    Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G.,
    Lepiniec, L., Caboche, M. and Lecharny, A.
    T-DNA integration into the Arabidopsis genome depends on sequences
    of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED
    12446565
REFERENCE
    2 (bases 1 to 14)
    Balzergue, S.
    Direct Submission
TITLE
    Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
    Gaston Cremieux, 91057 Evry cedex, FRANCE
JOURNAL
    PCR was performed on DNA from transformants of Arabidopsis thaliana
    plants from INRA (Versailles). The DNA fragment(s) resulting from
    the PCR were directly sequenced from the left or the right border
    to determine the genomic sequence flanking the insertion. T-DNA
    derived sequences were removed. Information to order the
    corresponding mutant line and a link to a database providing a
    graphical display of the insertion site are available at
    http://dbgap-versailles.inra.fr/publiclines/. This sequence has
    been generated in the framework of the French plant genomics
    program 'Genoplante' (http://www.genoplante.com and
    http://genoplante-info.infobiogen.fr).
    Location/Qualifiers
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            /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
        1..14
            /note="T-DNA flanking sequence
            left border"
misc_feature
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    Best Local Similarity 100.0%; Pred. No. 9.5e+06;
    Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
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Db 5 GTGGG 9

RESULT 24

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AJ682954/c
LOCUS AJ682954 15 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ682954 CSEQAN04 Sus scrofa cDNA clone C0001800_K20, mRNA
sequence.
ACCESSION AJ682954
VERSION AJ682954.1 GI:49415544
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 15)
AUTHORS Anderson, S.I., Finlayson, H.A. and Archibald, A.L.
TITLE Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
v0.020425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options. Vector:pBluescriptII(KS+) R. Site1: EcoRI
R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
from pig uterus. Clones available from UK Centre for Functional
Genomics in Farm Animals, Roslin Institute, Roslin, Midlothian, UK,
EH25 9PS, www.arkgenomics.org.
FEATURES
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Location/Qualifiers
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/db_xref="taxon:9823"
/clone="C0001800_K20"
/tissue_type="uterus"
/clone_lib="CSEQAN04"
/note="Vector: pBluescriptII(KS+); Site 1: EcoRI; Site 2:
NotI; Single pass sequencing. Normalised library
constructed from pig uterus."
ORIGIN
Query Match 100.0%; Score 5; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 13 GTGGG 9
RESULT 25
BQ594756
LOCUS BQ594756 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012441-024-024-IL3-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-024-IL3 5-PRIME, mRNA sequence.
ACCESSION BQ594756
VERSION BQ594756.1 GI:26124339
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z

```

```

Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
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Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES
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Location/Qualifiers
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/clone="024-024-IL3"
/tissue_type="developing root"
/lab_hosts="EMDH10B"
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN
Query Match 100.0%; Score 5; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GTGGG 5
Db 8 GTGGG 12
RESULT 26
BQ595235
LOCUS BQ595235 15 bp mRNA linear EST 06-DEC-2002
DEFINITION E012708-024-023-C01-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-023-C01 5-PRIME, mRNA sequence.
ACCESSION BQ595235
VERSION BQ595235.1 GI:26124818
KEYWORDS EST.
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE 1 (bases 1 to 15)
AUTHORS Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
and Radelof, U.
TITLE Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL Plant J. 32 (5), 845-857 (2002)
MEDLINE 22362189
PUBMED 12472698
COMMENT Contact: Weishaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaa@mpiz-koeln.mpg.de
Insert Length: 15 Std Error: 0.00
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Seq primer: SP6; CATACGATTAGTGACACTATAG.
FEATURES
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Location/Qualifiers
1..15

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/tissue\_type="developing root"  
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/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinvanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 8 GTGGG 12

## RESULT 27

CAB851710  
LOCUS  
DEFINITION CAB851710 15 bp mRNA linear EST 01-AUG-2003  
D16F12 L24 12.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max  
cDNA clone D16F12 5', mRNA sequence.

ACCESSION CAB851710  
VERSION CAB851710.1 GI:33388503  
KEYWORDS EST.  
SOURCE Glycine max (soybean)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Glycine.

1 (bases 1 to 15)

Alkharouf, N.W., Khan, R. and Matthews, B.F.  
Analysis of expressed sequence tags from roots of resistant soybean infected by the soybean cyst nematode  
unpublished (2002)

## JOURNAL

COMMENT  
Contact: Alkharouf, N.W.  
Soybean Genomics and Improvement Laboratory (SGIL)  
US Department of Agriculture (USDA), ARS, PSI  
Bldg. 006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,  
USA

Tel: 301 504 5750

Fax: 301 504 5728

Email: alkharouf@ba.ars.usda.gov.

## FEATURES

source  
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Location/Qualifiers  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Peking"  
/db\_xref="taxon:3847"  
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/dev\_stages="Seedlings"  
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## ORIGIN

Query Match 100.0%; Score 5; DB 6; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTGGG 5  
|||||  
Db 7 GTGGG 3

## RESULT 28

CF543306/c  
LOCUS  
DEFINITION CF543306 15 bp mRNA linear EST 22-SEP-2003  
S014668-024-029-F24-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone  
024-029-F24 5-PRIME, mRNA sequence.

ACCESSION CF543306  
VERSION CF543306.1 GI:34891746  
KEYWORDS EST.

## SOURCE

Beta vulgaris  
Beta vulgaris  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Caryophyllales; Amaranthaceae; Beta.

## REFERENCE

AUTHORS  
Herwig, R., Schulz, B., Weishaar, B., Hennig, S., Steinfath, M.,  
Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.  
and Radelof, U.  
Construction of a 'unigene' cDNA clone set by oligonucleotide  
fingerprinting allows access to 25 000 potential sugar beet genes  
Plant J. 32 (5), 845-857 (2002)

## JOURNAL

MEDLINE  
PUBMED  
COMMENT

Contact: Weishaar B

ADIS DNA core facility at MPIZ

Max-Planck-Institute for Plant Breeding Research

Carl-von-Linne Weg 10, 50829 Koeln, Germany

Fax: 00492215062851

Email: weishaar@mpiz-koeln.mpg.de

Insert Length: 15 Std Error: 0.00

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Seq primer: SP6.

## FEATURES

Location/Qualifiers  
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/clone="024-029-F24"  
/tissue\_type="leaf"  
/lab\_host="EMDH10B"  
/clone\_lib="MPIZ-ADIS-024-leaf"

/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI; cDNA library from sugar beet, library provided by KWS Kleinvanzlebener Saatzzucht AG Einbeck, Germany, contact: b.schulz@kws.de; cloning sites SalI-NotI, primer sites and orientation:  
SP6-Sali-CCACGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note: Sequencing granted in the context of the GABI-Beet project, local PI: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GABI-Primary database: http://gabi.rzpd.de"

## ORIGIN

Query Match 100.0%; Score 5; DB 7; Length 15;  
Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
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Db 5 GTGGG 1

## RESULT 29

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CF543404/c
LOCUS       CF543404               15 bp   mRNA       linear       EST 22-SEP-2003
DEFINITION   S014668-024-029-D20-SP6 MPZ-ADIS-024-leaf Beta vulgaris cDNA clone
              024-029-D20 5-PRIME, mRNA sequence.
ACCESSION   CF543404
VERSION     CF543404.1   GI:34891844
KEYWORDS    EST.
SOURCE      Beta vulgaris
            Euteleostomi;
ORGANISM    Euteleostomi;
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
AUTHORS     Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
            and Radelof, U.
TITLE       Construction of a 'unigenes' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@piiz-koeln.mpg.de
            Insert Length: 15 Std Error: 0.00
            Plate: 29 row: D column: 20
            Seq primer: SP6.

FEATURES             source
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            /mol_type="mRNA"
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            /db_xref="GABI:936359"
            /db_xref="taxon:161934"
            /clone="024-029-D20"
            /tissue_type="leaf"
            /lab_host="EMDH10B"
            /clone_lib="MPZ-ADIS-024-leaf"
            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
Query Match      100.0%; Score 5; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
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Db 5 GTGGG 1

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LOCUS       AA937364               16 bp   mRNA       linear       EST 19-MAY-1998
DEFINITION   oJ08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3,
            similar to SM:ACRO.FABIT P48038 ACROSSIN PRECURSOR ;contains MSR1.b2
            MSR1 repetitive element ;, mRNA sequence.
ACCESSION   AA937364
VERSION     AA937364.1   GI:3095475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)

CF543404/c
LOCUS       CF543404               15 bp   mRNA       linear       EST 22-SEP-2003
DEFINITION   S014668-024-029-D20-SP6 MPZ-ADIS-024-leaf Beta vulgaris cDNA clone
              024-029-D20 5-PRIME, mRNA sequence.
ACCESSION   CF543404
VERSION     CF543404.1   GI:34891844
KEYWORDS    EST.
SOURCE      Beta vulgaris
            Euteleostomi;
ORGANISM    Euteleostomi;
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 15)
AUTHORS     Drungowski, M., Stahl, D., Wruck, W., Menze, A., O'Brien, J., Lehrach, H.
            and Radelof, U.
TITLE       Construction of a 'unigenes' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL     Plant J. 32 (5), 845-857 (2002)
MEDLINE     22362189
PUBMED      12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaar@piiz-koeln.mpg.de
            Insert Length: 15 Std Error: 0.00
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            Seq primer: SP6.

FEATURES             source
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            /tissue_type="leaf"
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            /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
            cDNA library from sugar beet, library provided by KWS
            Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
            b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
            orientation:
            SP6-Sali-CCACGGCTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
            Sequencing granted in the context of the GABI-Beet
            project, local PI: Dr. Katharina Schneider, coordinator:
            Prof. Christian Jung; Sequence submission managed by
            RZPD/GABI-Primary database:http://gabi.rzpd.de"

ORIGIN
Query Match      100.0%; Score 5; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 5 GTGGG 1

RESULT 30
AA937364
LOCUS       AA937364               16 bp   mRNA       linear       EST 19-MAY-1998
DEFINITION   oJ08f10.s1 NCI CGAP Mel3 Homo sapiens cDNA clone IMAGE:1491595.3,
            similar to SM:ACRO.FABIT P48038 ACROSSIN PRECURSOR ;contains MSR1.b2
            MSR1 repetitive element ;, mRNA sequence.
ACCESSION   AA937364
VERSION     AA937364.1   GI:3095475
KEYWORDS    EST.
SOURCE      Homo sapiens (human)

```

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
AUTHORS     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL     Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-r@mail.nih.gov
            unknown library type
            Trace considered overall poor quality
            Insert Length: 1265 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
            Location/Qualifiers
                1..16
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:1491595"
                /tissue_type="metastatic melanoma to bowel"
                /lab_host="DH10B"
                /clone_lib="NCI CGAP Mel3"
                /note="Organ: bowel (skin primary); Vector: pCMV-SPORT4;
                Site 1: SalI; Site 2: NotI; Cloned unidirectionally.
                Primer: Oligo dT. Average insert size 0.9 kb. Life
                Technologies catalog #: 10981-017"

ORIGIN
Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 2 GTGGG 6

RESULT 31
AI248882/c
LOCUS       AI248882               16 bp   mRNA       linear       EST 10-NOV-1998
DEFINITION   qu73e07.x1 NCI CGAP Brn35 Homo sapiens cDNA clone IMAGE:1977732.3,
            similar to SW:CA13_BOVIN P04258 COLLAGEN ALPHA 1(III) CHAIN. ;,
            mRNA sequence.
ACCESSION   AI248882
VERSION     AI248882.1   GI:3844279
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
AUTHORS     NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
            National Cancer Institute / National Institute of Neurological
            Disorders and Stroke, Brain Tumor Genome Anatomy Project
            (CGAP/BTCAP), Tumor Gene Index
JOURNAL     Unpublished (1998)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapsb-r@mail.nih.gov
            unknown library type
            Trace considered overall poor quality
            Insert Length: 1913 Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
            Location/Qualifiers
                1..16
                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clone="IMAGE:1977732"
                /tissue_type="tumor, 5 pooled (see description)"
                /lab_host="DH10B"

```

/clone\_lib="NCI CGAP Brn35"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site: 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.33 kb. Tumor types include:  
 meningioma, oligodendroglioma, astrocytoma (grade II),  
 medulloblastoma, astrocytoma (grade IV). Life Technologies  
 catalog #: 11544-012"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 8 GTGGG 4

## RESULT 32

AI564478/c  
 LOCUS  
 DEFINITION  
 tq57g09.x1 NCI CGAP Ut1 Homo sapiens cDNA clone IMAGE:2212960 3',  
 similar to TR:O00599 O00599 CON1.; contains element MSRI repetitive  
 element.; mRNA sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

AI564478.1 GI:4522935  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 16)  
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS  
 TITLE  
 JOURNAL

COMMENT  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 1.

## FEATURES

source

1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2212960"  
 /tissue\_type="well-differentiated endometrial  
 adenocarcinoma, 7 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut1"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.75 kb. Life Technologies catalog #:  
 11538-014"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
 |||||  
 Db 14 GTGGG 10

## RESULT 33

AI569544/c

LOCUS

DEFINITION

16 bp mRNA linear EST 12-MAY-1999  
 to28d10.x1 NCI CGAP Ut4 Homo sapiens cDNA clone IMAGE:2180371 3',  
 similar to TR:Q18444 Q18444 COSMID C34D4.; contains MSRI.b2 MSRI  
 repetitive element.; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AI569544.1 GI:4532918  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality  
 Insert Length: 1683 Std Error: 0.00  
 Seq primer: -40UP from Gibco

High quality sequence stop: 1  
 POLYA-No.

## FEATURES

source

1..16  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2180371"  
 /tissue\_type="serous papillary carcinoma, high grade, 2  
 pooled tumors"  
 /lab\_host="DH10B"  
 /clone\_lib="NCI CGAP Ut4"  
 /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;  
 Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.48 kb. Life Technologies catalog #:  
 11542-016"

## ORIGIN

Query Match 100.0%; Score 5; DB 1; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5

|||||

Db 14 GTGGG 10

## RESULT 34

AI590540/c

LOCUS

DEFINITION

16 bp mRNA linear EST 14-MAY-1999  
 tw11c02.x1 NCI CGAP Brn52 Homo sapiens cDNA clone IMAGE:2259362 3',  
 similar to TR:O00599 O00599 CON1.; mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AI590540.1 GI:4599588  
 EST.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS 1 (bases 1 to 16)
TITLE NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
JOURNAL National Cancer Institute / National Institute of Neurological
COMMENT Disorders and Stroke, Brain Tumor Genome Anatomy Project
(CGAP/BTGP), Tumor Gene Index
Unpublished (1998)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

FEATURES
source Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2259362"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/clone_lib="NCI CGAP Brn52"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; This library represents the normalized
version of NCI CGAP Brn35. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.19 kb. Tumor
types include: meningioma, oligodendroglioma, astrocytoma
(grade II), medulloblastoma, astrocytoma (grade IV).
Constructed by Life Technologies."

ORIGIN
Query Match 100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
|||||
Db 8 GTGGG 4

RESULT 35
AI684114/c 16 bp mRNA linear EST 16-DEC-1999
LOCUS tx79d02.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:225779 3'
DEFINITION similar to TR:Q09084 Q09084 EXTENSIN CLASS II PRECURSOR ;, mRNA
sequence.
ACCESSION AI684114.1 GI:4895408
VERSION AI684114
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2335755"
/sex="male"

FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2335755"
/sex="male"

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Insert Length: 1454 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2275779"
/tissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP Utl1"
/notes="Organ: uterus; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
11538-014"

ORIGIN
Query Match 100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
|||||
Db 15 GTGGG 11

RESULT 36
AI735054/c 16 bp mRNA linear EST 14-JUN-1999
LOCUS as88b02.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
DEFINITION IMAGE:2335755 3' similar to WP:T28C6.1 CE03746 ;contains MSR1.b2
MSR1 repetitive element ;, mRNA sequence.
ACCESSION AI735054.1 GI:5056653
VERSION AI735054
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 16)
Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2335755"
/sex="male"

FEATURES
source
1..16
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2335755"
/sex="male"

```

```

/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/clone_lib="Barstead colon HPLRB7"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACGAATCTGAAGTCGGAGCGCCCTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5' AATTCACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob
Barstead."

```

## ORIGIN

```

Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GTGGG 5
        |||||
DB      6 GTGGG 2

```

## RESULT 37

```

A1749229/c
LOCUS      16 bp mRNA linear EST 22-JUN-1999
DEFINITION at41a02.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
IMAGE:2374538.3 similar to TR:Q91810 Q91810 PROLINE RICH PROTEIN.
CONTAINS MSRI.b3 MSRI repetitive element ;; mRNA sequence.

```

```

ACCESSION A1749229.1 GI:5127493
VERSION A1749229.1
KEYWORDS EST.
SOURCE Homo sapiens (human)

```

## ORGANISM

```

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

## REFERENCE

```

AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.

```

## TITLE

```

WashU-NCI human EST Project

```

## JOURNAL

```

Unpublished (1997)

```

## COMMENT

```

Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: -400P from Gibco
High quality sequence stop: 1.

```

## FEATURES

## source

```

1..16
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2374538"
/sex="male"
/dev_stage="adult, age 25"
/lab_host="DH10B (phage resistant)"
/clone_lib="Barstead colon HPLRB7"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoRI; Site 2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTACGAATCTGAAGTCGGAGCGCCCTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5' AATTCACTAGTAAT 3' and 5' ATTACTAGTG 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified pT73 vector. Library constructed by Bob

```

## Barstead."

## ORIGIN

```

Query Match      100.0%; Score 5; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GTGGG 5
        |||||
DB      14 GTGGG 10

```

## RESULT 38

```

BE586084/c
LOCUS      16 bp mRNA linear EST 17-AUG-2000
DEFINITION Est#8PT7_G06_g6_040 KSU wheat Fusarium graminearum infected spike
CDNA library Triticum aestivum cDNA clone Est#8PT7_G06_g6_040, mRNA
sequence.

```

```

ACCESSION BE586084.1 GI:9839116
VERSION BE586084.1
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)

```

## ORGANISM

```

Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```

## REFERENCE

```

AUTHORS Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S.

```

## TITLE

```

The structure and function of the expressed portion of the wheat
genomes - Kansas State University. Fusarium graminearum infected
spike cDNA library

```

## JOURNAL

```

Unpublished (2000)

```

## COMMENT

```

Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA

```

```

Tel: 785-532-2367
Fax: 785-532-6167

```

```

Email: jof@alfalfa.ksu.edu

```

```

Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20

```

```

Seq primer: T7.

```

```

Location/Qualifiers

```

## FEATURES

## source

```

1..16
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Sumai3"
/db_xref="taxon:4565"
/clone="Est#8PT7_G06_g6_040"
/tissue_type="Spike"
/dev_stage="Adult plant"
/lab_host="E. coli JM109"
/clone_lib="KSU wheat Fusarium graminearum infected spike
cDNA library"
/note="Vector: pGEM-T easy; Site 1: SacII; Site 2: SpeI;
Plants were grown in the greenhouse. Spikes were sprayed
with Fusarium graminearum (at what stage). Total RNA, and
poly(A) RNA were prepared from infected spikes. cDNA was
prepared using the SmartTM PCR cDNA synthesis kit from
Clontech. cDNA was cloned into the pGEM-T easy vector
from Promega."

```

## ORIGIN

```

Query Match      100.0%; Score 5; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GTGGG 5
        |||||
DB      5 GTGGG 1

```

```

RESULT 39
BM396802
LOCUS
DEFINITION
5009-0-25-D06.t.1 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM396802
VERSION
BM396802.1 GI:18196855
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
Location/Qualifiers
1..16
/molecule="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Query Match 100.0%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 2 GTGGG 6

RESULT 40
BM399406
LOCUS
DEFINITION
5009-0-57-D08.t.2 Chilcoat/Turkewitz cDNA (large fraction)
Tetrahymena thermophila cDNA, mRNA sequence.
ACCESSION
BM399406
VERSION
BM399406.1 GI:18199459
KEYWORDS
EST.
SOURCE
Tetrahymena thermophila
ORGANISM
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E.,
Frankel,J. and Klobutcher,L.
TITLE
EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL
Unpublished (2002)
COMMENT
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.
FEATURES
Location/Qualifiers
1..16
/molecule="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Query Match 100.0%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 2 GTGGG 6

RESULT 41
BM392176/c
LOCUS
DEFINITION
E012696-024-021-004-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-021-004 5-PRIME, mRNA sequence.
ACCESSION
BM392176
VERSION
BM392176.1 GI:26121759
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Kadelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 21 row: 0 column: 04
Seq primer: SP6; CATACGATTGATGGTGACACTATAG.
FEATURES
Location/Qualifiers
1..16
/organism="Beta vulgaris"
/molecule="mRNA"
/cultivar="KWS23320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:190799"
/db_xref="taxon:161934"
/clone="024-021-004"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

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/organism="Tetrahymena thermophila"
/molecule="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
ORIGIN
Query Match 100.0%; Score 5; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 6 GTGGG 10

RESULT 41
BM392176/c
LOCUS
DEFINITION
E012696-024-021-004-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
cDNA clone 024-021-004 5-PRIME, mRNA sequence.
ACCESSION
BM392176
VERSION
BM392176.1 GI:26121759
KEYWORDS
EST.
SOURCE
Beta vulgaris
ORGANISM
Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE
1 (bases 1 to 16)
AUTHORS
Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Kadelof,U.
TITLE
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL
Plant J. 32 (5), 845-857 (2002)
MEDLINE
22362189
PUBMED
12472698
COMMENT
Contact: Weisshaar B
ADIS DNA core facility at MP1Z
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Plate: 21 row: 0 column: 04
Seq primer: SP6; CATACGATTGATGGTGACACTATAG.
FEATURES
Location/Qualifiers
1..16
/organism="Beta vulgaris"
/molecule="mRNA"
/cultivar="KWS23320 (double haploid, monogerm breeding
line)"
/db_xref="GABI:190799"
/db_xref="taxon:161934"
/clone="024-021-004"
/tissue_type="developing root"
/lab_host="EMDH10B"
/clone_lib="MP1Z-ADIS-024-developing root"
/note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzaucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
orientation:
SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

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Query Match 100.0%; Score 5; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
 Db 5 GTGGG 1

RESULT 42  
 BQ593213  
 LOCUS  
 DEFINITION BQ593213 16 bp mRNA linear EST 06-DEC-2002  
 CDNA clone 024-027-K15-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
 BQ593213  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 16)  
 Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 PUBMED 12472698  
 COMMENT  
 Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 16 Std Error: 0.00  
 Plate: 27 row: K column: 15  
 Seq primer: SP6; CATACGATTAGTGACACTATAG.

#### FEATURES

source  
 1..16  
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 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:193643"  
 /db\_xref="taxon:161934"  
 /clones="024-027-K15"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP1Z-ADIS-024-developing root"  
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

#### ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
 Db 6 GTGGG 10

#### RESULT 43

BQ595114  
 LOCUS  
 DEFINITION BQ595114 16 bp mRNA linear EST 06-DEC-2002  
 CDNA clone 024-023-M09-SP6 MP1Z-ADIS-024-developing root Beta vulgaris  
 BQ595114  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM Beta vulgaris  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 Caryophyllales; Amaranthaceae; Beta.  
 1 (bases 1 to 16)  
 Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,  
 Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.  
 and Radelof,U.  
 Construction of a 'unigene' cDNA clone set by oligonucleotide  
 fingerprinting allows access to 25 000 potential sugar beet genes  
 Plant J. 32 (5), 845-857 (2002)  
 22362189  
 PUBMED 12472698  
 COMMENT  
 Contact: Weishaar B  
 ADIS DNA core facility at MP1Z  
 Max-Planck-Institute for Plant Breeding Research  
 Carl-von-Linne Weg 10, 50829 Koeln, Germany  
 Fax: 00492215062851  
 Email: weishaar@mpiz-koeln.mpg.de  
 Insert Length: 16 Std Error: 0.00  
 Plate: 23 row: M column: 09  
 Seq primer: SP6; CATACGATTAGTGACACTATAG.

#### FEATURES

source  
 1..16  
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 /mol\_type="mRNA"  
 /cultivar="KWS2320 (double haploid, monogerm breeding  
 line)"  
 /db\_xref="GABI:191733"  
 /db\_xref="taxon:161934"  
 /clones="024-023-M09"  
 /tissue\_type="developing root"  
 /lab\_host="EMDH10B"  
 /clone\_lib="MP1Z-ADIS-024-developing root"  
 /note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;  
 cDNA library from sugar beet, library provided by KWS  
 Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:  
 b.schulz@kws.de; cloning sites Sali-NotI, primer sites and  
 orientation:  
 SP6-Sali-CCACGGCTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:  
 Sequencing granted in the context of the GABI-Beet  
 project, local PI: Dr. Katharina Schneider, coordinator:  
 Prof. Christian Jung; Sequence submission managed by  
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

#### ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
 Db 8 GTGGG 12

#### ORIGIN

Query Match 100.0%; Score 5; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 9.5e+06;  
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
 Db 8 GTGGG 12

#### RESULT 44

CF543332  
 LOCUS  
 DEFINITION CF543332 16 bp mRNA linear EST 22-SEP-2003  
 S014665-024-029-O21-SP6 MP1Z-ADIS-024-leaf Beta vulgaris cDNA clone  
 024-029-O21 5-PRIME, mRNA sequence.  
 CF543332  
 VERSION  
 KEYWORDS

Oy 1 GTGGG 5  
 Db 8 GTGGG 12

```

SOURCE      Beta vulgaris
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
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Seq primer: SP6.
FEATURES     source
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             line)"
             /db_xref="GABI:936425"
             /cl_xref="taxon:161934"
             /clone="024-029-021"
             /tissue type="leaf"
             /lab_host="EMDH10B"
             /clone_lib="MPIZ-ADIS-024-leaf"
             /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
             cDNA library from sugar beet, library provided by KWS
             Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
             b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
             orientation:
             SP6-Sali-CCACGGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
             Sequencing granted in the context of the GABI-Beet
             project, local PI: Dr. Katharina Schneider, coordinator:
             Prof. Christian Jung; Sequence submission managed by
             RZPD/GABI-Primary database:http://gabi.rzpd.de"
ORIGIN
Query Match      100.0%; Score 5; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 8 GTGGG 12

RESULT 45
AJ596548
LOCUS      Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 435H06, genomic survey sequence.
ACCESSION  AJ596548.1 GI:37946176
VERSION     GSS; left border; T-DNA flanking sequence.
KEYWORDS    Arabidopsis thaliana (thale cress)
SOURCE      Arabidopsis thaliana
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE    1
AUTHORS      Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.

SOURCE      Beta vulgaris
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE    1 (bases 1 to 16)
AUTHORS      Herwig,R., Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruick,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
TITLE        Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL      Plant J. 32 (5), 845-857 (2002)
MEDLINE      22362189
PUBMED       12472698
COMMENT      Contact: Weishaar B
ADIS DNA core facility at MPZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weishaar@mpiz-koeln.mpg.de
Insert Length: 16 Std Error: 0.00
Place: 29. row: 0 column: 21
Seq primer: SP6.
FEATURES     source
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             /mol_type="mRNA"
             /cultivar="KWS2320 (double haploid, monogerm breeding
             line)"
             /db_xref="GABI:936425"
             /cl_xref="taxon:161934"
             /clone="024-029-021"
             /tissue type="leaf"
             /lab_host="EMDH10B"
             /clone_lib="MPIZ-ADIS-024-leaf"
             /note="Vector: pCMVSPORT6; Site 1: SalI; Site 2: NotI;
             cDNA library from sugar beet, library provided by KWS
             Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
             b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
             orientation:
             SP6-Sali-CCACGGCGTCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
             Sequencing granted in the context of the GABI-Beet
             project, local PI: Dr. Katharina Schneider, coordinator:
             Prof. Christian Jung; Sequence submission managed by
             RZPD/GABI-Primary database:http://gabi.rzpd.de"
ORIGIN
Query Match      100.0%; Score 5; DB 7; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
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Db 8 GTGGG 12

RESULT 45
AJ596548
LOCUS      Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 435H06, genomic survey sequence.
ACCESSION  AJ596548.1 GI:37946176
VERSION     GSS; left border; T-DNA flanking sequence.
KEYWORDS    Arabidopsis thaliana (thale cress)
SOURCE      Arabidopsis thaliana
ORGANISM     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE    1
AUTHORS      Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
Lepiniec,L., Caboche,M. and Lecharny,A.

```

```

TITLE        T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL      EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE      22363535
PUBMED       12448565
REFERENCE    2 (bases 1 to 16)
AUTHORS      Balzergue,S.
Direct Submission
Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment (6) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomes
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
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             /mol_type="genomic DNA"
             /cultivar="Wassiliewskija"
             /db_xref="taxon:3702"
             /clone="435H06"
             /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
             /misc_feature
             1. .16
             /note="T-DNA flanking sequence
             left border"
ORIGIN
Query Match      100.0%; Score 5; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 9.5e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 5 GTGGG 9

RESULT 46
AJ666397/c
LOCUS      AJ666397 CSEQRAN09 Sus scrofa cDNA clone C0000033_K10, mRNA
DEFINITION  AJ666397 CSEQRAN09 Sus scrofa cDNA clone C0000033_K10, mRNA
sequence.
ACCESSION  AJ666397
VERSION     AJ666397.1 GI:49350848
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
ORGANISM     Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE    1 (bases 1 to 17)
AUTHORS      Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE        Development of cDNA and EST resources for studying reproduction and
embryo development in pigs and cattle
JOURNAL      Unpublished (2004)
COMMENT      Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with the -minscore 20
v0.020425.c. Vector identified by cross match with the -minscore 20
and -mismatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
EcoRI R. Site 2: NotI Description: Normalised library constructed
from pooled tissue from day 30 placentas. Clones available from UK
Centre for Functional Genomics in Farm Animals, Roslin Institute,
Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES     source
             1. .17

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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone="C000033_K10"
/tissue_type="placenta"
/clone_lib="CSORAN09"
/note="Vector: pBlueScriptII(KS+); Site1: EcoRI; Site_2:
NotI; Single pass sequencing. Normalised library
constructed from pooled tissue from day 30 placentas."

ORIGIN
Query Match          100.0%; Score 5; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 5 GTGGG 1

RESULT 47
BM395627
LOCUS          17 bp mRNA linear EST 17-JAN-2002
DEFINITION    Tetrahymena thermophila cDNA (large fraction)
ACCESSION     BM395627
VERSION       1 (bases 1 to 17)
KEYWORDS      EST.
SOURCE        Tetrahymena thermophila
ORGANISM      Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE     1 (bases 1 to 17)
AUTHORS       Turkewitz A.P., Karrer K.M., Jahn C., Orlas E., Kirk K.E.,
Frankel J. and Klobutcher L.
TITLE         EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL       Unpublished (2002)
COMMENT       Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

FEATURES
source          Location/Qualifiers
1..17
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/db_xref="taxon:9823"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN
Query Match          100.0%; Score 5; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
    |||||
Db 9 GTGGG 5

RESULT 49
BM590447
LOCUS          17 bp mRNA linear EST 06-DEC-2002
DEFINITION    E012839-024-019-O05-SP6 MP12-ADIS-024-storage root Beta vulgaris
ACCESSION     BM590447
VERSION       B0590447.1 GI:36120030
KEYWORDS      EST.
SOURCE        Beta vulgaris
ORGANISM      Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
REFERENCE     1 (bases 1 to 17)
AUTHORS       Herwig R., Schulz B., Weisshaar B., Hennig S., Steinfath M.,
Drungowski M., Stahl D., Wruick W., Menze A., O'Brien J., Lehrach H.
and Radelof U.
TITLE         Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
JOURNAL       Plant J. 32 (5), 845-857 (2002)
MEDLINE       2362189
PUBMED        12472698
COMMENT       Contact: Weisshaar B
ADIS DNA core facility at MP12
Max-Planck-Institute for plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaar@mpiz-koeln.mpg.de
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Seq primer: SP6; CATACGATTAGTGACACTATAG.

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constructed from pooled tissue from day 30 placentas."

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Db 5 GTGGG 1

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LOCUS          17 bp mRNA linear EST 17-JAN-2002
DEFINITION    Tetrahymena thermophila cDNA (large fraction)
ACCESSION     BM395627
VERSION       1 (bases 1 to 17)
KEYWORDS      EST.
SOURCE        Tetrahymena thermophila
ORGANISM      Tetrahymena thermophila
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Hymenostomatida; Tetrahymenina; Tetrahymena.
REFERENCE     1 (bases 1 to 17)
AUTHORS       Turkewitz A.P., Karrer K.M., Jahn C., Orlas E., Kirk K.E.,
Frankel J. and Klobutcher L.
TITLE         EST from Tetrahymena thermophila, strain CU428.1, growing cells
JOURNAL       Unpublished (2002)
COMMENT       Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
Tel: 773 702 4374
Fax: 773 702 3172
Email: apturkew@midway.uchicago.edu
Seq primer: T3.

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Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS          17 bp mRNA linear EST 17-JAN-2002
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ACCESSION     BM397301
VERSION       BM397301.1 GI:18197354

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cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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## ORIGIN

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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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## RESULT 50

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DEFINITION      17 bp mRNA linear EST 06-DEC-2002
cDNA clone 024-023-M09-SP6 MP1Z-ADIS-024-developing root Beta vulgaris
BQ594949
ACCESSION      BQ594949
VERSION
KEYWORDS
SOURCE

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## ORGANISM

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Beta vulgaris
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
1 (bases 1 to 17)
Herwig,R.; Schulz,B., Weishaar,B., Hennig,S., Steinfath,M.,
Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
and Radelof,U.
Construction of a 'unigene' cDNA clone set by oligonucleotide
fingerprinting allows access to 25 000 potential sugar beet genes
Plant J. 32 (5), 845-857 (2002)
22362189
PUBMED
12472698
Contact: Weishaar B
ADIS DNA core facility at MPIZ
Max-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weissshaar@piz-koeln.mpg.de
Insert Length: 17 Std Error: 0.00
Plate: 23 row: M column: 09
Seq primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
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## FEATURES

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/note="Vector: pCMVSPORT6; Site 1: Sali; Site 2: NotI;
cDNA library from sugar beet, library provided by KWS
Kleinwanzlebener Saatzzucht AG Einbeck, Germany, contact:
b.schulz@kws.de; cloning sites Sali-NotI, primer sites and
orientation:
SP6-Sali-CCAGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
Sequencing granted in the context of the GABI-Beet
project, local PI: Dr. Katharina Schneider, coordinator:
Prof. Christian Jung; Sequence submission managed by
RZPD/GABI-Primary database: http://gabi.rzpd.de"

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## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.6e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GTGGG 5
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Db      8 GTGGG 12

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Search completed: January 7, 2005, 11:01:27
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 7, 2005, 05:37:38 ; Search time 58 Seconds  
(without alignments)  
61.275 Million cell updates/sec

Title: GTGGG  
Perfect score: 5  
Sequence: 1 gtggg 5

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 896372

Minimum DB seq length: 10  
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Post-processing: Minimum Match 0%  
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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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249	5	100.0	13	3	US-09-429-130-49	Sequence 49, Appl	322	5	100.0	14	4	US-09-230-652-23	Sequence 23, Appl
250	5	100.0	13	3	US-09-345-294-2	Sequence 2, Appl	323	5	100.0	14	4	US-09-230-652-25	Sequence 25, Appl
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## ALIGNMENTS

RESULT 1  
US-07-651-710A-8  
; Sequence 8, Application US/07651710A  
; Patent No. 5362864  
; GENERAL INFORMATION:  
; APPLICANT: Chua, Nam-Hai  
; TITLE OF INVENTION: Trans-Activating Factor-1  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/651,710A  
; FILING DATE: 19910206  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mirock, S. Leslie  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 3288-014  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 790-9090  
; TELEFAX: 212 8698864/9741  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 8:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
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; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-8

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      5 GTGGG 9

RESULT 2
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; Patent No. 5362864
; GENERAL INFORMATION:
; APPLICANT: Chua, Nan-Hai
; TITLE OF INVENTION: Trans-Activating Factor-1
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/651,710A
; FILING DATE: 19910206
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 3288-014
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
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; TOPOLOGY: unknown
; MOLECULE TYPE: TAF-1 binding motif
US-07-651-710A-12

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;
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Qy      1 GTGGG 5
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RESULT 3
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; Sequence 27, Application US/08061697
; Patent No. 5498696
; GENERAL INFORMATION:
; APPLICANT: Brown, Michael S.; Briggs, Michael R.; Wang,
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; APPLICANT: Xiaodong; Goldstein, Joseph L.
; TITLE OF INVENTION: Sterol Regulatory Element Binding Proteins
; TITLE OF INVENTION: and Their Use in Screening Assays
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P. O. Box 4433
; CITY: Houston
; STATE: Texas
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; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:347/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 320-7200
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-061-697-27

Query Match      100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      10 GTGGG 6

RESULT 4
US-08-229-515A-17
; Sequence 17, Application US/08229515A
; Patent No. 5518885
; GENERAL INFORMATION:
; APPLICANT: RAZIUDIN
; APPLICANT: SARKAR, FAZLUL H
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN
; TITLE OF INVENTION: NEOPLASTIC DISEASE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG PC
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: usa
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/229,515A
; FILING DATE: 19 APR 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PERRYMAN, DAVID G
```

REGISTRATION NUMBER: 33,438  
REFERENCE/DOCKET NUMBER: 1414.608  
TELEPHONE: 404-688-0770  
TELEFAX: 404-688-9880  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-229-515A-17

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 2 GTGGG 6

## RESULT 5

US-08-229-515A-18  
Sequence 18, Application US/08229515A  
Patent No. 5518885

## GENERAL INFORMATION:

APPLICANT: RAZIUDIN  
APPLICANT: SARKAR, FAZLUL H  
TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN  
TITLE OF INVENTION: NEOPLASTIC DISEASE  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:

ADDRESSEE: NEEDLE & ROSENBERG PC  
STREET: 127 Peachtree Street, Suite 1200  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: usa  
ZIP: 30303

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/229,515A  
FILING DATE: 19 APR 1994  
CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: PERRYMAN, DAVID G  
REGISTRATION NUMBER: 33,438  
REFERENCE/DOCKET NUMBER: 1414.608  
TELEPHONE: 404-688-0770  
TELEFAX: 404-688-9880

## INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-229-515A-18

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 1 GTGGG 5

## RESULT 6

US-08-131-365B-27/c  
Sequence 27, Application US/08131365B  
Patent No. 5527690  
GENERAL INFORMATION:  
APPLICANT: Brown, Michael S.  
APPLICANT: Briggs, Michael R.  
APPLICANT: Wang, Xiaodong  
APPLICANT: Goldstein, Joseph L.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77210

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/131,365B

FILING DATE: 01-OCT-1993

CLASSIFICATION: 435

## ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

## INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"

US-08-131-365B-27

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 10 GTGGG 6

## RESULT 7

US-08-131-365B-43  
Sequence 43, Application US/08131365B  
Patent No. 5527690

## GENERAL INFORMATION:

APPLICANT: Brown, Michael S.  
APPLICANT: Briggs, Michael R.  
APPLICANT: Wang, Xiaodong  
APPLICANT: Goldstein, Joseph L.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.

Qy 1 GTGGG 5  
Db 1 GTGGG 5



ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/131,365B  
FILING DATE: 01-OCT-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-131-365B-43

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GTGGG 5  
DB 3 GTGGG 7

## RESULT 8

US-07-990-303A-3/c  
Sequence 3, Application US/07990303A  
Patent No. 5582972  
GENERAL INFORMATION:  
APPLICANT: Lima, Walter F.  
APPLICANT: Monia, Brett P.  
APPLICANT: Freier, Susan M.  
APPLICANT: Ecker, David J.  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES  
TITLE OF INVENTION: TO THE ras GENE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz  
ADDRESSEE: Mackiewicz & No. 5582972ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/990,303A  
FILING DATE: 19921214  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 715,196  
FILING DATE: June 14, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISIS-0786  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
ANTI-SENSE: YES  
US-07-990-303A-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GTGGG 5  
DB 8 GTGGG 4

## RESULT 9

US-07-990-303A-6/c  
Sequence 6, Application US/07990303A  
Patent No. 5582972  
GENERAL INFORMATION:  
APPLICANT: Lima, Walter F.  
APPLICANT: Monia, Brett P.  
APPLICANT: Freier, Susan M.  
APPLICANT: Ecker, David J.  
TITLE OF INVENTION: ANTISENSE OLIGONUCLEOTIDES  
TITLE OF INVENTION: TO THE ras GENE  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz  
ADDRESSEE: Mackiewicz & No. 5582972ris  
STREET: One Liberty Place - 46th Floor  
CITY: Philadelphia  
STATE: PA  
COUNTRY: USA  
ZIP: 19103

COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: WORDPERFECT 5.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/990,303A  
FILING DATE: 19921214  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 715,196  
FILING DATE: June 14, 1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Jane Massey Licata  
REGISTRATION NUMBER: 32,257  
REFERENCE/DOCKET NUMBER: ISIS-0786  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
ANTI-SENSE: YES  
US-07-990-303A-6

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 1 GTGGG 5

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Db      8 GTGGG 4
|||||
RESULT 10
US-08-197-463-4/c
; Sequence 4, Application US/08197463
; Patent No. 5627047
; GENERAL INFORMATION:
; APPLICANT: Brenner, Michael
; APPLICANT: Beznard, Francois
; APPLICANT: Nakatani, Yoshihiro
; TITLE OF INVENTION: Astrocyte-Specific Transcription
; TITLE OF INVENTION: of Human Genes
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Birch, Stewart, Koslasch & Birch
; STREET: 301 N. Washington St.
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22046-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08197,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07769,626
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Svensson, Leonard R.
; REGISTRATION NUMBER: 30330
; REFERENCE/DOCKET NUMBER: 1173-362P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-241-1300
; TELEFAX: 703-241-2848
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: protein_bind
; LOCATION: 1..10
; OTHER INFORMATION: /function= "transcription enhancer"
; OTHER INFORMATION: /bound_moiety= "AP-2"
; OTHER INFORMATION: /standard_name= "AP-2 site"
US-08-197-463-4
Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
|||||
Db      6 GTGGG 2

RESULT 11
US-08-317-403A-44
; Sequence 44, Application US/08317403A
; Patent No. 5629155
; GENERAL INFORMATION:
; APPLICANT: WIEGAND, T., GOLD, L., AND TASSET, D.
; TITLE OF INVENTION: HIGH-AFFINITY

;
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
; TITLE OF INVENTION: TO IMMUNOGLOBIN E
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08317,403A
; FILING DATE: 3-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-317-403A-44
Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
|||||
Db      3 GUGGG 7

RESULT 12
US-08-202-927-20/c
; Sequence 20, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
```

```

; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note="Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
;
US-08-202-927-20

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Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTGGG 5
Db 5 GTGGG 1

```

```

RESULT 13
US-08-202-927-38
; Sequence 38, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994

```

```

; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 10
; OTHER INFORMATION: /mod_base= OTHER
; OTHER INFORMATION: /note="Nucleotide 10 has a tail which comprises
; OTHER INFORMATION: a cholesterol moiety which has its A ring linked to
; OTHER INFORMATION: the 3'-phosphate through a carbonyl group attached
; OTHER INFORMATION: to the ring nitrogen of a moiety derived from
; OTHER INFORMATION: 4-hydroxy-2-hydroxymethylpyrrolidine (see
; OTHER INFORMATION: formula 3)."
;
US-08-202-927-38

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Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTGGG 5
Db 1 GTGGG 5

```

```

RESULT 14
US-08-202-927-38/c
; Sequence 38, Application US/08202927
; Patent No. 5646126
; GENERAL INFORMATION:
; APPLICANT: Cheng, Yung-chi
; APPLICANT: Lukhtanov, Eugeny A.
; APPLICANT: Meyer Jr., Rich B.
; APPLICANT: Pai, Balakrishna S.
; APPLICANT: Reed, Michael W.
; APPLICANT: Zhou, James H.
; TITLE OF INVENTION: Modified Oligonucleotide Duplexes Having
; TITLE OF INVENTION: Anticancer Activity
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klein & Szekeres
; STREET: 4199 Campus Drive, Suite 700
; CITY: Irvine
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92715
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,927
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Szekeres, Gabor L.
; REGISTRATION NUMBER: 28,675
; REFERENCE/DOCKET NUMBER: 491-07-PA
; TELEPHONE: (714) 854-5502
; TELEFAX: (714) 854-4897
; INFORMATION FOR SEQ ID NO: 38:

```

SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: modified\_base  
LOCATION: 10  
OTHER INFORMATION: /mod\_base= OTHER  
OTHER INFORMATION: /note= "Nucleotide 10 has a tail which comprises a cholesterol moiety which has its A ring linked to the 3'-phosphate through a carbonyl group attached to the ring nitrogen of a moiety derived from 4-hydroxy-2-hydroxymethylpyrrolidine (see formula 3)."  
US-08-202-927-38

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
DB 10 GTGGG 6

RESULT 15  
US-08-645-865-17  
; Sequence 17, Application US/08645865  
; Patent No. 5654406  
; GENERAL INFORMATION:  
; APPLICANT: RAZIUDIN  
; APPLICANT: SARKAR, FAZLUL H  
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN  
; TITLE OF INVENTION: NEOPLASTIC DISEASE  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEEDLE & ROSENBERG PC  
; STREET: 127 Peachtree Street, Suite 1200  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: usa  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/645,865  
; FILING DATE: 14 MAY 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PERRYMAN, DAVID G  
; REGISTRATION NUMBER: 33,438  
; REFERENCE/DOCKET NUMBER: 1414.608  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-688-0770  
; TELEFAX: 404-688-9880  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-645-865-17

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||

Db 2 GTGGG 6  
RESULT 16  
US-08-645-865-18  
; Sequence 18, Application US/08645865  
; Patent No. 5654406  
; GENERAL INFORMATION:  
; APPLICANT: RAZIUDIN  
; APPLICANT: SARKAR, FAZLUL H  
; TITLE OF INVENTION: ERBB2 PROMOTER BINDING PROTEIN IN  
; TITLE OF INVENTION: NEOPLASTIC DISEASE  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NEEDLE & ROSENBERG PC  
; STREET: 127 Peachtree Street, Suite 1200  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: usa  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/645,865  
; FILING DATE: 14 MAY 1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PERRYMAN, DAVID G  
; REGISTRATION NUMBER: 33,438  
; REFERENCE/DOCKET NUMBER: 1414.608  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404-688-0770  
; TELEFAX: 404-688-9880  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-645-865-18

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGG 5  
|||||  
DB 1 GTGGG 5

RESULT 17  
US-08-330-000-3/c  
; Sequence 3, Application US/08330000  
; Patent No. 5686242  
; GENERAL INFORMATION:  
; APPLICANT: Bruice, Thomas W.  
; APPLICANT: Lima, Walter F.  
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES  
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSEE: NO. 5686242r18  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-000-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 8 GTGGG 4

RESULT 18  
US-08-330-000-4/c  
; Sequence 4, Application US/08330000  
; Patent No. 5686242  
; GENERAL INFORMATION:  
; APPLICANT: Bruice, Thomas W.  
; APPLICANT: Lima, Walter F.  
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSEE: No. 5686242ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-000-6

Query Match 100.0%; Score 5; DB 1; Length 10;

; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-000-4

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 8 GTGGG 4

RESULT 19  
US-08-330-000-6/c  
; Sequence 6, Application US/08330000  
; Patent No. 5686242  
; GENERAL INFORMATION:  
; APPLICANT: Bruice, Thomas W.  
; APPLICANT: Lima, Walter F.  
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSEE: No. 5686242ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-000-6

Query Match

Best Local Similarity 100.0%; Pred. No. 2.3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 8 GTGGG 4

## RESULT 20

US-08-330-000-9  
; Sequence 9, Application US/083300000  
; Patent No. 5686242  
; GENERAL INFORMATION:  
; APPLICANT: Bruice, Thomas W.  
; APPLICANT: Lima, Walter F.  
; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES  
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSEE: No. 5686242ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA (genomic)  
US-08-330-000-9

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.3e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 3 GUGGG 7

## RESULT 21

US-08-330-000-15/c  
; Sequence 15, Application US/083300000  
; Patent No. 5686242  
; GENERAL INFORMATION:  
; APPLICANT: Bruice, Thomas W.  
; APPLICANT: Lima, Walter F.

; TITLE OF INVENTION: DETERMINATION OF OLIGONUCLEOTIDES  
; TITLE OF INVENTION: FOR THERAPEUTICS, DIAGNOSTICS AND RESEARCH REAGENTS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and  
; ADDRESSEE: No. 5686242ris  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: U.S.A.  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/330,000  
; FILING DATE:  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER: 755,485  
; FILING DATE: September 5, 1991  
; PRIOR APPLICATION NUMBER: PCT/US92/07489  
; FILING DATE: September 4, 1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ralph, Rebecca Lynne  
; REGISTRATION NUMBER: 35,152  
; REFERENCE/DOCKET NUMBER: ISIS-1723  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-568-3100  
; TELEFAX: 215-568-3439  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-330-000-15

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 8 GTGGG 4

## RESULT 22

US-08-471-985A-44  
; Sequence 44, Application US/08471985A  
; Patent No. 5686592  
; GENERAL INFORMATION:  
; APPLICANT: WIEGAND, Torsten Walter  
; APPLICANT: GOLD, Larry  
; APPLICANT: TASSET, Diane  
; TITLE OF INVENTION: HIGH-AFFINITY  
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS TO  
; TITLE OF INVENTION: IMMUNOGLOBIN E  
; NUMBER OF SEQUENCES: 112  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Swanson & Bratschun, L.L.C.  
; STREET: 8400 East Prentice Avenue, Suite 200  
; CITY: Englewood  
; STATE: Colorado  
; COUNTRY: USA  
; ZIP: 80111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage  
; COMPUTER: IBM compatible

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; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,985A
; FILING DATE: 06-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/317,403
; FILING DATE: 03-OCTOBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX23/CIP
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; FEATURE:
; OTHER INFORMATION: All C's are 2'-NH2 cytosine
; FEATURE:
; OTHER INFORMATION: All U's are 2'-NH2 uracil
US-08-471-985A-44

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.3e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 3 GUGGG 7

RESULT 23
US-08-171-718-30/c
; Sequence 30, Application US/08171718
; Patent No. 5707863
; GENERAL INFORMATION:
; APPLICANT: Trofatter, James A.
; APPLICANT: MacCollin, Mia M.
; APPLICANT: Gusella, James F.
; TITLE OF INVENTION: Tumor Suppressor Gene Merlin and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/171,718
; FILING DATE: 22-DEC-1993
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/108,808

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; FILING DATE: 19-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/022,034
; FILING DATE: 25-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/026,063
; FILING DATE: 04-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Anne
; REGISTRATION NUMBER: 36,463
; REFERENCE/DOCKET NUMBER: 0609.3850003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-171-718-30

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 24
US-08-463-660-13/c
; Sequence 13, Application US/08463660
; Patent No. 5759776
; GENERAL INFORMATION:
; APPLICANT: SMITH, HELENE S.
; APPLICANT: CHEN, LING-CHUN
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND TREATMENT
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,660
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 28888-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-463-660-13

Query Match 100.0%; Score 5; DB 1; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 2.3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 10 GTGGG 6

RESULT 25  
US-08-280-13/c  
; Sequence 13, Application US/08678280  
; Patent No. 5776683  
; GENERAL INFORMATION:  
; APPLICANT: SMITH, HELENE S.  
; APPLICANT: CHUN, LING-CHEN  
; TITLE OF INVENTION: TARGETS FOR BREAST CANCER DIAGNOSIS AND  
; TREATMENT  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 Page Mill Road  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/678,280  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schiff, J. Michael  
; REGISTRATION NUMBER: 40,253  
; REFERENCE/DOCKET NUMBER: 28888-20001.20  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 813-5600  
; TELEFAX: (415) 494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-678-280-13

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 10 GTGGG 6

RESULT 26  
US-08-590-804-13  
; Sequence 13, Application US/08590804  
; Patent No. 5780273  
; GENERAL INFORMATION:  
; APPLICANT: Burg, J. Lawrence  
; TITLE OF INVENTION: INSERTION ELEMENTS AND AMPLIFIABLE  
; TITLE OF INVENTION: NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amoco Corporation  
; STREET: 55 Shuman Blvd., Suite 600  
; CITY: Naperville  
; STATE: Illinois

COUNTRY: USA  
ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,804  
FILING DATE: 24-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/357,779  
FILING DATE:  
APPLICATION NUMBER: US 08/045,587  
ATTORNEY/AGENT INFORMATION:  
NAME: Galloway, No. 5780273val B  
REGISTRATION NUMBER: 33,595  
REFERENCE/DOCKET NUMBER: 32,468  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 708-717-2447  
TELEFAX: 708-717-2430  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-590-804-13

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 4 GTGGG 8

RESULT 27  
US-08-590-804-18  
; Sequence 18, Application US/08590804  
; Patent No. 5780273  
; GENERAL INFORMATION:  
; APPLICANT: Burg, J. Lawrence  
; TITLE OF INVENTION: INSERTION ELEMENTS AND AMPLIFIABLE  
; TITLE OF INVENTION: NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Amoco Corporation  
; STREET: 55 Shuman Blvd., Suite 600  
; CITY: Naperville  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60563  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,804  
FILING DATE: 24-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/357,779  
FILING DATE:  
APPLICATION NUMBER: US 08/045,587  
FILING DATE: 09-APR-1993  
ATTORNEY/AGENT INFORMATION:



NAME: Galloway, No. 5780273val B  
REGISTRATION NUMBER: 33,595  
REFERENCE/DOCKET NUMBER: 32,468  
TELEPHONE: 708-717-2447  
TELEFAX: 708-717-2430  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-590-804-18

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 6 GTGGG 10

RESULT 28  
US-08-540-448-16  
Sequence 16, Application US/08540448  
Patent No. 5786145  
GENERAL INFORMATION:  
APPLICANT: KARN, JONATHAN  
APPLICANT: GAIT, MICHAEL J.  
APPLICANT: HEAPHY, SHAUN  
APPLICANT: DINGWALL, COLIN  
TITLE OF INVENTION: VIRAL GROWTH INHIBITION  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/540,448  
FILING DATE:

CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/030,102  
FILING DATE: 18-MAR-1993  
APPLICATION NUMBER: GB 9020541.0  
FILING DATE: 20-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Obion, No. 5786145man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 3077-007-0 PCT  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: Other nucleic acid;

DESCRIPTION: RNA (synthetic)  
US-08-540-448-16

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.3e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 2 GUGGG 6

RESULT 29  
US-08-729-447-3/c  
Sequence 3, Application US/08729447  
Patent No. 5789174  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: DETECTION OF PERIODONTAL PATHOGENS INCLUDING  
BACTEROIDES FORSYTHUS, PORPHYROMONAS GINGIVALIS,  
PREVOTELLA INTERMEDIA AND PREVOTELLA NIGRESCENS  
NUMBER OF SEQUENCES: 20  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/729,447  
FILING DATE:

CLASSIFICATION: 435  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "AP-PCR primer for P.  
DESCRIPTION: intermedia and P. nigrescens"  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-729-447-3

Query Match 100.0%; Score 5; DB 1; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 10 GTGGG 6

RESULT 30  
US-08-597-467-9  
Sequence 9, Application US/08597467  
Patent No. 5824787  
GENERAL INFORMATION:  
APPLICANT: Singer, Paul A.  
TITLE OF INVENTION: POLYNUCLEOTIDE SIZING REAGENT  
NUMBER OF SEQUENCES: 20  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Spensley Horn Jubas & Lubitz  
STREET: 1880 Century Park East, Suite 500  
CITY: Los Angeles  
STATE: California  
COUNTRY: USA  
ZIP: 90067  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25

```
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/597.467
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/161,901
; FILING DATE: 03-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Wetherell, Jr., Ph.D., John R.
; REGISTRATION NUMBER: 31,678
; REFERENCE/DOCKET NUMBER: PD-3006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; IMMEDIATE SOURCE:
; CLONE: EP
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..10
;
US-08-597-467-9

Query Match 100.0%; Score 5; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 6 GTGGG 10

RESULT 31
US-08-590-571-17
; Sequence 17, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590.571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-590-571-17

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 1 GTGGG 5

RESULT 33
US-08-590-571-29
; Sequence 29, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
```

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;
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-590-571-17

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 4 GTGGG 8

RESULT 32
US-08-590-571-28
; Sequence 28, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590.571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
US-08-590-571-28

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 1 GTGGG 5

RESULT 33
US-08-590-571-29
; Sequence 29, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
```

```
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-29

Query Match          100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      1 GTGGG 5

RESULT 34
US-08-590-571-45
; Sequence 45, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
```

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-45

Query Match          100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      1 GTGGG 5

RESULT 35
US-08-590-571-48
; Sequence 48, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
; STREET: 25 Skytop Drive
; CITY: Trumbull
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06611
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: Macintosh
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/590,571
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: George M. Yahwak
; REGISTRATION NUMBER: 26,824
; REFERENCE/DOCKET NUMBER: Yale
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203)268-1951
; TELEFAX: (203)268-1951
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-590-571-48

Query Match          100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      1 GTGGG 5

RESULT 36
US-08-590-571-49
; Sequence 49, Application US/08590571
; Patent No. 5861246
; GENERAL INFORMATION:
; APPLICANT: Sherman Weissman and Girish N. Nallur
; TITLE OF INVENTION: MULTIPLE SELECTION PROCESS
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Yahwak & Associates
```

STREET: 25 Skytop Drive  
CITY: Trumbull  
STATE: Connecticut  
COUNTRY: USA  
ZIP: 06611  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Macintosh  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 5.1  
CURRENT APPLICATION DATA:  
APPLICANT: US/08/590.571  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: George M. Yahwak  
REGISTRATION NUMBER: 26,824  
REFERENCE/DOCKET NUMBER: Yale  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (203)268-1951  
TELEFAX: (203)268-1951  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-590-571-49

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 1 GTGGG 5

RESULT 37  
US-08-276-567A-6/c  
Sequence 6, Application US/08276567A  
Patent No. 5866699  
GENERAL INFORMATION:  
APPLICANT: Adrienne Smyth  
TITLE OF INVENTION: Oligonucleotides Having Anti-MDR-1 Gene Activity  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lappin & Kusner  
STREET: 200 State Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICANT NUMBER: US/08/276.567A  
FILING DATE:  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Kerner, Ann-Louise  
REGISTRATION NUMBER: 33,523  
REFERENCE/DOCKET NUMBER: HVZ-022  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-330-1300  
TELEFAX: 617-330-1311  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: YES  
US-08-276-567A-6

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 10 GTGGG 6

RESULT 38  
US-08-668-123-27/c  
Sequence 27, Application US/08668123  
Patent No. 5891631  
GENERAL INFORMATION:  
APPLICANT: Brown, Michael S.  
APPLICANT: Briggs, Michael R.  
APPLICANT: Wang, Xiaodong  
APPLICANT: Goldstein, Joseph L.  
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
TITLE OF INVENTION: TO STEROL REGULATORY ELEMENT BINDING  
TITLE OF INVENTION: PROTEINS  
NUMBER OF SEQUENCES: 64  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICANT NUMBER: US/08/668.123  
FILING DATE: 14-JUN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/131,365  
FILING DATE: 01-OCT-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "DNA"  
US-08-668-123-27

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 10 GTGGG 6

RESULT 39  
US-08-668-123-43  
; Sequence 43, Application US/08668123  
; Patent No. 5891631  
; GENERAL INFORMATION:  
; APPLICANT: Brown, Michael S.  
; APPLICANT: Briggs, Michael R.  
; APPLICANT: Wang, Xiaodong  
; APPLICANT: Goldstein, Joseph L.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING  
; TO STEROL REGULATORY ELEMENT BINDING  
; TITLE OF INVENTION: PROTEINS  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: U.S.A.  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/668,123  
; FILING DATE: 14-JUN-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/131,365  
; FILING DATE: 01-OCT-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTSD:372/PAR  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 43:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "DNA"  
US-08-668-123-43

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
Db 3 GTGGG 7

RESULT 40  
US-08-403-888A-108  
; Sequence 108, Application US/08403888A  
; Patent No. 5952490  
; GENERAL INFORMATION:  
; APPLICANT: Hanecak et al.  
; TITLE OF INVENTION: Oligonucleotides Having A Conserved G4 Core  
; TITLE OF INVENTION: Sequence  
; NUMBER OF SEQUENCES: 146  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5952490ris LLP  
; STREET: One Liberty Place - 46th Floor  
; CITY: Philadelphia

STATE: PA  
COUNTRY: U.S.A.  
ZIP: 19103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch disk, 1.44 Mb  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,888A  
FILING DATE: 12-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/954,185  
FILING DATE: 29-SEP-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul K. Legaard  
REGISTRATION NUMBER: 38,534  
REFERENCE/DOCKET NUMBER: ISIS-1229  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-568-3100  
TELEFAX: 215-568-3439  
INFORMATION FOR SEQ ID NO: 108:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-403-888A-108

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
Db 3 GTGGG 7

RESULT 41  
US-08-481-658B-19/c  
; Sequence 19, Application US/08481658B  
; Patent No. 5955075  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 6 Mariposa Court  
; CITY: Tiburon  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94920  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/481,658B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/260,190  
FILING DATE: 15-JUN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Lauder, Leona L.  
REGISTRATION NUMBER: 30,863  
REFERENCE/DOCKET NUMBER: D-0021.3E  
TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
US-08-481-658B-19

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 42
US-08-477-504A-19/c
; Sequence 19, Application US/08477504A
; Patent No. 5972353
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,504A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
US-08-477-504A-19

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 43
US-08-486-756A-19/c
; Sequence 19, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
US-08-486-756A-19

Query Match 100.0%; Score 5; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 44
US-08-485-862B-19/c
; Sequence 19, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
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;; COUNTRY: USA  
;; ZIP: 94920  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/485,862B  
;; FILING DATE: 07-JUN-1995  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/477,504  
;; FILING DATE: 07-JUN-1995  
;; APPLICATION NUMBER: US 08/260,190  
;; FILING DATE: 15-JUN-1994  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Lauder, Leona L.  
;; REGISTRATION NUMBER: 30,863  
;; REFERENCE/DOCKET NUMBER: D-0021.3D  
;; TELEPHONE: 415-435-2034  
;; TELEFAX: 415-435-0727  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; DESCRIPTION: AP-2 transcription factor  
US-08-485-862B-19

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
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Db 8 GTGGG 4

RESULT 45  
US-08-265-484B-15  
; Sequence 15, Application US/08265484B  
; Patent No. 5998193  
; GENERAL INFORMATION:  
; APPLICANT: Keese, Paul  
; APPLICANT: Stapper, Marianne  
; APPLICANT: Perriman, Rhonda  
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing  
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded  
; TITLE OF INVENTION: Ribozymes and Compositions Thereof  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper & Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/265,484B  
; FILING DATE: 24-JUN-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678

;; REFERENCE/DOCKET NUMBER: 45284  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 278-0400  
;; TELEFAX: (212) 391-0525  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 10 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: Other Nucleic Acid  
US-08-265-484B-15

Query Match 100.0%; Score 5; DB 2; Length 10;  
Best Local Similarity 80.0%; Pred. No. 2.3e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
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Db 5 GUGGG 9

RESULT 46  
US-08-388-353-84  
; Sequence 84, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 84:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-84

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
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Db 5 GUGGG 9

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Db          6 GTGGG 10

RESULT 47
US-08-388-353-85
; Sequence 85, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learnmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-86

Query Match          100.0%; Score 5; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GTGGG 5
Db          4 GTGGG 8

RESULT 49
US-08-388-353-87
; Sequence 87, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learnmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 86:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-85

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Best Local Similarity 100.0%; Pred. No. 2.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          1 GTGGG 5
Db          5 GTGGG 9

RESULT 48
US-08-388-353-86
; Sequence 86, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learnmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
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Search completed: January 7, 2005, 11:05:41  
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TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 87:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-87

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
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Db 3 GTGGG 7

RESULT 50  
US-08-388-353-88  
; Sequence 88, Application US/08388353  
; Patent No. 6010895  
; GENERAL INFORMATION:  
; APPLICANT: Deacon, Nicholas J.  
; APPLICANT: Learmont, Jennifer C.  
; APPLICANT: McPhee, Dale A.  
; APPLICANT: Crowe, Suzanne  
; APPLICANT: Cooper, David  
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1  
; NUMBER OF SEQUENCES: 800  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Scully, Scott, Murphy & Presser  
; STREET: 400 Garden City Plaza  
; CITY: Garden City  
; STATE: New York  
; COUNTRY: United States  
; ZIP: 11530  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/388,353  
; FILING DATE: 14-FEB-1995  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Digiglio, Frank S.  
; REGISTRATION NUMBER: 31,346  
; REFERENCE/DOCKET NUMBER: 9606  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (516) 742-4343  
; TELEFAX: (516) 742-4366  
; TELEX: 230 901 SANS UR  
; INFORMATION FOR SEQ ID NO: 88:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-388-353-88

Query Match 100.0%; Score 5; DB 3; Length 10;  
Best Local Similarity 100.0%; Pred.No. 2.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGGG 5  
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Db 2 GTGGG 6

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: GTGGG

Perfect score: 5

Sequence: 1 gt999 5

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

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Minimum DB seq length: 10

Maximum DB seq length: 50

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Listing first 500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	5	100.0	10	9	US-09-989-789-630
6	5	100.0	10	9	US-09-989-789-1273
7	5	100.0	10	9	US-09-989-789-1645
8	5	100.0	10	9	US-09-989-789-1646
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c 87	5	100.0	10	13	US-10-033-145-1668	Sequence 1668, App	c 160	5	100.0	10	15	US-10-330-627-1015	Sequence 1015, App
c 88	5	100.0	10	13	US-10-033-145-1710	Sequence 1710, App	c 161	5	100.0	10	15	US-10-330-627-1058	Sequence 1058, App
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c 90	5	100.0	10	13	US-10-033-145-1728	Sequence 1728, App	c 163	5	100.0	10	15	US-10-330-627-1101	Sequence 1101, App
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c 115	5	100.0	10	15	US-10-215-647-4	Sequence 4, Appl	c 188	5	100.0	10	15	US-10-401-194-95	Sequence 95, Appl
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C 297	5	100.0	11	17	US-10-450-797-692	Sequence 692, App	c 370	5	100.0	12	18	US-10-257-017B-267100	Sequence 267100, App
C 298	5	100.0	11	17	US-10-450-797-712	Sequence 712, App	c 371	5	100.0	12	18	US-10-257-017B-267276	Sequence 267276, App
C 299	5	100.0	11	17	US-10-450-797-791	Sequence 791, App	c 372	5	100.0	12	18	US-10-257-017B-267283	Sequence 267283, App
C 300	5	100.0	11	17	US-10-450-797-845	Sequence 845, App	c 373	5	100.0	12	18	US-10-257-017B-267343	Sequence 267343, App
C 301	5	100.0	11	17	US-10-450-797-893	Sequence 893, App	c 374	5	100.0	12	18	US-10-257-017B-267455	Sequence 267455, App
C 302	5	100.0	11	17	US-10-450-797-910	Sequence 910, App	c 375	5	100.0	12	18	US-10-257-017B-267715	Sequence 267715, App
C 303	5	100.0	11	17	US-10-450-797-919	Sequence 919, App	c 376	5	100.0	12	18	US-10-257-017B-267747	Sequence 267747, App
C 304	5	100.0	11	17	US-10-450-797-953	Sequence 953, App	c 377	5	100.0	12	18	US-10-257-017B-267756	Sequence 267756, App

378	5	100.0	12	18	US-10-257-017B-267780	Sequence 267780,
379	5	100.0	12	18	US-10-257-017B-268055	Sequence 268055,
380	5	100.0	12	18	US-10-257-017B-268254	Sequence 268254,
381	5	100.0	12	18	US-10-257-017B-268822	Sequence 268822,
382	5	100.0	12	18	US-10-257-017B-268829	Sequence 268829,
383	5	100.0	12	18	US-10-257-017B-268830	Sequence 268830,
384	5	100.0	12	18	US-10-257-017B-268862	Sequence 268862,
385	5	100.0	12	18	US-10-257-017B-268908	Sequence 268908,
386	5	100.0	12	18	US-10-257-017B-268987	Sequence 268987,
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389	5	100.0	12	18	US-10-257-017B-269204	Sequence 269204,
390	5	100.0	12	18	US-10-257-017B-269205	Sequence 269205,
391	5	100.0	12	18	US-10-257-017B-269315	Sequence 269315,
392	5	100.0	12	18	US-10-257-017B-269319	Sequence 269319,
393	5	100.0	12	18	US-10-257-017B-269332	Sequence 269332,
394	5	100.0	12	18	US-10-257-017B-269526	Sequence 269526,
395	5	100.0	12	18	US-10-257-017B-269587	Sequence 269587,
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397	5	100.0	12	18	US-10-257-017B-269660	Sequence 269660,
398	5	100.0	12	18	US-10-257-017B-269910	Sequence 269910,
399	5	100.0	12	18	US-10-257-017B-269911	Sequence 269911,
400	5	100.0	12	18	US-10-257-017B-270006	Sequence 270006,
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402	5	100.0	12	18	US-10-257-017B-270111	Sequence 270111,
403	5	100.0	12	18	US-10-257-017B-270119	Sequence 270119,
404	5	100.0	12	18	US-10-257-017B-270134	Sequence 270134,
405	5	100.0	12	18	US-10-257-017B-270224	Sequence 270224,
406	5	100.0	12	18	US-10-257-017B-270510	Sequence 270510,
407	5	100.0	12	18	US-10-257-017B-270552	Sequence 270552,
408	5	100.0	12	18	US-10-257-017B-270552	Sequence 270552,
409	5	100.0	12	18	US-10-257-017B-270652	Sequence 270652,
410	5	100.0	12	18	US-10-257-017B-270653	Sequence 270653,
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413	5	100.0	12	18	US-10-257-017B-270987	Sequence 270987,
414	5	100.0	12	18	US-10-257-017B-271011	Sequence 271011,
415	5	100.0	12	18	US-10-257-017B-271084	Sequence 271084,
416	5	100.0	12	18	US-10-257-017B-271110	Sequence 271110,
417	5	100.0	12	18	US-10-257-017B-271113	Sequence 271113,
418	5	100.0	12	18	US-10-257-017B-271244	Sequence 271244,
419	5	100.0	12	18	US-10-257-017B-271245	Sequence 271245,
420	5	100.0	12	18	US-10-257-017B-271402	Sequence 271402,
421	5	100.0	12	18	US-10-257-017B-271403	Sequence 271403,
422	5	100.0	12	18	US-10-257-017B-271436	Sequence 271436,
423	5	100.0	12	18	US-10-257-017B-271437	Sequence 271437,
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425	5	100.0	12	18	US-10-257-017B-271515	Sequence 271515,
426	5	100.0	12	18	US-10-257-017B-271572	Sequence 271572,
427	5	100.0	12	18	US-10-257-017B-271595	Sequence 271595,
428	5	100.0	12	18	US-10-257-017B-271596	Sequence 271596,
429	5	100.0	12	18	US-10-257-017B-271829	Sequence 271829,
430	5	100.0	12	18	US-10-257-017B-271863	Sequence 271863,
431	5	100.0	12	18	US-10-257-017B-271960	Sequence 271960,
432	5	100.0	12	18	US-10-257-017B-271967	Sequence 271967,
433	5	100.0	12	18	US-10-257-017B-271978	Sequence 271978,
434	5	100.0	12	18	US-10-257-017B-272083	Sequence 272083,
435	5	100.0	12	18	US-10-257-017B-272084	Sequence 272084,
436	5	100.0	12	18	US-10-257-017B-272090	Sequence 272090,
437	5	100.0	12	18	US-10-257-017B-272097	Sequence 272097,
438	5	100.0	12	18	US-10-257-017B-272218	Sequence 272218,
439	5	100.0	12	18	US-10-257-017B-272436	Sequence 272436,
440	5	100.0	12	18	US-10-257-017B-272442	Sequence 272442,
441	5	100.0	12	18	US-10-257-017B-272443	Sequence 272443,
442	5	100.0	12	18	US-10-257-017B-272454	Sequence 272454,
443	5	100.0	12	18	US-10-257-017B-272455	Sequence 272455,
444	5	100.0	12	18	US-10-257-017B-272456	Sequence 272456,
445	5	100.0	12	18	US-10-257-017B-272500	Sequence 272500,
446	5	100.0	12	18	US-10-257-017B-272534	Sequence 272534,
447	5	100.0	12	18	US-10-257-017B-272714	Sequence 272714,
448	5	100.0	12	18	US-10-257-017B-272851	Sequence 272851,
449	5	100.0	12	18	US-10-257-017B-272988	Sequence 272988,
450	5	100.0	12	18	US-10-257-017B-273422	Sequence 273422,
451	5	100.0	12	18	US-10-257-017B-273512	Sequence 273512,
452	5	100.0	12	18	US-10-257-017B-273513	Sequence 273513,
453	5	100.0	12	18	US-10-257-017B-273514	Sequence 273514,
454	5	100.0	12	18	US-10-257-017B-273515	Sequence 273515,
455	5	100.0	12	18	US-10-257-017B-273561	Sequence 273561,
456	5	100.0	12	18	US-10-257-017B-273642	Sequence 273642,
457	5	100.0	12	18	US-10-257-017B-273666	Sequence 273666,
458	5	100.0	12	18	US-10-257-017B-273679	Sequence 273679,
459	5	100.0	12	18	US-10-257-017B-273796	Sequence 273796,
460	5	100.0	12	18	US-10-257-017B-273935	Sequence 273935,
461	5	100.0	12	18	US-10-257-017B-274147	Sequence 274147,
462	5	100.0	12	18	US-10-257-017B-274414	Sequence 274414,
463	5	100.0	12	18	US-10-257-017B-274651	Sequence 274651,
464	5	100.0	12	18	US-10-257-017B-274652	Sequence 274652,
465	5	100.0	12	18	US-10-257-017B-274735	Sequence 274735,
466	5	100.0	12	18	US-10-257-017B-274818	Sequence 274818,
467	5	100.0	12	18	US-10-257-017B-274853	Sequence 274853,
468	5	100.0	12	18	US-10-257-017B-274854	Sequence 274854,
469	5	100.0	12	18	US-10-257-017B-275025	Sequence 275025,
470	5	100.0	12	18	US-10-257-017B-275026	Sequence 275026,
471	5	100.0	12	18	US-10-257-017B-275042	Sequence 275042,
472	5	100.0	12	18	US-10-257-017B-275043	Sequence 275043,
473	5	100.0	12	18	US-10-257-017B-275044	Sequence 275044,
474	5	100.0	12	18	US-10-257-017B-275045	Sequence 275045,
475	5	100.0	12	18	US-10-257-017B-275103	Sequence 275103,
476	5	100.0	12	18	US-10-257-017B-275104	Sequence 275104,
477	5	100.0	12	18	US-10-257-017B-275178	Sequence 275178,
478	5	100.0	12	18	US-10-257-017B-275354	Sequence 275354,
479	5	100.0	12	18	US-10-257-017B-275356	Sequence 275356,
480	5	100.0	12	18	US-10-257-017B-275359	Sequence 275359,
481	5	100.0	12	18	US-10-257-017B-275540	Sequence 275540,
482	5	100.0	12	18	US-10-257-017B-275598	Sequence 275598,
483	5	100.0	12	18	US-10-257-017B-275741	Sequence 275741,
484	5	100.0	12	18	US-10-257-017B-275792	Sequence 275792,
485	5	100.0	12	18	US-10-257-017B-275811	Sequence 275811,
486	5	100.0	12	18	US-10-257-017B-275812	Sequence 275812,
487	5	100.0	12	18	US-10-257-017B-275868	Sequence 275868,
488	5	100.0	12	18	US-10-257-017B-275870	Sequence 275870,
489	5	100.0	12	18	US-10-257-017B-275925	Sequence 275925,
490	5	100.0	12	18	US-10-257-017B-275961	Sequence 275961,
491	5	100.0	12	18	US-10-257-017B-275962	Sequence 275962,
492	5	100.0	12	18	US-10-257-017B-275995	Sequence 275995,
493	5	100.0	12	18	US-10-257-017B-275996	Sequence 275996,
494	5	100.0	12	18	US-10-257-017B-276174	Sequence 276174,
495	5	100.0	12	18	US-10-257-017B-276195	Sequence 276195,
496	5	100.0	12	18	US-10-257-017B-276202	Sequence 276202,
497	5	100.0	12	18	US-10-257-017B-276295	Sequence 276295,
498	5	100.0	12	18	US-10-257-017B-276383	Sequence 276383,
499	5	100.0	12	18	US-10-257-017B-276424	Sequence 276424,
500	5	100.0	12	18	US-10-257-017B-306238	Sequence 306238,

## ALIGNMENTS

## RESULT 1

US-09-154-750A-9/c  
; Sequence 9, Application US/09154750A  
; Publication No. US20020055097A1  
; GENERAL INFORMATION:  
; APPLICANT: Vogelstein, Bert  
; APPLICANT: Kinzler, Kenneth  
; APPLICANT: Polyak, Kornelia  
; TITLE OF INVENTION: p53-Induced Apoptosis  
; FILE REFERENCE: 1107.75357  
; CURRENT APPLICATION NUMBER: US/09/154,750A  
; CURRENT FILING DATE: 1998-09-17  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/059,153  
; PRIOR FILING DATE: 1997-09-17  
; PRIOR APPLICATION NUMBER: 60/079817  
; PRIOR FILING DATE: 1998-03-30  
; NUMBER OF SEQ ID NOS: 93  
; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 9  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-154-750A-9

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
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Db 8 GTGGG 4

## RESULT 2

US-09-989-789-562  
; Sequence 562, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 562  
; LENGTH: 10

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA

## US-09-989-789-562

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 1 GTGGG 5

## RESULT 3

US-09-989-789-624  
; Sequence 624, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 624  
; LENGTH: 10

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA

## US-09-989-789-624

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5

Db  
|||||  
4 GTGGG 8

## RESULT 4

US-09-989-789-625  
; Sequence 625, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 625  
; LENGTH: 10

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA

## US-09-989-789-625

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 4 GTGGG 8

## RESULT 5

US-09-989-789-630  
; Sequence 630, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,789  
; CURRENT FILING DATE: 2002-03-25  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 630  
; LENGTH: 10

; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA

## US-09-989-789-630

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||||  
Db 4 GTGGG 8

## RESULT 6

US-09-989-789-1273  
; Sequence 1273, Application US/09989789  
; Patent No. US20020063379A1  
; GENERAL INFORMATION:

; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE

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; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1273

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 4 GTGGG 8

RESULT 7
US-09-989-789-1645
; Sequence 1645, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1645

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 4 GTGGG 8

RESULT 8
US-09-989-789-1646
; Sequence 1646, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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RESULT 11
US-09-989-789-1670
; Sequence 1670, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1670
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1670

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Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTGGG 5
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Db 5 GTGGG 9

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RESULT 12
US-09-989-789-1673
; Sequence 1673, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1673
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1673

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```

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTGGG 5
   |||||
Db 4 GTGGG 8

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RESULT 13
US-09-989-789-1687
; Sequence 1687, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2

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; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1687
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1687

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Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GTGGG 5
   |||||
Db 4 GTGGG 8

```

```

RESULT 14
US-09-989-789-1705
; Sequence 1705, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1705
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-789-1705

```

```

Query Match      100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GTGGG 5
   |||||
Db 3 GTGGG 7

```

```

RESULT 15
US-09-989-789-1706
; Sequence 1706, Application US/09989789
; Patent No. US20020063379A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,789
; CURRENT FILING DATE: 2002-03-25
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1706
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA

```

US-09-989-789-1706

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GTGGG 5  
| | | | |  
Db 3 GTGGG 7

## RESULT 16

US-09-761-116-2  
; Sequence 2, Application US/09761116  
; Patent No. US20020102552A1  
; GENERAL INFORMATION:  
; APPLICANT: American Home Products Corp.  
; APPLICANT: Sueilic, Vedrana S.  
; APPLICANT: Duzic, Edmir  
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATION OF THE HUMAN  
; FILE REFERENCE: 0630/0E791  
; CURRENT APPLICATION NUMBER: US/09/761,116  
; CURRENT FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: 09/243,335  
; PRIOR FILING DATE: 1999-02-01  
; NUMBER OF SEQ ID NOS: 49  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-09-761-116-2

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GTGGG 5  
| | | | |  
Db 3 GTGGG 7

## RESULT 17

US-09-942-325A-5/c  
; Sequence 5, Application US/09942325A  
; Patent No. US20020106794A1  
; GENERAL INFORMATION:  
; APPLICANT: Iacovitti, Lorraine  
; APPLICANT: Kessler, Mark  
; TITLE OF INVENTION: The Human Tyrosine Hydroxylase Promoter  
; FILE REFERENCE: IAC01.NP001  
; CURRENT APPLICATION NUMBER: US/09/942,325A  
; CURRENT FILING DATE: 2001-08-29  
; PRIOR APPLICATION NUMBER: 60/228931  
; PRIOR FILING DATE: 2000-02-30  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-942-325A-5

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GTGGG 5  
| | | | |

Db 8 GTGGG 4

## RESULT 18

US-09-816-763-110/c  
; Sequence 110, Application US/09816763  
; Patent No. US20020110814A1  
; GENERAL INFORMATION:  
; APPLICANT: Remacle, Jose  
; APPLICANT: Renard, Patricia  
; APPLICANT: Arc, Muriel  
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE  
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL  
; TITLE OF INVENTION: FACTORS  
; FILE REFERENCE: VANM212.001AUS  
; CURRENT APPLICATION NUMBER: US/09/816,763  
; CURRENT FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: EP 00870057.7  
; PRIOR FILING DATE: 2000-03-24  
; NUMBER OF SEQ ID NOS: 150  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 110  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Consensus sequence for transcriptional factor  
; OTHER INFORMATION: SREBP1  
; NAME/KEY: misc\_binding  
; LOCATION: (0)...(0)  
; OTHER INFORMATION: non E-Box consensus binding sequence  
US-09-816-763-110

Query Match 100.0%; Score 5; DB 9; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06; Indels 0;  
Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 GTGGG 5  
| | | | |  
Db 10 GTGGG 6

## RESULT 19

US-09-772-719-19/c  
; Sequence 19, Application US/09772719  
; Patent No. US20020137910A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: AP-2 transcription factor
US-09-772-719-19

Query Match 100.0%; Score 5; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 8 GTGGG 4

RESULT 20
US-09-846-033B-140
; Sequence 140, Application US/09846033B
; Publication No. US2003004404A1
; GENERAL INFORMATION:
; APPLICANT: Rebar, Edward
; APPLICANT: Jamieson, Andrew
; APPLICANT: Liu, Qiang
; APPLICANT: Liu, Pei-Qi
; APPLICANT: Wolffe, Alan
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Jarvis, Eric
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
; FILE REFERENCE: 019496-005820US
; CURRENT APPLICATION NUMBER: US/09/846,033B
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 09/733,604
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 09/736,083
; PRIOR FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 252
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 140
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: target
US-09-846-033B-140

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 3 GTGGG 7

RESULT 21
US-09-990-186-562
; Sequence 562, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
```

```
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 562
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-562

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 1 GTGGG 5

RESULT 22
US-09-990-186-624
; Sequence 624, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 624
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-624

Query Match 100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5
Db 4 GTGGG 8

RESULT 23
US-09-990-186-625
; Sequence 625, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

```
;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-625

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 24
US-09-990-186-630
; Sequence 630, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-630

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 25
US-09-990-186-1273
; Sequence 1273, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1273

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 26
US-09-990-186-1645
; Sequence 1645, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1645

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 27
US-09-990-186-1646
; Sequence 1646, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1646

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 28
US-09-990-186-1668
; Sequence 1668, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
```

```
Db      4 GTGGG 8

RESULT 26
US-09-990-186-1645
; Sequence 1645, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1645

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 27
US-09-990-186-1646
; Sequence 1646, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1646

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
      |||||
Db      4 GTGGG 8

RESULT 28
US-09-990-186-1668
; Sequence 1668, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
```

; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1668  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-990-186-1668

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 1 GTGGG 5

## RESULT 29

US-09-990-186-1669  
; Sequence 1669, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.21 / S11-US3  
; CURRENT APPLICATION NUMBER: US/09/990,186

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1669

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA

## US-09-990-186-1669

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 5 GTGGG 9

## RESULT 30

US-09-990-186-1670  
; Sequence 1670, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.21 / S11-US3

; CURRENT APPLICATION NUMBER: US/09/990,186

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1670

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target

; OTHER INFORMATION: DNA  
US-09-990-186-1670

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 5 GTGGG 9

## RESULT 31

US-09-990-186-1673  
; Sequence 1673, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.21 / S11-US3

; CURRENT APPLICATION NUMBER: US/09/990,186

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1673

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA

## US-09-990-186-1673

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 4 GTGGG 8

## RESULT 32

US-09-990-186-1687  
; Sequence 1687, Application US/09990186  
; Publication No. US20030068675A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang

; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

; FILE REFERENCE: 8325-0011.21 / S11-US3

; CURRENT APPLICATION NUMBER: US/09/990,186

; CURRENT FILING DATE: 2001-11-20

; NUMBER OF SEQ ID NOS: 4085

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1687

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA

## US-09-990-186-1687

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
Db 4 GTGGG 8

```
RESULT 33
US-09-990-186-1705
; Sequence 1705, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1705
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-1705

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      3 GTGGG 7

RESULT 34
US-09-990-186-1706
; Sequence 1706, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1706
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-990-186-1706

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      3 GTGGG 7

RESULT 35
US-09-996-484-62
; Sequence 62, Application US/09996484
; Publication No. US20030092010A1
; GENERAL INFORMATION:
; APPLICANT: CHOO, Yen
; APPLICANT: ULLMAN, Christopher G.
; TITLE OF INVENTION: MOLECULAR SWITCHES
; FILE REFERENCE: 8325-2004 / G8-US1
; CURRENT APPLICATION NUMBER: US/09/996,484
```

```
; CURRENT FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 62
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA
; OTHER INFORMATION: recognition site
US-09-996-484-62

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      3 GTGGG 7

RESULT 36
US-09-748-710-14
; Sequence 14, Application US/09748710
; Publication No. US20030104369A1
; GENERAL INFORMATION:
; APPLICANT: WANG, SAN MING
; APPLICANT: CHEN, JIANJUN
; APPLICANT: ROWLEY, JANET D.
; TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER CDNA FRAGMENTS
; TITLE OF INVENTION: FROM SAGE TAGS FOR GENE IDENTIFICATION
; FILE REFERENCE: ARCD.343US
; CURRENT APPLICATION NUMBER: US/09/748,710
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/174,391
; PRIOR FILING DATE: 2000-01-03
; PRIOR APPLICATION NUMBER: 60/173,617
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-748-710-14

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      3 GTGGG 7

RESULT 37
US-09-748-710-27
; Sequence 27, Application US/09748710
; Publication No. US20030104369A1
; GENERAL INFORMATION:
; APPLICANT: WANG, SAN MING
; APPLICANT: CHEN, JIANJUN
; APPLICANT: ROWLEY, JANET D.
; TITLE OF INVENTION: METHOD FOR GENERATION OF LONGER CDNA FRAGMENTS
; TITLE OF INVENTION: FROM SAGE TAGS FOR GENE IDENTIFICATION
; FILE REFERENCE: ARCD.343US
; CURRENT APPLICATION NUMBER: US/09/748,710
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/174,391
; PRIOR FILING DATE: 2000-01-03
```

```

; PRIOR APPLICATION NUMBER: 60/173,617
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-09-748-710-27

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      3 GTGGG 7

RESULT 38
US-09-989-994-562
; Sequence 562, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 562
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-562

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      3 GTGGG 7

RESULT 39
US-09-989-994-624
; Sequence 624, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 624
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-624

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      1 GTGGG 5

RESULT 40
US-09-989-994-625
; Sequence 625, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-625

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      4 GTGGG 8

RESULT 41
US-09-989-994-630
; Sequence 630, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-630

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      4 GTGGG 8
```

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US-09-989-994-624

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      4 GTGGG 8

RESULT 40
US-09-989-994-625
; Sequence 625, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 625
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-625

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      4 GTGGG 8

RESULT 41
US-09-989-994-630
; Sequence 630, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-630

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
Db      4 GTGGG 8
```

```
RESULT 42
US-09-989-994-1273
; Sequence 1273, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1273
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1273

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
        |||||
Db      4 GTGGG 8

RESULT 43
US-09-989-994-1645
; Sequence 1645, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1645
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1645

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
        |||||
Db      4 GTGGG 8

RESULT 44
US-09-989-994-1646
; Sequence 1646, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
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; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1646
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1646

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
        |||||
Db      4 GTGGG 8

RESULT 45
US-09-989-994-1668
; Sequence 1668, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1668
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1668

Query Match      100.0%; Score 5; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GTGGG 5
        |||||
Db      1 GTGGG 5

RESULT 46
US-09-989-994-1669
; Sequence 1669, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1669
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1669
```



Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||  
Db 5 GTGGG 9

## RESULT 47

US-09-989-994-1670  
; Sequence 1670, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1670  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1670

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||  
Db 5 GTGGG 9

## RESULT 48

US-09-989-994-1673  
; Sequence 1673, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1673  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1673

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||  
Db 4 GTGGG 8

## RESULT 49

US-09-989-994-1687

; Sequence 1687, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1687  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1687

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||  
Db 4 GTGGG 8

## RESULT 50

US-09-989-994-1705  
; Sequence 1705, Application US/09989994  
; Publication No. US20030104526A1  
; GENERAL INFORMATION:  
; APPLICANT: LIU, Qiang  
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE  
; FILE REFERENCE: 8325-0011.20 / S11-US2  
; CURRENT APPLICATION NUMBER: US/09/989,994  
; CURRENT FILING DATE: 2001-11-20  
; NUMBER OF SEQ ID NOS: 4085  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1705  
; LENGTH: 10  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: example target  
; OTHER INFORMATION: DNA  
US-09-989-994-1705

Query Match 100.0%; Score 5; DB 10; Length 10;  
Best Local Similarity 100.0%; Pred. No. 2.2e+06;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGGG 5  
|||  
Db 3 GTGGG 7

Search completed: January 7, 2005, 11:31:26  
Job time : 272.2 secs

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